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☐ 1: [Zhou X, Qian X, Zhao Q, Lu Y, Xiong M.](#) [Related Articles, Links](#)

Efficient expression of modified human papillomavirus 16 e6/e7 fusion protein and the antitumor efficacy in a mouse model.  
Biol Pharm Bull. 2004 Mar;27(3):303-7.  
PMID: 14993792 [PubMed - indexed for MEDLINE]

☐ 2: [Daemen T, Pries F, Bungener L, Kraak M, Regts J, Wilschut J.](#) [Related Articles, Links](#)

Genetic immunization against cervical carcinoma: induction of cytotoxic T lymphocyte activity with a recombinant alphavirus vector expressing human papillomavirus type 16 E6 and E7.  
Gene Ther. 2000 Nov;7(21):1859-66.  
PMID: 11110419 [PubMed - indexed for MEDLINE]

☐ 3: [Daemen T, Regts J, Holtrop M, Wilschut J.](#) [Related Articles, Links](#)

Immunization strategy against cervical cancer involving an alphavirus vector expressing high levels of a stable fusion protein of human papillomavirus 16 E6 and E7.  
Gene Ther. 2002 Jan;9(2):85-94.  
PMID: 11857066 [PubMed - indexed for MEDLINE]

☐ 4: [Pokorna D, Mackova J, Duskova M, Rittich S, Ludvikova V, Smahel M.](#) [Related Articles, Links](#)

Combined immunization with fusion genes of mutated E7 gene of human papillomavirus type 16 did not enhance antitumor effect.  
J Gene Med. 2005 Jun;7(6):696-707.  
PMID: 15712328 [PubMed - indexed for MEDLINE]








☐ 5: [Chu NR, Wu HB, Wu T, Boux LJ, Siegel MI, Mizzen LA.](#) [Related Articles, Links](#)

Immunotherapy of a human papillomavirus (HPV) type 16 E7-expressing tumour by administration of fusion protein comprising Mycobacterium bovis bacille Calmette-Guerin (BCG) hsp65 and HPV16 E7.  
Clin Exp Immunol. 2000 Aug;121(2):216-25.  
PMID: 10931134 [PubMed - indexed for MEDLINE]








☐ 6: [Cassetti MC, McElhiney SP, Shahabi V, Pullen JK, Le Poole IC, Eiben GL, Smith LR, Kast WM.](#) [Related Articles, Links](#)

Antitumor efficacy of Venezuelan equine encephalitis virus replicon particles encoding mutated HPV16 E6 and E7 genes.  
Vaccine. 2004 Jan 2;22(3-4):520-7.  
PMID: 14670335 [PubMed - indexed for MEDLINE]

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- ☐ 7: [Smahel M, Sima P, Ludvikova V, Vonka V.](#) [Related Articles, Links](#)  
 Modified HPV16 E7 Genes as DNA Vaccine against E7-Containing Oncogenic Cells.  
Virology. 2001 Mar 15;281(2):231-8.  
PMID: 11277695 [PubMed - indexed for MEDLINE]
- ☐ 8: [Ressing ME, Sette A, Brandt RM, Ruppert J, Wentworth PA, Hartman M, Oseroff C, Grey HM, Melief CJ, Kast WM.](#) [Related Articles, Links](#)  
 Human CTL epitopes encoded by human papillomavirus type 16 E6 and E7 identified through in vivo and in vitro immunogenicity studies of HLA-A\*0201-binding peptides.  
J Immunol. 1995 Jun 1;154(11):5934-43.  
PMID: 7538538 [PubMed - indexed for MEDLINE]
- ☐ 9: [Chu NR, Wu HB, Wu TC, Boux LJ, Mizzen LA, Siegel MI.](#) [Related Articles, Links](#)  
 Immunotherapy of a human papillomavirus type 16 E7-expressing tumor by administration of fusion protein comprised of Mycobacterium bovis BCG Hsp65 and HPV16 E7.  
Cell Stress Chaperones. 2000 Nov;5(5):401-5.  
PMID: 11189443 [PubMed - indexed for MEDLINE]
- ☐ 10: [De Bruijn ML, Schuurhuis DH, Vierboom MP, Vermeulen H, de Cock KA, Ooms ME, Ressing ME, Toebes M, Franken KL, Drijfhout JW, Ottenhoff TH, Offringa R, Melief CJ.](#) [Related Articles, Links](#)  
 Immunization with human papillomavirus type 16 (HPV16) oncoprotein-loaded dendritic cells as well as protein in adjuvant induces MHC class I-restricted protection to HPV16-induced tumor cells.  
Cancer Res. 1998 Feb 15;58(4):724-31.  
PMID: 9485027 [PubMed - indexed for MEDLINE]
- ☐ 11: [Kim TY, Myoung HJ, Kim JH, Moon IS, Kim TG, Ahn WS, Sin JI.](#) [Related Articles, Links](#)  
 Both E7 and CpG-oligodeoxynucleotide are required for protective immunity against challenge with human papillomavirus 16 (E6/E7) immortalized tumor cells: involvement of CD4+ and CD8+ T cells in protection.  
Cancer Res. 2002 Dec 15;62(24):7234-40.  
PMID: 12499264 [PubMed - indexed for MEDLINE]
- ☐ 12: [Daemen T, Riezebos-Brilman A, Regts J, Dontje B, van der Zee A, Wilschut J.](#) [Related Articles, Links](#)  
 Superior therapeutic efficacy of alphavirus-mediated immunization against human papilloma virus type 16 antigens in a murine tumour model: effects of the route of immunization.  
Antivir Ther. 2004 Oct;9(5):733-42.  
PMID: 15535411 [PubMed - indexed for MEDLINE]
- ☐ 13: [Baez-Astua A, Herraez-Hernandez E, Garbi N, Pasolli HA, Juarez V, Zur Hausen H, Cid-Arregui A.](#) [Related Articles, Links](#)  
 Low-dose adenovirus vaccine encoding chimeric hepatitis B virus surface antigen-human papillomavirus type 16 E7 proteins induces enhanced E7-specific antibody and cytotoxic T-cell responses.  
J Virol. 2005 Oct;79(20):12807-17.  
PMID: 16188983 [PubMed - indexed for MEDLINE]

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- ☐ **14:** [Lasaro MO, Diniz MO, Reyes-Sandoval A, Ertl HC, Ferreira LC.](#) Related Articles, Links  
 Anti-tumor DNA vaccines based on the expression of human papillomavirus-16 E6/E7 oncoproteins genetically fused with the glycoprotein D from herpes simplex virus-1.  
 Microbes Infect. 2005 Dec;7(15):1541-50. Epub 2005 Sep 9.  
 PMID: 16213178 [PubMed - indexed for MEDLINE]
- ☐ **15:** [Sun Q, Tang SC, Pater MM, Pater A.](#) Related Articles, Links  
 Different HPV16 E6/E7 oncogene expression patterns in epithelia reconstructed from HPV16-immortalized human endocervical cells and genital keratinocytes.  
 Oncogene. 1997 Nov 13;15(20):2399-408.  
 PMID: 9395236 [PubMed - indexed for MEDLINE]
- ☐ **16:** [Azoury-Ziadeh R, Herd K, Fernando GJ, Frazer IH, Tindle RW.](#) Related Articles, Links  
 T-helper epitopes identified within the E6 transforming protein of cervical cancer-associated human papillomavirus type 16.  
 Viral Immunol. 1999;12(4):297-312.  
 PMID: 10630789 [PubMed - indexed for MEDLINE]
- ☐ **17:** [Indrova M, Reinis M, Bubenik J, Jandlova T, Bieblova J, Vonka V, Velek J.](#) Related Articles, Links  
 Immunogenicity of dendritic cell-based HPV16 E6/E7 peptide vaccines: CTL activation and protective effects.  
 Folia Biol (Praha). 2004;50(6):184-93.  
 PMID: 15709713 [PubMed - indexed for MEDLINE]
- ☐ **18:** [Fernando GJ, Murray B, Zhou J, Frazer IH.](#) Related Articles, Links  
 Expression, purification and immunological characterization of the transforming protein E7, from cervical cancer-associated human papillomavirus type 16.  
 Clin Exp Immunol. 1999 Mar;115(3):397-403.  
 PMID: 10193409 [PubMed - indexed for MEDLINE]
- ☐ **19:** [Peng S, Ji H, Trimble C, He L, Tsai YC, Yeatermeyer J, Boyd DA, Hung CF, Wu TC.](#) Related Articles, Links  
 Development of a DNA vaccine targeting human papillomavirus type 16 oncoprotein E6.  
 J Virol. 2004 Aug;78(16):8468-76.  
 PMID: 15280455 [PubMed - indexed for MEDLINE]
- ☐ **20:** [Kadish AS, Ho GY, Burk RD, Wang Y, Romney SL, Ledwidge R, Angeletti RH.](#) Related Articles, Links  
 Lymphoproliferative responses to human papillomavirus (HPV) type 16 proteins E6 and E7: outcome of HPV infection and associated neoplasia.  
 J Natl Cancer Inst. 1997 Sep 3;89(17):1285-93.  
 PMID: 9293919 [PubMed - indexed for MEDLINE]

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☐ 1. Document ID: CN 1160463 C, CN 1381583 A

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File: DWPI

Aug 4, 2004

DERWENT-ACC-NO: 2003-258260

DERWENT-WEEK: 200612

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TITLE: Human papillomavirus E6/E7 fusion gene and its efficient expression carrier and fusion protein vaccine

INVENTOR: ZHAO, Q

PRIORITY-DATA: 2002CN-0117143 (April 24, 2002)

PATENT-FAMILY:

PUB-NO	PUB-DATE	LANGUAGE	PAGES	MAIN-IPC
<u>CN 1160463 C</u>	August 4, 2004		000	C12N015/62
<u>CN 1381583 A</u>	November 27, 2002		000	C12N015/62

INT-CL (IPC): A61 K 48/00; A61 P 35/00; C07 K 19/00; C12 N 15/62; C12 N 15/63

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☐ 2. Document ID: NZ 505108 A, WO 9933868 A2, AU 9924191 A, ZA 9811848 A, EP 1040123 A2, BR 9814487 A, CZ 200002376 A3, AU 729336 B, HU 200100526 A2, JP 2001527091 W

L4: Entry 2 of 3

File: DWPI

Oct 25, 2002

DERWENT-ACC-NO: 1999-405485

DERWENT-WEEK: 200274

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TITLE: Composition comprising an E6, E7 or E6/E7 fusion protein from HPV to induce immune response to HPV

INVENTOR: DALEMANS, W L J; GERARD, C M G

PRIORITY-DATA: 1997GB-0027262 (December 24, 1997)

PATENT-FAMILY:

PUB-NO	PUB-DATE	LANGUAGE	PAGES	MAIN-IPC
<u>NZ 505108 A</u>	October 25, 2002		000	A61K039/02
<u>WO 9933868 A2</u>	July 8, 1999	E	062	C07K014/00

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<u>AU 9924191 A</u>	July 19, 1999		000	
<u>ZA 9811848 A</u>	July 26, 2000		063	C07K000/00
<u>EP 1040123 A2</u>	October 4, 2000	E	000	C07K014/00
<u>BR 9814487 A</u>	October 10, 2000		000	C07K014/00
<u>CZ 200002376 A3</u>	November 15, 2000		000	C07K014/01
<u>AU 729336 B</u>	February 1, 2001		000	C07K014/00
<u>HU 200100526 A2</u>	June 28, 2001		000	A61K039/12
<u>JP 2001527091 W</u>	December 25, 2001		093	C07K014/025

INT-CL (IPC): A61 K 38/16; A61 K 39/00; A61 K 39/02; A61 K 39/09; A61 K 39/102;  
A61 K 39/12; A61 K 39/385; A61 K 39/39; A61 P 35/00; C07 K 0/00; C07 K 14/00;  
C07 K 14/01; C07 K 14/025; C07 K 14/285; C07 K 14/315; C07 K 19/00; C12 N 15/09

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	KMC	Draw D
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☐ 3. Document ID: DE 69824013 T2, WO 9910375 A2, AU 9892639 A, ZA 9807591 A, NO 200000850 A, EP 1007551 A2, BR 9812139 A, CZ 200000634 A3, CN 1276833 A, HU 200004327 A2, AU 732946 B, MX 2000001813 A1, KR 2001023193 A, JP 2001513986 W, US 6342224 B1, NZ 502632 A, US 20020182221 A1, EP 1007551 B1, DE 69824013 E, ES 2221198 T3

L4: Entry 3 of 3

File: DWPI

Jun 2, 2005

DERWENT-ACC-NO: 1999-190587

DERWENT-WEEK: 200537

COPYRIGHT 2006 DERWENT INFORMATION LTD

TITLE: Human Papilloma Virus (HPV) fusion proteins - useful in vaccines for treatment or prophylaxis of HPV induced lesions

INVENTOR: BRUCK, C; DELISSE, A E F ; GERARD, C M G ; LOMBARDO-BENCHEIKH, A ; SILVA, T C ; CABEZON, S T ; CABEZON SILVA, T ; FERNANDE DELISSE, A E ; GHISLAINE GERARD, C M

PRIORITY-DATA: 1997GB-0017953 (August 22, 1997)

## PATENT-FAMILY:

PUB-NO	PUB-DATE	LANGUAGE	PAGES	MAIN-IPC
<u>DE 69824013 T2</u>	June 2, 2005		000	C07K014/025
<u>WO 9910375 A2</u>	March 4, 1999	E	095	C07K014/00
<u>AU 9892639 A</u>	March 16, 1999		000	C07K014/00
<u>ZA 9807591 A</u>	April 26, 2000		096	C07K000/00
<u>NO 200000850 A</u>	April 14, 2000		000	C07K019/00
<u>EP 1007551 A2</u>	June 14, 2000	E	000	C07K014/00
<u>BR 9812139 A</u>	July 18, 2000		000	C07K014/00
<u>CZ 200000634 A3</u>	January 17, 2001		000	C07K014/00
<u>CN 1276833 A</u>	December 13, 2000		000	C12N015/62
<u>HU 200004327 A2</u>	March 28, 2001		000	C07K014/00
<u>AU 732946 B</u>	May 3, 2001		000	C07K014/00
<u>MX 2000001813 A1</u>	October 1, 2000		000	C07K014/00
<u>KR 2001023193 A</u>	March 26, 2001		000	C12N015/62

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<u>JP 2001513986 W</u>	September 11, 2001	131	C12N015/09
<u>US 6342224 B1</u>	January 29, 2002	000	A61K039/00
<u>NZ 502632 A</u>	March 28, 2002	000	C07K014/285
<u>US 20020182221 A1</u>	December 5, 2002	000	A61K039/12
<u>EP 1007551 B1</u>	May 19, 2004	E 000	C07K014/025
<u>DE 69824013 E</u>	June 24, 2004	000	C07K014/025
<u>ES 2221198 T3</u>	December 16, 2004	000	C07K014/025

NZ 502632 A , US 20020182221 A1 INT-CL (IPC): A61 K 9/107; A61 K 38/02;  
A61 K 39/00; A61 K 39/12; A61 K 39/145; A61 K 39/39; A61 P 35/00; A61 P 37/00;  
C07 H 14/00; C07 H 21/04; C07 K 0/00; C07 K 1/00; C07 K 14/00; C07 K 14/025;  
C07 K 14/08; C07 K 14/11; C07 K 14/285; C07 K 16/08; C07 K 17/00; C07 K 19/00;  
C12 N 1/15; C12 N 1/19; C12 N 1/20; C12 N 1/21; C12 N 5/00; C12 N 5/02; C12 N 5/10;  
C12 N 15/00; C12 N 15/09; C12 N 15/62; C12 N 15/63; C12 N 15/70; C12 N 15/74;  
C12 P 21/02; C12 P 21/04

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L10: Entry 1 of 6

File: USPT

May 6, 2003

US-PAT-NO: 6558670

DOCUMENT-IDENTIFIER: US 6558670 B1

TITLE: Vaccine adjuvants

DATE-ISSUED: May 6, 2003

#### INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Friede; Martin	Court St Etienne			BE
Hermand; Philippe	Court St Etienne			BE

US-CL-CURRENT: [424/184.1](#); [424/278.1](#), [424/283.1](#), [514/25](#)

Full	Title	Citation	Front	Review	Classification	Date	Reference	Figures	Abstracts	Claims	KMC	Drawings
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☐ 2. Document ID: US 6544518 B1

L10: Entry 2 of 6

File: USPT

Apr 8, 2003

US-PAT-NO: 6544518

DOCUMENT-IDENTIFIER: US 6544518 B1

TITLE: Vaccines

DATE-ISSUED: April 8, 2003

#### INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Friede; Martin	Farnham			GB
Garcon; Nathalie	Wavre			BE
Gerard; Catherine Marie Ghislaine	Rhode Saint Genese			BE
Hermand; Philippe	Court-Saint-Etienne			BE

US-CL-CURRENT: [424/184.1](#); [424/208.1](#), [424/228.1](#), [424/229.1](#), [424/231.1](#), [424/249.1](#), [424/278.1](#), [424/283.1](#), [514/25](#)

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☐ 3. Document ID: US 6342224 B1

L10: Entry 3 of 6

File: USPT

Jan 29, 2002

US-PAT-NO: 6342224

DOCUMENT-IDENTIFIER: US 6342224 B1

TITLE: Recombinant papillomavirus vaccine and method for production and treatment

DATE-ISSUED: January 29, 2002

## INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Bruck; Claudine	Rixensart			BE
Silva; Teresa Cabezon	Lenkebeek			BE
Fernande Delisse; Anne-Marie Eva	Gosselies			BE
Ghislaine Gerard; Catherine Marie	Rhode Saint Genese			BE
Lombardo-Bencheikh; Angela	Wavre			BE

US-CL-CURRENT: 424/192.1; 424/185.1, 424/186.1, 424/204.1, 435/252.3, 435/320.1,  
435/325, 435/69.3, 435/69.7, 530/350, 536/23.4, 536/23.72

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	KWIC	Draw. D.
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☐ 4. Document ID: US 6306397 B1

L10: Entry 4 of 6

File: USPT

Oct 23, 2001

US-PAT-NO: 6306397

DOCUMENT-IDENTIFIER: US 6306397 B1

TITLE: Variants of human papilloma virus antigens

DATE-ISSUED: October 23, 2001

## INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Edwards; Stirling John	Northcote			AU
Cox; John Cooper	Bullengarook			AU
Webb; Elizabeth Ann	Eltham			AU
Frazer; Ian	St. Lucia			AU

US-CL-CURRENT: 424/192.1; 424/186.1, 424/204.1, 435/235.1, 435/69.1, 435/69.7,  
536/23.1, 536/23.72, 536/24.3

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	KWIC	Draw. D.
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☐ 5. Document ID: US 6303128 B1

L10: Entry 5 of 6

File: USPT

Oct 16, 2001

US-PAT-NO: 6303128

DOCUMENT-IDENTIFIER: US 6303128 B1

TITLE: Method for protein expression

DATE-ISSUED: October 16, 2001

## INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Webb; Elizabeth Ann	Eltham			AU
Edwards; Stirling John	Northcote			AU

US-CL-CURRENT: [424/199.1](#); [424/192.1](#), [435/235.1](#), [435/320.1](#), [435/325](#), [435/69.1](#),  
[435/69.7](#)

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	KMC	Draw D
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☐ 6. Document ID: US 6004557 A

L10: Entry 6 of 6

File: USPT

Dec 21, 1999

US-PAT-NO: 6004557

DOCUMENT-IDENTIFIER: US 6004557 A

TITLE: Variants of human papillomavirus antigens

DATE-ISSUED: December 21, 1999

## INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Edwards; Stirling John	Caburg			AU
Cox; John Cooper	Bullengarook			AU
Webb; Elizabeth Ann	Eltham			AU
Frazer; Ian	St. Lucia.			AU

US-CL-CURRENT: [424/192.1](#); [424/186.1](#), [424/199.1](#), [424/204.1](#), [435/235.1](#), [435/320.1](#),  
[435/69.1](#), [435/69.7](#), [536/23.1](#), [536/23.72](#) , [536/24.3](#)

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☐ 1: [Cassetti MC, McElhiney SP, Shahabi V, Pullen JK, Le Poole IC, Eiben GL, Smith LR, Kast WM.](#) Related Articles, Links

Antitumor efficacy of Venezuelan equine encephalitis virus replicon particles encoding mutated HPV16 E6 and E7 genes. Vaccine. 2004 Jan 2;22(3-4):520-7. PMID: 14670335 [PubMed - indexed for MEDLINE]

☐ 2: [Velders MP, McElhiney S, Cassetti MC, Eiben GL, Higgins T, Kovacs GR, Elmishad AG, Kast WM, Smith LR.](#) Related Articles, Links

Eradication of established tumors by vaccination with Venezuelan equine encephalitis virus replicon particles delivering human papillomavirus 16 E7 RNA. Cancer Res. 2001 Nov 1;61(21):7861-7. PMID: 11691804 [PubMed - indexed for MEDLINE]

☐ 3: [Eiben GL, Velders MP, Schreiber H, Cassetti MC, Pullen JK, Smith LR, Kast WM.](#) Related Articles, Links

Establishment of an HLA-A\*0201 human papillomavirus type 16 tumor model to determine the efficacy of vaccination strategies in HLA-A\*0201 transgenic mice. Cancer Res. 2002 Oct 15;62(20):5792-9. PMID: 12384540 [PubMed - indexed for MEDLINE]

☐ 4: [Zhou X, Qian X, Zhao Q, Lu Y, Xiong M.](#) Related Articles, Links

Efficient expression of modified human papillomavirus 16 e6/e7 fusion protein and the antitumor efficacy in a mouse model. Biol Pharm Bull. 2004 Mar;27(3):303-7. PMID: 14993792 [PubMed - indexed for MEDLINE]

☐ 5: [Peng S, Ji H, Trimble C, He L, Tsai YC, Yeatermeyer J, Boyd DA, Hung CF, Wu TC.](#) Related Articles, Links

Development of a DNA vaccine targeting human papillomavirus type 16 oncoprotein E6. J Virol. 2004 Aug;78(16):8468-76. PMID: 15280455 [PubMed - indexed for MEDLINE]


☐ 6: [Pushko P, Parker M, Ludwig GV, Davis NL, Johnston RE, Smith JF.](#) Related Articles, Links

Replicon-helper systems from attenuated Venezuelan equine encephalitis virus: expression of heterologous genes in vitro and immunization against heterologous pathogens in vivo.

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Virology. 1997 Dec 22;239(2):389-401.  
PMID: 9434729 [PubMed - indexed for MEDLINE]

- ☐ 7: [Smahel M, Sima P, Ludvikova V, Vonka V.](#) [Related Articles, Links](#)

 Modified HPV16 E7 Genes as DNA Vaccine against E7-Containing Oncogenic Cells.


Virology. 2001 Mar 15;281(2):231-8.  
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 Combined immunization with fusion genes of mutated E7 gene of human papillomavirus type 16 did not enhance antitumor effect.


J Gene Med. 2005 Jun;7(6):696-707.  
PMID: 15712328 [PubMed - indexed for MEDLINE]

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 Immunization strategy against cervical cancer involving an alphavirus vector expressing high levels of a stable fusion protein of human papillomavirus 16 E6 and E7.

Gene Ther. 2002 Jan;9(2):85-94.  
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 Immunotherapy of a human papillomavirus (HPV) type 16 E7-expressing tumour by administration of fusion protein comprising Mycobacterium

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bovis bacille Calmette-Guerin (BCG) hsp65 and HPV16 E7.  
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T-helper epitopes identified within the E6 transforming protein of cervical cancer-associated human papillomavirus type 16.

Viral Immunol. 1999;12(4):297-312.

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Immunological ignorance of an E7-encoded cytolytic T-lymphocyte epitope in transgenic mice expressing the E7 and E6 oncogenes of human papillomavirus type 16.

J Virol. 1997 May;71(5):3998-4004.

PMID: 9094677 [PubMed - indexed for MEDLINE]

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Superior therapeutic efficacy of alphavirus-mediated immunization against human papilloma virus type 16 antigens in a murine tumour model: effects of the route of immunization.

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Intervirology. 2002;45(4-6):300-7.

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- ☐ 19: [Indrova M, Reinis M, Bubenik J, Jandlova T, Bieblova J, Vonka V, Velek J.](#) Related Articles, Links



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Anti-tumor DNA vaccines based on the expression of human papillomavirus-16 E6/E7 oncoproteins genetically fused with the glycoprotein D from herpes simplex virus-1.

Microbes Infect. 2005 Dec;7(15):1541-50. Epub 2005 Sep 9.

PMID: 16213178 [PubMed - indexed for MEDLINE]

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☐ 1. Document ID: US 6558670 B1

L10: Entry 1 of 6

File: USPT

May 6, 2003

US-PAT-NO: 6558670

DOCUMENT-IDENTIFIER: US 6558670 B1

TITLE: Vaccine adjuvants

DATE-ISSUED: May 6, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Friede; Martin	Court St Etienne			BE
Hermand; Philippe	Court St Etienne			BE

US-CL-CURRENT: [424/184.1](#); [424/278.1](#), [424/283.1](#), [514/25](#)

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	KMC	Draw D
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☐ 2. Document ID: US 6544518 B1

L10: Entry 2 of 6

File: USPT

Apr 8, 2003

US-PAT-NO: 6544518

DOCUMENT-IDENTIFIER: US 6544518 B1

TITLE: Vaccines

DATE-ISSUED: April 8, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Friede; Martin	Farnham			GB
Garcon; Nathalie	Wavre			BE
Gerard; Catherine Marie Ghislaine	Rhode Saint Genese			BE
Hermand; Philippe	Court-Saint-Etienne			BE

US-CL-CURRENT: [424/184.1](#); [424/208.1](#), [424/228.1](#), [424/229.1](#), [424/231.1](#), [424/249.1](#), [424/278.1](#), [424/283.1](#), [514/25](#)

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Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	KWIC	Draw D
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☐ 3. Document ID: US 6342224 B1

L10: Entry 3 of 6

File: USPT

Jan 29, 2002

US-PAT-NO: 6342224

DOCUMENT-IDENTIFIER: US 6342224 B1

TITLE: Recombinant papillomavirus vaccine and method for production and treatment

DATE-ISSUED: January 29, 2002

## INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Bruck; Claudine	Rixensart			BE
Silva; Teresa Cabezon	Lenkebeek			BE
Fernande Delisse; Anne-Marie Eva	Gosselies			BE
Ghislaine Gerard; Catherine Marie	Rhode Saint Genese			BE
Lombardo-Bencheikh; Angela	Wavre			BE

US-CL-CURRENT: 424/192.1; 424/185.1, 424/186.1, 424/204.1, 435/252.3, 435/320.1,  
435/325, 435/69.3, 435/69.7, 530/350, 536/23.4, 536/23.72

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	KWIC	Draw D
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☐ 4. Document ID: US 6306397 B1

L10: Entry 4 of 6

File: USPT

Oct 23, 2001

US-PAT-NO: 6306397

DOCUMENT-IDENTIFIER: US 6306397 B1

TITLE: Variants of human papilloma virus antigens

DATE-ISSUED: October 23, 2001

## INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Edwards; Stirling John	Northcote			AU
Cox; John Cooper	Bullengarook			AU
Webb; Elizabeth Ann	Eltham			AU
Frazer; Ian	St. Lucia			AU

US-CL-CURRENT: 424/192.1; 424/186.1, 424/204.1, 435/235.1, 435/69.1, 435/69.7,  
536/23.1, 536/23.72, 536/24.3

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	KWIC	Draw D
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☐ 5. Document ID: US 6303128 B1

L10: Entry 5 of 6

File: USPT

Oct 16, 2001

US-PAT-NO: 6303128

DOCUMENT-IDENTIFIER: US 6303128 B1

TITLE: Method for protein expression

DATE-ISSUED: October 16, 2001

## INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Webb; Elizabeth Ann	Eltham			AU
Edwards; Stirling John	Northcote			AU

US-CL-CURRENT: 424/199.1; 424/192.1, 435/235.1, 435/320.1, 435/325, 435/69.1,  
435/69.7

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	KMC	Draw D
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☐ 6. Document ID: US 6004557 A

L10: Entry 6 of 6

File: USPT

Dec 21, 1999

US-PAT-NO: 6004557

DOCUMENT-IDENTIFIER: US 6004557 A

TITLE: Variants of human papillomavirus antigens

DATE-ISSUED: December 21, 1999

## INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Edwards; Stirling John	Caburg			AU
Cox; John Cooper	Bullengarook			AU
Webb; Elizabeth Ann	Eltham			AU
Frazer; Ian	St. Lucia.			AU

US-CL-CURRENT: 424/192.1; 424/186.1, 424/199.1, 424/204.1, 435/235.1, 435/320.1,  
435/69.1, 435/69.7, 536/23.1, 536/23.72 , 536/24.3

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	KMC	Draw D
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<input type="checkbox"/>	L5	CN-1381583-A.did.	0
	<i>DB=DWPI; PLUR=YES; OP=ADJ</i>		
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## OM protein - protein search, using sw model

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(without alignments)  
196.288 Million cell updates/sec

Title: US-10-530-253-14ED

Perfect score: 517  
Sequence: 1 MNCDFTLRHYMLDLPETT.....LEDLMGTGIVXPSQRP 98Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*  
9: geneseqp2005s:\*  
10: geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	514	99.4	248	AD044070	Ad044070 Amino aci
2	513	99.2	98	AE13079	AE13079 HPV16 E7
3	513	99.2	220	AA125378	AA125378 HPV fusio
4	513	99.2	220	AA102634	AA102634 Prot.D1/3
5	513	99.2	220	AE152640	AE152640 Fusion pr
6	513	99.2	248	AD044068	Ad044068 Amino aci
7	513	99.2	805	ADA27366	Ada27366 HPV-16 L2
8	513	99.2	805	ADA25444	Ada25444 HPV-16 L2
9	513	99.2	805	ADA14293	Ada14293 HPV-16 L2
10	513	99.2	805	AE138618	AE138618 HPV-16 L2
11	512	99.0	98	AA122767	AA122767 HPV E7 pe
12	512	99.0	98	AA12361	AA12361 Human pap
13	512	99.0	98	AA146886	AA146886 Amino aci
14	512	99.0	98	AA158474	AA158474 Human pap
15	512	99.0	98	AA157721	AA157721 Human pap
16	512	99.0	98	AA158421	AA158421 Human pap
17	512	99.0	98	AA101718	AA101718 Human pap
18	512	99.0	98	AA172607	AA172607 Human pap
19	512	99.0	98	AA167546	AA167546 Amino aci
20	512	99.0	98	AA186332	AA186332 HPV 16 E7
21	512	99.0	98	AA177713	AA177713 Human pap
22	512	99.0	98	AA10810	AA10810 Human pap
23	512	99.0	98	AB182375	AB182375 Wild-type

24	512	99.0	98	AA16630	AA16630 Human pap
25	512	99.0	98	AD109516	AD109516 Human pap
26	512	99.0	98	AD118632	AD118632 Human pap
27	512	99.0	98	AD190076	AD190076 Human pap
28	512	99.0	98	AD132916	AD132916 Amino aci
29	512	99.0	98	AD044073	Ad044073 Amino aci
30	512	99.0	98	AD149005	AD149005 Human pap
31	512	99.0	98	AD166362	AD166362 Human pap
32	512	99.0	98	AD15532	AD15532 Human pap
33	512	99.0	98	AD169083	AD169083 HPV 16 E7
34	512	99.0	98	AE140816	AE140816 Ant1-apop
35	512	99.0	98	AE111989	AE111989 HPV16 E7
36	512	99.0	98	AE16392	AE16392 HPV prote
37	512	99.0	98	AE198871	AE198871 HPV 16 En
38	512	99.0	98	AE13078	AE13078 HPV16 E7
39	512	99.0	98	AE14360	AE14360 Human pap
40	512	99.0	98	AE194089	AE194089 HPV16 E7
41	512	99.0	99	AD108451	AD108451 HPV16 E7
42	512	99.0	99	AD192615	AD192615 HPV16 E7
43	512	99.0	121	AA131608	AA131608 Amino aci
44	512	99.0	198	AA131616	AA131616 Novel Pve
45	512	99.0	212	AD175831	AD175831 Novel Pve
46	512	99.0	220	AA125375	AA125375 HPV fusio
47	512	99.0	220	AA102631	AA102631 ProtDch1
48	512	99.0	220	AE152631	AE152631 Fusion pr
49	512	99.0	239	AA125380	AA125380 HPV fusio
50	512	99.0	239	AA102636	AA102636 CXTA-E7-
51	512	99.0	239	AE152644	AE152644 Fusion pr
52	512	99.0	248	AD044066	Ad044066 Amino aci
53	512	99.0	253	AA143480	AA143480 Amino aci
54	512	99.0	253	AA101502	AA101502 Amino ter
55	512	99.0	253	AA197612	AA197612 Amino ter
56	512	99.0	253	AA11132	AA11132 CXTA4/E7
57	512	99.0	253	AA181586	AA181586 CXTA4/E7
58	512	99.0	253	AA187562	AA187562 CXTA4-E7
59	512	99.0	256	ADR47005	ADR47005 Human pap
60	512	99.0	256	AE140157	AE140157 Human pap
61	512	99.0	266	AA197561	AA197561 Human pap
62	512	99.0	268	AA102129	AA102129 Flt-3 lig
63	512	99.0	285	AA131615	AA131615 Amino aci
64	512	99.0	324	AA131613	AA131613 Amino aci
65	512	99.0	334	AA1022926	AA1022926 HbAg-E7
66	512	99.0	349	AE140828	AE140828 Ant1-apop
67	512	99.0	349	AE140831	AE140831 Ant1-apop
68	512	99.0	371	AA125377	AA125377 HPV fusio
69	512	99.0	371	AA102633	AA102633 Prot.D1/3
70	512	99.0	371	AE152638	AE152638 Fusion pr
71	512	99.0	390	AA125381	AA125381 HPV fusio
72	512	99.0	390	AA102637	AA102637 CXTA-E6E
73	512	99.0	390	AE152646	AE152646 Fusion pr
74	512	99.0	421	AA150663	AA150663 Thioedox
75	512	99.0	493	AA131610	AA131610 Amino aci
76	512	99.0	638	AA1803790	AA1803790 Heat choc
77	512	99.0	639	AA131609	AA131609 Amino aci
78	512	99.0	641	AA131619	AA131619 Amino aci
79	512	99.0	647	AA131620	AA131620 Amino aci
80	511	98.8	98	AD118635	AD118635 Human pap
81	511	98.8	248	AD044064	Ad044064 Amino aci
82	511	98.6	248	AD044062	Ad044062 Amino aci
83	509	98.5	248	AD044060	Ad044060 Amino aci
84	507	98.1	98	AA150703	AA150703 HPV16 E7
85	507	98.1	98	AA149453	AA149453 HPV 16E7
86	507	98.1	98	AA102639	AA102639 HPV-16 pr
87	507	98.1	111	AA1022923	AA1022923 Human pap
88	505	97.7	262	AA127724	AA127724 HPV 16 E7
89	504	97.5	98	AA108020	AA108020 Human pap
90	504	97.5	98	AD132548	AD132548 Human pap
91	503	97.3	98	AA131607	AA131607 Amino aci
92	503	97.3	490	AD142209	AD142209 N. mening
93	503	97.3	648	AA131614	AA131614 Amino aci
94	503	97.3	711	AA131617	AA131617 Amino aci
95	503	97.3	724	AA131618	AA131618 Amino aci
96	500	96.7	99	AB181111	AB181111 HPV E7 an

97	500	96.7	99	5	ABB82376	Modified
98	500	96.7	99	7	ADE21865	HPV-16 E7
99	500	96.7	99	8	ADO05276	Human pap
100	500	96.7	99	8	ADU66377	Human pap

## ALIGNMENTS

## RESULT 1

ADO44070 standard; protein; 248 AA.

ADO44070;

15-JUL-2004 (first entry)

Amino acid sequence of a fusion protein designated E7E6PentM.

E6 protein; E7 protein; fusion protein; HPV16; HPV-associated cancer;

cervical cancer; immune response; lower gastrointestinal tract cancer;

anal cancer; reproductive system cancer; penile cancer; vulvar cancer;

gene; 98.

Human papillomavirus type 16.

Synthetic.

WO2004030636-A2.

15-APR-2004.

02-OCT-2003; 2003WO-US031726.

03-OCT-2002; 2002US-0415929P.

(AMHP ) WYETH HOLDINGS CORP.

Smith L, Caesetti MC;

WPI; 2004-316326/29.

N-PSDB; ADO44071.

New polypeptide comprising human papillomavirus E6 and E7 polypeptides,

useful for treating or preventing human papillomavirus (HPV)-associated

cancers, e.g. cervical cancer.

Claim 22; Page 75-76; 101pp; English.

The present sequence represents a fusion protein, comprising E7 and E6

polypeptides from human papillomavirus type 16 (HPV16). The fusion

protein is designated E7E6PentM, and comprises an E7 amino terminus

(where residues 24, 26 and 91 have been replaced with glycine) and an E6

carboxy terminus (where residues 63 and 106 have been replaced with

glycine). E7E6PentM is representative of fusion proteins of the

invention. The specification describes human papillomavirus E6 and E7

polypeptides, where the E7 polypeptide has mutations at any one or more

of the amino acids corresponding to amino acids 24, 26 or 91 of the

sequence given in ADO44073 and the E6 polypeptide has no mutations or has

mutations at any one or more of the amino acids corresponding to amino

acids 63 or 106 of the sequence given in ADO44072. The polypeptides of

the invention are useful for treating or preventing human papillomavirus

(HPV)-associated cancers, such as cervical cancer. The fusion proteins

and nucleic acids encoding the fusion proteins are useful for generating

immune responses against HPV. They are also useful for treating lower

gastrointestinal tract cancers, e.g. anal cancer, and other cancers of

the reproductive system, including penile and vulvar cancer.

Sequence 248 AA;

Query Match 99.4%; Score 514; DB 8; Length 248;

Best Local Similarity 96.9%; Pred. No. 3.9e-57;

Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy	1	MHGDTPLHEMYMDLQPEETDLYXXYQJNDSSSEEDIDEPAGQAEPPDRAHYNIIVTFCK 60
Db	1	MHGDTPLHEMYMDLQPEETDLYGYGQJNDSSSEEDIDEPAGQAEPPDRAHYNIIVTFCK 60
Qy	61	CDSTLRLCVQSTHVDIRLTEDLMGTIGIVPICSGKP 98
Db	61	CDSTLRLCVQSTHVDIRLTEDLMGTIGIVPICSGKP 98

## RESULT 2

AED13079 standard; protein; 98 AA.

AED13079;

15-DEC-2005 (first entry)

HPV16 E7 variant protein sequence.

mutagen; vaccine; antigen; virucide; antibacterial.

Human papillomavirus type 16.

FR2868781-A1.

14-OCT-2005.

13-APR-2004; 2004FR-00003848.

13-APR-2004; 2004FR-00003848.

(IMMU-) IMMUTEP.

Triebel F;

WPI; 2005-678227/70.

N-PSDB; AED13077.

Therapeutic vaccine, for viral and bacterial conditions, comprises an

antigen protein and a viral or bacterial protein, coupled together by

stable hydrogen or covalence bonds in biological media.

Disclosure; Fig 1; 51pp; French.

The invention relates to a novel vaccine composed of an antigen protein

and a second protein as an s-(methyl) mercury)-L-cysteine (CMH class II)

ligand. The second protein is taken from a group including human

Lymphocyte Activation Gene (hLAG)-3. The first protein is a viral or

bacterial antigen, a tumor antigen, parasitic antigen, or their mixtures.

The viral antigens can be for hepatitis B (HBV), human papillomavirus

(HPV), hepatitis C (HCV), human immunodeficiency virus (HIV), Epstein-

Barr virus (EBV), cytomegalovirus (CMV), and their combinations. The

bacterial antigens can be intracellular bacteria of tuberculosis, leprosy

and listeria. A vaccine of the invention has virucide, and antibacterial

activity. The present sequence represents the HPV16 variant E7 protein

sequence.

Sequence 98 AA;

Query Match 99.2%; Score 513; DB 9; Length 98;

Best Local Similarity 96.9%; Pred. No. 1.6e-57;

Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEMYMDLQPEETDLYXXYQJNDSSSEEDIDEPAGQAEPPDRAHYNIIVTFCK 60

Db 1 MHGDTPLHEMYMDLQPEETDLYGYGQJNDSSSEEDIDEPAGQAEPPDRAHYNIIVTFCK 60

Qy 61 CDSTLRLCVQSTHVDIRLTEDLMGTIGIVPICSGKP 98

Db 61 CDSTLRLCVQSTHVDIRLTEDLMGTIGIVPICSGKP 98

RESULT 3

AAV25378  
ID AAV25378 standard; protein; 220 AA.  
XX  
AC AAV25378;  
XX  
DT 06-SEP-1999 (first entry)  
XX  
DE HPV fusion protein DI/3-E7-Mutated (C24G, E26Q)/HPV16.  
XX  
KW Fusion protein; E6 protein; E7 protein; E6/E7; immunomodulator; tumour;  
KM immunological fusion partner; Cpg oligonucleotide; immune response;  
KM HPV antigen; prevention; treatment.  
XX  
OS Synthetic.  
OS Human papillomavirus.  
XX  
PN WO933868-A2.  
XX  
PD 08-JUL-1999.  
XX  
PF 18-DEC-1998; 98WO-EP008563.  
XX  
PR 24-DEC-1997; 97GB-00027262.  
XX  
XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
XX  
PI Dalemans WLJ, Gerard CMG;  
XX  
DR WPI; 1999-405485/34.  
XX  
DR N-PSDB; AAX78794.  
XX  
PT Composition comprising an E6, E7 or E6/E7 fusion protein from HPV to  
PS induce immune response to HPV.  
XX  
PS Example V; Page 51; 62pp; English.  
XX  
CC AAX78791-X78801 represent nucleic acid sequences which encode novel  
CC constructs comprising an E6 or E7 protein or E6/E7 fusion protein from  
CC HPV (represented in AAV25375-Y25386). These constructs are optionally  
CC linked to an immunological fusion partner and an immunomodulatory Cpg  
CC oligonucleotide. The products of the invention can be used to induce an  
CC immune response in a patient to an HPV antigen. They can also be used for  
CC preventing or treating HPV induced tumours  
XX  
SQ Sequence 220 AA;  
XX  
Query Match 99.2%; Score 513; DB 2; Length 220;  
Best Local Similarity 96.9%; Pred. No. 4.6e-57;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
XX  
QY 1 MGGDTPTLHEHYMLDLOPETTDLYXXQLNDSSEEDIDGPAGAPDRAHYNIIVTFCK 60  
DB 114 MGGDTPTLHEHYMLDLOPETTDLYGYQLNDSSEEDIDGPAGAPDRAHYNIIVTFCK 173  
QY 61 CDSTLRLCVQSTHVDIRTLEDLMGTIGIYXPTCSQKP 98  
DB 174 CDSTLRLCVQSTHVDIRTLEDLMGTIGIYXPTCSQKP 211

RESULT 4  
AAV02634  
ID AAV02634 standard; protein; 220 AA.  
XX  
AC AAV02634;  
XX  
DT 17-OCT-2003 (revised)  
DT 22-JUN-1999 (first entry)  
XX  
DE Prot. DI/3-E7-mut (C24G, E26Q)/HPV16 protein.  
XX  
KM Chimeric; E6; E7; fusion protein; protein D; vaccine; immunotherapy;  
KM tumour; lesion; benign; malignant; virus; infection.  
XX

OS Human papillomavirus.  
OS Haemophilus influenzae.  
OS Chimeric.  
XX  
PN WO910375-A2.  
XX  
PD 04-MAR-1999.  
XX  
PF 17-AUG-1998; 98WO-EP005285.  
XX  
PR 22-AUG-1997; 97GB-00017953.  
XX  
XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
XX  
PI Bruck C, Cabezon Silva T, Delisse AEF, Gerard CMG;  
XX  
PI Lombardo-Bencheikh A;  
XX  
DR WPI; 1999-190587/16.  
DR N-PSDB; AAX29783.  
XX  
XX Human Papilloma Virus (HPV) fusion proteins - useful in vaccines for  
PT treatment or prophylaxis of HPV induced lesions.  
XX  
PS Disclosure; Fig 8; 95pp; English.  
XX  
CC This sequence represents a chimeric E6 or E7 protein or E6/E7 fusion  
CC protein from Human papillomavirus (HPV) linked to an immunological fusion  
CC partner, in this case, a fragment of the Haemophilus influenzae B protein  
CC D. The sequence also contains a histidine tag at the C-terminus of the  
CC encoded protein. The protein can be used in a vaccine, for immuno-  
CC therapeutically treating HPV induced tumour lesions (benign or malignant)  
CC and preventing HPV viral infection. (Updated on 17-OCT-2003 to  
CC standardise OS field)  
XX  
SQ Sequence 220 AA;  
XX  
Query Match 99.2%; Score 513; DB 2; Length 220;  
Best Local Similarity 96.9%; Pred. No. 4.6e-57;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
XX  
QY 1 MGGDTPTLHEHYMLDLOPETTDLYXXQLNDSSEEDIDGPAGAPDRAHYNIIVTFCK 60  
DB 114 MGGDTPTLHEHYMLDLOPETTDLYGYQLNDSSEEDIDGPAGAPDRAHYNIIVTFCK 173  
QY 61 CDSTLRLCVQSTHVDIRTLEDLMGTIGIYXPTCSQKP 98  
DB 174 CDSTLRLCVQSTHVDIRTLEDLMGTIGIYXPTCSQKP 211

RESULT 5  
AED52640  
ID AED52640 standard; protein; 220 AA.  
XX  
AC AED52640;  
XX  
DT 29-DEC-2005 (first entry)  
XX  
DE Fusion protein DI/3-E7-His (HPV16), C137G/E139Q.  
XX  
KW Fusion protein; vaccine; papilloma; cytosstatic; papillomavirus infection;  
KM virucide; uterine cervix tumor; E7; muten; D protein.  
XX  
OS Haemophilus influenzae; strain 772.  
OS Human papillomavirus type 16.  
OS Synthetic.  
OS Chimeric.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 137 /note= "Wild-type Cys substituted by Gly"  
FT FT Misc-difference 139 /note= "Wild-type Gln substituted by Gln"  
FT FT

PN IN9801903-14.  
XX  
PD 04-MAR-2005.  
XX  
PF 24-AUG-1998; 98IN-CH001903.  
XX  
PR 22-AUG-1997; 97EP-00179535.  
XX  
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
XX  
PI Tyrell AMR;  
XX  
DR WPI; 2005-557648/57.  
XX  
DR N-PSDB; AED52639.  
XX  
PT Vaccine.  
XX  
PS Example 8; Fig 8; 96pp; English.  
XX  
CC The invention relates to human Papilloma virus (HPV) fusion proteins,  
CC linked to an immunological fusion partner that provides T helper epitopes  
CC to the HPV antigen. Vaccine formulations comprising the fusion proteins  
CC are useful in the treatment or prophylaxis of HPV induced lesions  
CC (papillomas, warts and cervical cancer). HPV 16 (and HPV 18) E6 and E7  
CC proteins (singly, as an E6-E7 fusion or mutated) were fused to either  
CC Haemophilus influenzae D protein (20-127), the C-terminus of  
CC Streptococcus pneumoniae Lyta protein (glycA) or thiorodoxin. The present  
CC sequence represents a mutated HPV-H. influenzae D protein, fusion protein  
CC of the invention.  
XX  
SQ Sequence 220 AA;  
  
Query Match 99.2%; Score 513; DB 9; Length 220;  
Best Local Similarity 96.9%; Pred. No. 4.6e-57;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 MHGDTPTLHEYM L D L Q P E T T D L Y X X X Q L N D S S E E D E I D G P A G Q A E P D R A H Y N I V T F C C K 60  
DB 114 MHGDTPTLHEYM L D L Q P E T T D L Y X X X Q L N D S S E E D E I D G P A G Q A E P D R A H Y N I V T F C C K 173  
  
QY 61 CDSTLR L C V O S T H Y D I R T L E D L M G T L G I V X P I C S Q K P 98  
DB 174 CDSTLR L C V O S T H Y D I R T L E D L M G T L G I V C P I C S Q K P 211  
  
RESULT 6  
ADA044068  
ID ADO44068 standard; protein; 248 AA.  
XX  
AC ADO44068;  
XX  
DT 15-JUL-2004 (first entry)  
XX  
DE Amino acid sequence of a fusion protein designated E7E6TetM.  
XX  
KW E6 protein; E7 protein; fusion protein; HPV16; HPV-associated cancer;  
KW cervical cancer; immune response; lower gastrointestinal tract cancer;  
KW anal cancer; reproductive system cancer; penile cancer; vulvar cancer.  
XX  
OS Human papillomavirus type 16.  
OS Synthetic.  
XX  
PN WO2004030636-A2.  
XX  
PD 15-APR-2004.  
XX  
PF 02-OCT-2003; 2003WO-US0311726.  
XX  
PR 03-OCT-2002; 2002US-0415929P.  
XX  
PA (AMHP ) WYETH HOLDINGS CORP.  
XX  
PI Smith L, Caesetti MC;

XX  
DR WPI; 2004-316328/29.  
XX  
DR N-PSDB; ADO44069.  
XX  
PT New polypeptide comprising human papillomavirus E6 and E7 polypeptides,  
XX useful for treating or preventing human papillomavirus (HPV)-associated  
XX cancers, e.g. cervical cancer.  
XX  
PS Claim 22; Page 73-74; 101pp; English.  
XX  
CC The present sequence represents a fusion protein, comprising E7 and E6  
CC polypeptides from human papillomavirus type 16 (HPV16). The fusion  
CC protein is designated E7E6TetM, and comprises an E7 amino terminus (where  
CC residues 24 and 26 have been replaced with glycine) and an E6 carboxy  
CC terminus (where residues 63 and 106 have been replaced with glycine).  
CC E7E6TetM is representative of fusion proteins of the invention. The  
CC specification describes human papillomavirus E6 and E7 polypeptides,  
CC where the E7 polypeptide has mutations at any one or more of the amino  
CC acids corresponding to amino acids 24, 26 or 91 of the sequence given in  
CC ADO44073 and the E6 polypeptide has no mutations or has mutations at any  
CC one or more of the amino acids corresponding to amino acids 63 or 106 of  
CC there sequence given in ADO44072. The polypeptides of the invention are  
CC useful for treating or preventing human papillomavirus (HPV)-associated  
CC cancers, such as cervical cancer. The fusion proteins and nucleic acids  
CC encoding the fusion proteins are useful for generating immune responses  
CC against HPV. They are also useful for treating lower gastrointestinal  
CC tract cancers, e.g. anal cancer, and other cancers of the reproductive  
CC system, including penile and vulvar cancer.  
XX  
SQ Sequence 248 AA;  
  
Query Match 99.2%; Score 513; DB 8; Length 248;  
Best Local Similarity 96.9%; Pred. No. 5.3e-57;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 MHGDTPTLHEYM L D L Q P E T T D L Y X X X Q L N D S S E E D E I D G P A G Q A E P D R A H Y N I V T F C C K 60  
DB 1 MHGDTPTLHEYM L D L Q P E T T D L Y X X X Q L N D S S E E D E I D G P A G Q A E P D R A H Y N I V T F C C K 60  
  
QY 61 CDSTLR L C V O S T H Y D I R T L E D L M G T L G I V X P I C S Q K P 98  
DB 61 CDSTLR L C V O S T H Y D I R T L E D L M G T L G I V C P I C S Q K P 98  
  
RESULT 7  
ADA27366  
ID ADA27366 standard; protein; 805 AA.  
XX  
AC ADA27366;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE HPV-16 L2/E7/E2 fusion protein SEQ ID NO:9.  
XX  
KW cell line; American Type Culture Collection PTA-4047; ATCC-4047;  
KW baculoviruses; viral recombinant protein; virus-like particle; vaccine;  
KW diagnostic reagent; human papillomavirus type 16; HPV-16; L2/E7/E2;  
KW fusion protein.  
XX  
OS Synthetic.  
OS Human papillomavirus type 16.  
XX  
PN WO2003068804-A2.  
XX  
PD 21-AUG-2003.  
XX  
PF 14-FEB-2003; 2003WO-US004516.  
XX  
PR 14-FEB-2002; 2002US-0356113P.  
XX  
PR 14-FEB-2002; 2002US-0356118P.  
XX  
PR 14-FEB-2002; 2002US-0356119P.  
XX  
PR 14-FEB-2002; 2002US-0356123P.  
XX  
PR 14-FEB-2002; 2002US-0356126P.

PR 14-FEB-2002; 2002US-0356133P.  
PR 14-FEB-2002; 2002US-0356135P.  
PR 14-FEB-2002; 2002US-0356150P.  
PR 14-FEB-2002; 2002US-0356151P.  
PR 14-FEB-2002; 2002US-0356152P.  
PR 14-FEB-2002; 2002US-0356154P.  
PR 14-FEB-2002; 2002US-0356156P.  
PR 14-FEB-2002; 2002US-0356157P.  
PR 14-FEB-2002; 2002US-0356161P.  
PR 14-FEB-2002; 2002US-0356162P.  
XX  
PA (NOVA-) NOVAVAX INC.  
XX  
PI Robinson RA;  
XX  
DR WPI; 2003-646475/61.  
DR N-PSDB; ADA27374.  
XX  
PT New insect cell line designated ATCC PTA-4047, useful for replicating  
PT baculoviruses to produce large amounts of recombinant proteins of  
PT medical, pharmaceutical and veterinary importance.  
XX  
PS Disclosure; Page 59-60; 63pp; English.  
XX  
CC The present invention describes a cell line comprising a cell that is a  
CC clone, derivative, mutant and/or transfectant of a cell line designated  
CC American Type Culture Collection (ATCC) PTA-4047. The cell upon culture  
CC grows continuously and retains the identifying characteristics of the  
CC cell line designated ATCC-4047. Also described is a process of making a  
CC cell line. The insect cell line is useful in replicating baculoviruses,  
CC as a host substrate for baculovirus plaque assays, as a source of insect  
CC proteins, acts as a depot for cell transfection to produce recombinant  
CC baculoviruses, and in expressing viral recombinant proteins.  
CC Extracellular and intracellular viral recombinant proteins and virus-like  
CC particles expressed from the cell line are useful as pharmaceutical  
CC compositions, vaccines or diagnostic reagents. The present sequence  
CC represents a human papillomavirus type 16 (HPV-16) L2/E7/E2 fusion  
CC protein, which is used in the exemplification of the present invention.  
XX  
SQ Sequence 805 AA;  
XX  
Query Match 99.2%; Score 513; DB 6; Length 805;  
Best Local Similarity 96.9%; Pred. No. 2.4e-56;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 MHGDTPLHEHYMLDLOPETTDLYXXQLNDSSEDEIDGPAGAEPRRAHYNIIVTFCK 60  
Db 471 MHGDTPLHEHYMLDLOPETTDLYGYEQUNDSSEDEIDGPAGAEPRRAHYNIIVTFCK 530  
QY 61 CDSTLRICVOSTHVDITRTLEDLMGTIGIYXPICSQRP 98  
Db 531 CDSTLRICVOSTHVDITRTLEDLMGTIGIYCPICSQRP 568  
RESULT 8  
ADA92544  
ID ADA92544 standard; protein; 805 AA.  
XX  
AC ADA92544;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
XX HPV-16 L2/E7/E2 fusion amino acid sequence SEQ ID NO:9.  
XX  
DE  
XX  
XX codon optimised; viral capsid protein; virus-like particle; VLP;  
KM antigenic; human papillomavirus infection; virucide; vaccine;  
KM gene therapy; human papillomavirus type 16; dysplasia; infection; HPV-16;  
XX fusion protein.  
XX  
OS Synthetic.  
OS Human papillomavirus type 16.  
XX  
PN W02003068933-A2.

XX  
PD 21-AUG-2003.  
XX  
XX 14-FEB-2003; 2003WO-US004480.  
XX  
PR 14-FEB-2002; 2002US-0356113P.  
PR 14-FEB-2002; 2002US-0356118P.  
PR 14-FEB-2002; 2002US-0356119P.  
PR 14-FEB-2002; 2002US-0356123P.  
PR 14-FEB-2002; 2002US-0356126P.  
PR 14-FEB-2002; 2002US-0356133P.  
PR 14-FEB-2002; 2002US-0356135P.  
PR 14-FEB-2002; 2002US-0356150P.  
PR 14-FEB-2002; 2002US-0356151P.  
PR 14-FEB-2002; 2002US-0356152P.  
PR 14-FEB-2002; 2002US-0356154P.  
PR 14-FEB-2002; 2002US-0356156P.  
PR 14-FEB-2002; 2002US-0356157P.  
PR 14-FEB-2002; 2002US-0356161P.  
PR 14-FEB-2002; 2002US-0356162P.  
XX  
PA (NOVA-) NOVAVAX INC.  
XX  
PI Robinson RA;  
XX  
DR WPI; 2003-689664/65.  
DR N-PSDB; ADA92552.  
XX  
XX New codon optimised polynucleotide encoding a viral capsid protein that  
PT self assembles into a virus-like particle, useful for diagnosing,  
PT preventing or treating human papillomavirus infections or associated  
PT disorders.  
XX  
PS Disclosure; Page 119-120; 123pp; English.  
XX  
CC The present invention describes a codon optimised polynucleotide encoding  
CC a viral capsid protein that self assembles into a virus-like particle  
CC (VLP) that exhibits conformational antigenic epitopes capable of raising  
CC neutralising antibodies, where the VLP is expressed from a host cell  
CC extracellularly. Also described: (1) a vector comprising the above codon  
CC optimised polynucleotide operably linked to a eukaryotic or prokaryotic  
CC regulatory control element, capable of replication in prokaryotic and/or  
CC eukaryotic host; (2) a host cell comprising the vector; (3) a  
CC pharmaceutical or vaccine composition for treating, ameliorating or  
CC preventing a papillomavirus related disease or disorder, comprising a  
CC multiplicity of VLPs that exhibit conformational antigenic epitopes, and  
CC a carrier, diluent or adjuvant; (4) a diagnostic kit for detecting a  
CC papillomavirus infection, comprising a multiplicity of VLPs that exhibit  
CC conformational antigenic epitopes, and a detection agent comprising a  
CC detectable label; (5) a method for preparing the above codon optimised  
CC polynucleotide, comprising replacing codons that are underutilised in  
CC insect cells with codons that are utilised at high levels in insect  
CC cells, to create an initially-modified nucleotide sequence, and modifying  
CC the initially-modified nucleotide sequence by choosing a preferred codon  
CC for the initially-modified sequence, where the ratio of GC nucleotide  
CC pairs to AT nucleotide pairs in the further-modified nucleotide sequence  
CC trends towards about 1:1, where the number of palindromic and stem-loop  
CC DNA structures in the further-modified nucleotide sequence is minimised,  
CC and where the number of transcription and post-transcription repressor  
CC elements are minimised; and (6) methods for treating, ameliorating or  
CC preventing a papillomavirus related disease or disorder, or for  
CC protecting an individual against a papillomavirus infection, comprising  
CC administering to an individual an amount of the composition or vaccine  
CC cited above. The VLP has virucide activity and can be used in vaccines  
CC and in gene therapy. The composition and methods of the present invention  
CC are useful in diagnosing, preventing or treating human papillomavirus  
CC infections or associated disorders, such as dysplasia. The present  
CC sequence represents an HPV-16 codon optimised L2/E7/E2 fusion amino acid  
CC sequence from the present invention.  
XX  
SQ Sequence 805 AA;  
XX  
Query Match 99.2%; Score 513; DB 7; Length 805;

Best Local Similarity 96.9%; Pred. No. 2.4e-56;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDTPTLHEHYMLDLOPETTDLYXXYQUNDSSSEDEIDGPAQAEPRRAHYNIVTFCK 60  
|||||  
DB 471 MHGDTPTLHEHYMLDLOPETTDLYGYEQUNDSSSEDEIDGPAQAEPRRAHYNIVTFCK 530  
|||||

OY 61 CDSTLRICVOSTHVDIRTLIEDLIMGTLGIYXPCISQKP 98  
|||||  
DB 531 CDSTLRICVOSTHVDIRTLIEDLIMGTLGIYXPCISQKP 568  
|||||

RESULT 9  
ADA14293  
ID ADA14293 standard; protein; 805 AA.  
XX  
AC ADA14293;  
XX  
DT 06-NOV-2003 (first entry)  
XX  
DE HPV-16 L2/E7/E2 fusion protein SEQ ID NO:9.  
XX  
XX purification; recombinant extracellular virus-like particle;  
KM recombinant intracellular virus-like particle; virus-like particle; VLP;  
KM virucide; vaccine; gene therapy; human papillomavirus; HPV; infection;  
KM dysplasia; HPV-16; fusion protein.  
XX  
OS Synthetic.  
OS Human papillomavirus type 16.  
XX  
PN WO2003068993-A1.  
XX  
PD 21-AUG-2003.  
XX  
PF 14-FEB-2003; 2003WO-US004474.  
XX  
XX 14-FEB-2002; 2002US-0356113P.  
XX  
PR 14-FEB-2002; 2002US-0356118P.  
PR 14-FEB-2002; 2002US-0356119P.  
PR 14-FEB-2002; 2002US-0356123P.  
PR 14-FEB-2002; 2002US-0356126P.  
PR 14-FEB-2002; 2002US-0356133P.  
PR 14-FEB-2002; 2002US-0356135P.  
PR 14-FEB-2002; 2002US-0356150P.  
PR 14-FEB-2002; 2002US-0356151P.  
PR 14-FEB-2002; 2002US-0356152P.  
PR 14-FEB-2002; 2002US-0356154P.  
PR 14-FEB-2002; 2002US-0356156P.  
PR 14-FEB-2002; 2002US-0356157P.  
PR 14-FEB-2002; 2002US-0356161P.  
PR 14-FEB-2002; 2002US-0356162P.  
XX  
PA (NOVA-) NOVAVAX INC.  
XX  
PI Robinson RA, Thompson MW;  
XX  
DR WPI; 2003-679645/64.  
XX  
DR N-PSDB; ADA14301.  
XX  
PT Purifying a recombinant human papillomavirus (HPV) L1, useful for  
PT diagnosing, preventing or treating HPV infections, comprises clarifying,  
PT concentrating and dialyzing cells containing HPV particles.  
XX  
PS Disclosure; Page 103-104; 11pp; English.  
XX  
XX The present invention describes a method for purifying a recombinant  
XX extracellular or intracellular virus-like particle (VLP). The method  
XX comprises harvesting a cell suspension comprising cells containing a  
XX plurality of VLPs to produce a harvested supernatant, optionally  
XX disrupting the harvested cells to produce cell lysates containing the  
XX VLP, clarifying the harvested supernatant, concentrating the clarified  
XX supernatant, dialyzing the concentrated supernatant, and recovering  
XX the purified recombinant VLP. Also described: (1) a cell line designated

CC as sf-9s deposited as American Type Culture Collection (ATCC) PTA-4047;  
CC (2) producing the cell line described above; (3) host cells that express  
CC one or more recombinant gene products with an enhanced yield; (4)  
CC producing a foreign protein in an insect cell; (5) nucleic acid sequences  
CC that correspond to, and code for human papillomavirus (HPV) polypeptides;  
CC and (6) pharmaceutical compositions comprising an amount of the  
CC recombinant viral gene products, VLPs, agonists, antagonists, or the  
CC active fragment of a viral gene product. The VLPs have virucide activity,  
CC and can be used in vaccines and in gene therapy. The method is useful in  
CC isolating and purifying expressed viral gene products, including VLPs, in  
CC vitro. The gene products or particles may be used in detecting,  
CC preventing or treating HPV infections and associated symptoms like  
CC dysplasia. The present sequence represents an HPV-16 L2/E7/E2 fusion  
CC protein, which is given in the exemplification of the present invention.  
XX  
SQ Sequence 805 AA;

Query Match 99.2%; Score 513; DB 7; Length 805;  
Best Local Similarity 96.9%; Pred. No. 2.4e-56;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDTPTLHEHYMLDLOPETTDLYXXYQUNDSSSEDEIDGPAQAEPRRAHYNIVTFCK 60  
|||||  
DB 471 MHGDTPTLHEHYMLDLOPETTDLYGYEQUNDSSSEDEIDGPAQAEPRRAHYNIVTFCK 530  
|||||

OY 61 CDSTLRICVOSTHVDIRTLIEDLIMGTLGIYXPCISQKP 98  
|||||  
DB 531 CDSTLRICVOSTHVDIRTLIEDLIMGTLGIYXPCISQKP 568  
|||||

RESULT 10  
AAE38618  
ID AAE38618 standard; protein; 805 AA.  
XX  
AC AAE38618;  
XX  
DT 04-DEC-2003 (first entry)  
XX  
DE HPV-16 L2/E7/E2 fusion protein.  
XX  
XX Vaccine; humoral immunity; cell-mediated immunity; gene therapy; HPV;  
KM virucide; papillomavirus infection; Human papillomavirus; fusion protein.  
XX  
OS Human Papillomavirus.  
OS Synthetic.  
XX  
PN WO2003068163-A2.  
XX  
PD 21-AUG-2003.  
XX  
PF 14-FEB-2003; 2003WO-US004473.  
XX  
XX 14-FEB-2002; 2002US-0356113P.  
XX  
PR 14-FEB-2002; 2002US-0356118P.  
PR 14-FEB-2002; 2002US-0356119P.  
PR 14-FEB-2002; 2002US-0356123P.  
PR 14-FEB-2002; 2002US-0356126P.  
PR 14-FEB-2002; 2002US-0356133P.  
PR 14-FEB-2002; 2002US-0356135P.  
PR 14-FEB-2002; 2002US-0356150P.  
PR 14-FEB-2002; 2002US-0356151P.  
PR 14-FEB-2002; 2002US-0356152P.  
PR 14-FEB-2002; 2002US-0356154P.  
PR 14-FEB-2002; 2002US-0356156P.  
PR 14-FEB-2002; 2002US-0356157P.  
PR 14-FEB-2002; 2002US-0356161P.  
PR 14-FEB-2002; 2002US-0356162P.  
XX  
PA (NOVA-) NOVAVAX INC.  
XX  
PI Robinson RA, Cioce V;  
XX  
DR WPI; 2003-689598/65.

DR N-PSDB; AAD58574.  
 XX  
 XX New chimeric virus-like particles comprising a recombinant viral capsid  
 PT protein encapsulating a recombinant viral protein, useful for inducing  
 PT humoral and/or cell-mediated immunity against papillomavirus infection.  
 XX  
 PS Disclosure; Page 122-123; 126pp; English.  
 XX  
 XX The present invention relates to chimeric virus-like particle comprising  
 CC a recombinant viral capsid protein that encapsulates a recombinant viral  
 CC protein during self assembly into a chimeric virus-like particle and  
 CC exhibiting conformational antigenic epitopes capable of eliciting  
 CC neutralising antibodies. The vaccine comprising the chimeric virus-like  
 CC particles are useful for inducing immunity (humoral and/or cell-mediated  
 CC immunity) against papillomavirus infection. The invention is also useful  
 CC in gene therapy. The present sequence is HPV (human papillomavirus)-16  
 CC L2/E7/E2 fusion protein  
 XX  
 SQ Sequence 805 AA;  
 Query Match 99.2%; Score 513; DB 7; Length 805;  
 Best Local Similarity 96.9%; Pred. No. 2.4e-56;  
 Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 MGGDTPLHEHYMDLQPEETDLYXXQLNDSSEEDIDGPAGQAEPRAHYNIIVTFCK 60  
 DB 471 MGGDTPLHEHYMDLQPEETDLYGYEQLNDSSEEDIDGPAGQAEPRAHYNIIVTFCK 530  
 QY 61 CDSTLRLCVOSTHYDITLEDLMGTGIVXPCISQKP 98  
 DB 531 CDSTLRLCVOSTHYDITLEDLMGTGIVXPCISQKP 568  
 RESULT 11  
 AAR22767  
 ID AAR22767 standard; peptide; 98 AA.  
 XX  
 AC AAR22767;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 21-SEP-1992 (first entry)  
 XX  
 DE HPV E7 peptide.  
 XX  
 XX Human; papillomavirus; immunogenic; cervical; warts; carcinoma; cancer.  
 KW  
 XX Synthetic.  
 OS Homo sapiens.  
 XX  
 FN W09205248-A.  
 XX  
 PD 02-APR-1992.  
 XX  
 PF 26-SEP-1991; 91WO-US007081.  
 XX  
 PR 26-SEP-1990; 90US-00588384.  
 XX  
 PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
 XX  
 PI Thomas EK, Chen L, Blake J, Hellstrom K, Hellstrom I, Hu SL;  
 XX  
 DR WPI; 1992-132119/16.  
 XX  
 XX Immunogenic peptide(s) derived from E6 or E7 region of HPV16 - and  
 PT recombinant cells encoding them, useful in treatment and prophylaxis of  
 PT cervical warts or cancer resulting from HPV infection.  
 XX  
 PS Disclosure; Fig 7; 81pp; English.  
 XX  
 CC The peptide is the sequence of the human papillomavirus HPV 16 E7  
 CC nucleoprotein. Peptides corresponding to regions (pref. epitopic regions)  
 CC of HPV 16 E7 were synthesised by standard Merrifield synthesis. Examples  
 CC of such peptides are E7 1-10, 29-50 or 70-81. Compositions contg. these

CC peptides, antibodies against the peptides, or recombinant cells contg.  
 CC the gene encoding the immunogenic peptides may be utilised in methods for  
 CC inhibiting and treating HPV infection and tumour initiation and  
 CC progression e.g. in the prevention or retardation of cervical warts and  
 CC cervical carcinoma resulting from HPV infection. See also AAR22766.  
 CC (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to  
 CC correct PI field.)  
 XX  
 SQ Sequence 98 AA;  
 Query Match 99.0%; Score 512; DB 2; Length 98;  
 Best Local Similarity 96.9%; Pred. No. 2.2e-57;  
 Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 MGGDTPLHEHYMDLQPEETDLYXXQLNDSSEEDIDGPAGQAEPRAHYNIIVTFCK 60  
 DB 1 MGGDTPLHEHYMDLQPEETDLYCYEQLNDSSEEDIDGPAGQAEPRAHYNIIVTFCK 60  
 QY 61 CDSTLRLCVOSTHYDITLEDLMGTGIVXPCISQKP 98  
 DB 61 CDSTLRLCVOSTHYDITLEDLMGTGIVXPCISQKP 98  
 RESULT 12  
 AAR42361  
 ID AAR42361 standard; protein; 98 AA.  
 XX  
 AC AAR42361;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 21-MAY-1994 (first entry)  
 XX  
 XX Human papillomavirus 16 E7 protein and fragments.  
 DE  
 XX Tumours; cows; horses; donkeys; regression; udder warts; HPV16.  
 KW  
 XX Synthetic.  
 OS  
 XX W09320844-A1.  
 XX  
 PD 28-OCT-1993.  
 XX  
 PF 01-APR-1993; 93WO-GB000679.  
 XX  
 PR 08-APR-1992; 92GB-00007701.  
 XX  
 PA (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.  
 XX  
 PI Camp MS;  
 XX  
 DR WPI; 1993-351368/44.  
 XX  
 XX Use of papilloma-virus E7 protein or fragments for the therapy of  
 PT papilloma-virus disease - for the regression of tumours e.g. removal of  
 PT warts from udders or mouth of milking cows or for treatment of horses or  
 PT donkeys.  
 XX  
 PS Disclosure; Fig 2; 31pp; English.  
 XX  
 CC The sequence is that of the human papillomavirus type 16 E7 protein. The  
 CC protein sequence was aligned with that of bovine papillomavirus type 4.  
 CC See also AAR42360. (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 98 AA;  
 Query Match 99.0%; Score 512; DB 2; Length 98;  
 Best Local Similarity 96.9%; Pred. No. 2.2e-57;  
 Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 MGGDTPLHEHYMDLQPEETDLYXXQLNDSSEEDIDGPAGQAEPRAHYNIIVTFCK 60  
 DB 1 MGGDTPLHEHYMDLQPEETDLYCYEQLNDSSEEDIDGPAGQAEPRAHYNIIVTFCK 60

Qy 61 CDSTLRLCVOSTHVDIRLTEDLLMGTIGIVXPCISQKP 98  
 Db 61 CDSTLRLCVOSTHVDIRLTEDLLMGTIGIVPCISQKP 98

## RESULT 13

AAW46886  
 ID AAW46886 standard; protein; 98 AA.

XX AAW46886;

DT 25-MAR-2003 (revised)  
 DT 15-JUN-1998 (first entry)

XX Amino acid sequence of the HPV-16 E7 oncoprotein.

XX E7 oncoprotein; proliferative state; HPV; kinase activity;  
 KM cyclin/cyclin-dependent kinase; p21CIP1; interaction; inactivation;  
 KM cyclin/cyclin-dependent kinase inhibitor.

XX Human papillomavirus.

XX US5736318-A.

XX 07-APR-1998.

XX 17-MAR-1995; 95US-00406248.

XX 17-MAR-1995; 95US-00406248.

XX (HARD ) UNIV HARVARD.

XX (HARD ) HARVARD COLLEGE.

XX Muenger K, Jones DL;

XX WPI; 1998-239202/21.

XX N-PSDB; AAV16717.

PT Evaluation of proliferative state of cells transformed with human  
 PT papilloma virus - by determining cyclin-dependent kinase activity induced  
 PT by E7 onco-protein.

XX Disclosure; Col 19-20; 14pp; English.

XX The present sequence represents Human papillomavirus (HPV), strain 16, E7  
 CC oncoprotein. The proliferative state of a cell transformed with HPV can  
 CC be evaluated in the following manner. Cyclin/cyclin-dependent kinase  
 CC complexes containing protein p21CIP1 (AAW46887-88) are isolated from the  
 CC transformed cell, and the HPV E7 oncoprotein added to the isolated  
 CC protein. Cyclin/cyclin-dependent kinase complexes are isolated from an  
 CC untransformed cell that is substantially homologous with the transformed  
 CC cell, and the HPV E7 oncoprotein added. The kinase activities of the 2  
 CC samples are measured, where a proliferating transformed cell has a  
 CC greater kinase activity than the untransformed cell. The method is used  
 CC for determining the extent of interaction and/or inactivation between a  
 CC cyclin/cyclin-dependent kinase inhibitor and the HPV E7 oncoprotein and  
 CC thus evaluating the proliferative state of a transformed cell. (Updated  
 CC on 25-MAR-2003 to correct PI field.)

XX Sequence 98 AA;

Query Match 99.0%; Score 512; DB 2; Length 98;  
 Best Local Similarity 96.9%; Pred. No. 2.2e-57;  
 Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHMYMDLQPTTDLXXYXQUNDSSSEDEIDDPAGQAEPRRAHYNIYTFCK 60  
 Db 1 MHGDTPLHMYMDLQPTTDLXXYXQUNDSSSEDEIDDPAGQAEPRRAHYNIYTFCK 60

Qy 61 CDSTLRLCVOSTHVDIRLTEDLLMGTIGIVXPCISQKP 98  
 Db 61 CDSTLRLCVOSTHVDIRLTEDLLMGTIGIVPCISQKP 98

RESULT 14  
 ID AAY58474  
 XX AAY58474 standard; protein; 98 AA.

XX AAY58474;

DT 10-APR-2000 (first entry)

XX Human papillomavirus (HPV) E7 oncoprotein.

XX HPV E7 oncoprotein; proteasome activity; degradation; virus component;  
 KM viral infection; inflammatory disease; anti-inflammatory; anti-HIV;  
 KM virucide.

XX Human papillomavirus.

XX WO9966065-A2.

XX 23-DEC-1999.

XX 10-JUN-1999; 99WO-GB001840.

XX 13-JUN-1998; 98GB-00012756.

XX 13-JUN-1998; 98GB-00012757.

XX 13-JUN-1998; 98GB-00012758.

XX 13-JUN-1998; 98GB-00012759.

XX 13-JUN-1998; 98GB-00012760.

XX (BRID-) BRIDGEHEAD TECHNOLOGIES LTD.

XX Schmid H, Pelt F, Klotzel P, Jarrousse A, Gautier K, Badaoui S;  
 PI Mouzevar S, Nicolas P;

XX WPI; 2000-106109/09.

XX Novel assay methods for identifying compounds which modulate and/or  
 XX regulate proteasomal activity.

XX Disclosure; Page 8; 35pp; English.

XX The invention relates to a novel assay for identifying compounds which  
 CC inhibit viral replication and pathogenesis by increasing proteasomal  
 CC degradation of viral components or molecules induced by viral infection.  
 CC The method comprises reacting a compound with proteasomal protein (20S  
 CC proteasomes separately with or without 19S and 11S complexes), viral gene  
 CC product, and protein or peptide substrates; measuring protease activity;  
 CC and identifying the compound as an inhibitor if the protease activity of  
 CC the assay system is increased. The assays of the invention can be used to  
 CC identify compounds which inhibit viral replication and pathogenesis, and  
 CC modulate and/or regulate proteasome activity. Compounds which increase  
 CC proteasomal degradation of viral components or molecules induced by viral  
 CC infection are of value in the treatment of viral disease. Compounds which  
 CC modulate proteasomal nuclease activity have use in the treatment of  
 CC inflammatory disease, and AIDS in HIV infected patients. The methods may  
 CC also be used to generate resistance to bacterial or viral damage.  
 CC Sequences AAY58472-Y58474 represent examples of viral proteins which  
 CC affect proteasomal function

XX Sequence 98 AA;

Query Match 99.0%; Score 512; DB 3; Length 98;  
 Best Local Similarity 96.9%; Pred. No. 2.2e-57;  
 Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHMYMDLQPTTDLXXYXQUNDSSSEDEIDDPAGQAEPRRAHYNIYTFCK 60  
 Db 1 MHGDTPLHMYMDLQPTTDLXXYXQUNDSSSEDEIDDPAGQAEPRRAHYNIYTFCK 60

Qy 61 CDSTLRLCVOSTHVDIRLTEDLLMGTIGIVXPCISQKP 98  
 Db 61 CDSTLRLCVOSTHVDIRLTEDLLMGTIGIVPCISQKP 98

```
RESULT 15
AAV57721
ID AAV57721 standard; protein; 98 AA.
XX
AC AAV57721;
XX
DT 14-MAR-2000 (first entry)
XX
DE Human papillomavirus 16 E7 protein SEQ ID NO:4.
XX
KM Human papillomavirus; HPV; L1 fusion protein; vaccine; cytostatic;
KM viral capsomere; virucide; dermatological; malignant tumour formation;
KM cervical cancer; cervical intraepithelial neoplasia; genital wart;
KM condylomata acuminata.
XX
OS Human papillomavirus.
XX
CA2229955-A1.
XX
PD 20-AUG-1999.
XX
PF 20-FEB-1998; 98CA-02229955.
XX
PR 20-FEB-1998; 98CA-02229955.
XX
PA (MED1-) MEDIGENE GMBH.
XX
PI Burger A, Hallek M;
XX
DR WPI; 2000-063092/06.
XX
DR N-PSDB; AA248175.
XX
PT Fusion proteins comprising papillomavirus specific proteins useful for
PT vaccinating against malignant tumors of the anogenital tract such as
PT cervical carcinomas.
XX
XX Example 1; Page 34; 46pp; English.
XX
CC The present invention describes a fusion protein comprising 2 amino acids
CC sequences from 2 different papillomavirus specific (PVS) proteins. The
CC fusion protein may be administered for preventing and treating
CC papillomavirus infections in humans and animals. Papillomaviruses are
CC implicated in the pathology of malignant tumour formation in the
CC anogenital tract (of these tumours, cervical cancer is the most frequent
CC (500000 cases/year) and in the formation of precursor lesions of cervical
CC intraepithelial neoplasia (CIN). Papillomaviruses also cause benign
CC genital warts such as condylomata acuminata. However, the type and
CC severity of disease caused by the papillomavirus is dependent on the
CC strain causing the infection. The present sequence represents the human
CC papillomavirus 16 E7 protein
XX
SQ Sequence 98 AA;
XX
Query Match 99.0%; Score 512; DB 3; Length 98;
Best Local Similarity 96.9%; Pred. No. 2.2e-57;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 MHGDTPLHEHYMDLQPEETDLYXXYXQNDSSSEDEIDDPAGQAEPPRAHYNIVTFCK 60
Db 1 MHGDTPLHEHYMDLQPEETDLYCYEQNDSSSEDEIDDPAGQAEPPRAHYNIVTFCK 60
QY 61 CDSTLRLCVQSTHVDIRTLIEDLLMGTLGIYXPICQKP 98
Db 61 CDSTLRLCVQSTHVDIRTLIEDLLMGTLGIYXPICQKP 98
RESULT 16
AAB98421
ID AAB98421 standard; protein; 98 AA.
XX
AC AAB98421;
XX
```

```
DT 22-AUG-2001 (first entry)
XX
DE Human papillomavirus protein HPV16 E7.
XX
KM Human papillomavirus; human leukocyte antigen; HLA; immune response; HPV;
KM epitope; T cell; identification; vaccine; infection; genital wart;
KM neoplastic growth; antiviral.
XX
OS Human papillomavirus.
XX
WO20014179-A1.
XX
PD 14-JUN-2001.
XX
PF 11-DEC-2000; 2000MO-US033549.
XX
PR 10-DEC-1999; 99US-0172705P.
XX
PR 15-AUG-2000; 2000US-00641528.
XX
PA (EPIM-) EPIMMUNE INC.
XX
PI Sette A, Sidney J, Southwood S, Cheasnut R, Celis E, Grey HM;
XX
DR WPI; 2001-361497/40.
XX
PT An isolated human papilloma virus (HPV) epitope, useful in vaccines for
PT treating HPV infections.
XX
PS Disclosure; Page 21; 756pp; English.
XX
CC The present invention describes an isolated prepared human papillomavirus
CC (HPV) epitope (I). (I) has antiviral activity, and can be used in vaccine
CC production. Peptides and corresponding nucleic acid compositions from the
CC present invention are useful for stimulating an immune response to HPV by
CC stimulating the production of CTL or HTL responses, specifically in the
CC treatment or prophylaxis of HPV infection, in persons who have not
CC manifested symptoms e.g. genital warts or neoplastic growth. The peptides
CC can also be used in a tetramer staining assay to assess peripheral blood
CC mononuclear cells for the presence of antigen-specific CTLs following
CC exposure to a pathogen or immunogen, and as reagents to evaluate immune
CC recall responses or evaluate the efficacy of a vaccine. The vaccine
CC compositions are useful for removing warts or treating HPV infections.
CC The epitopes for inclusion in an epitope-base vaccine may be selected
CC from conserved regions of viral or tumour-associated antigens, which
CC reduces the likelihood of escape mutants, also immunosuppressive epitopes
CC that may be present in whole antigens can be avoided with the use of
CC epitope-base vaccines. An additional advantage is the ability to combine
CC selected epitopes (CTL and HTL) and to modify the composition of the
CC epitopes achieving enhanced immunogenicity, the major benefit of the
CC vaccine is that is safe and efficacious. AAB98391 to AAB98477 represent
CC polypeptide sequences used in the exemplification of the present
CC invention
XX
SQ Sequence 98 AA;
XX
Query Match 99.0%; Score 512; DB 4; Length 98;
Best Local Similarity 96.9%; Pred. No. 2.2e-57;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 MHGDTPLHEHYMDLQPEETDLYXXYXQNDSSSEDEIDDPAGQAEPPRAHYNIVTFCK 60
Db 1 MHGDTPLHEHYMDLQPEETDLYCYEQNDSSSEDEIDDPAGQAEPPRAHYNIVTFCK 60
QY 61 CDSTLRLCVQSTHVDIRTLIEDLLMGTLGIYXPICQKP 98
Db 61 CDSTLRLCVQSTHVDIRTLIEDLLMGTLGIYXPICQKP 98
RESULT 17
AAU01718
ID AAU01718 standard; protein; 98 AA.
XX
AC AAU01718;
XX
```

XX 29-AUG-2001 (first entry)  
DT Human papilloma virus-16 (HPV-16) E7 antigen.  
XX  
DE Mouse; granulocyte-macrophage-colony stimulating factor; GM-CSF;  
XX chimeric; heat shock protein; HSP; Flt-3 ligand; Flt-3 ligand A; E7A d11;  
XX antigenic; immunogenic; cytotoxic T cell response; tumour; vaccine;  
XX immunotherapy; HPV-16; E7 antigen.  
XX  
OS Human papillomavirus.  
XX  
PN WO200129233-A2.  
XX  
PD 26-APR-2001.  
XX  
PP 20-OCT-2000; 2000WO-US041422.  
XX  
XX 20-OCT-1999; 99US-00421608.  
PR 09-FEB-2000; 2000US-00501097.  
PR  
XX (UJJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.  
XX  
XX Wu T, Hung C;  
XX WPI; 2001-290921/30.  
DR N-PSDB; AAS02608.  
XX  
XX New chimeric polypeptide, useful as anti-tumor vaccines, comprises  
PT carboxy terminal fragment of heat shock protein, Flt-3 ligand or  
PT cytoplasmic translocation domain of Pseudomonas exotoxin A and antigenic  
PT polypeptide.  
XX  
PS Example 1; Page 39; 110pp; English.  
XX  
XX The sequence represents the amino acid sequence of human papilloma virus-  
CC 16 (HPV-16) E7 antigen used in construction of a chimeric polypeptide  
CC comprising: (a) a first polypeptide domain containing a carboxy terminal  
CC fragment of a heat shock protein (HSP), an Flt-3 ligand (FL), a  
CC cytoplasmic translocation domain of a Pseudomonas exotoxin A (E7A d11),  
CC or a granulocyte-macrophage colony stimulating factor (GM-CSF); and (b) a  
CC second polypeptide domain containing an antigenic polypeptide. A  
CC composition comprising the chimeric polypeptide is useful for inducing an  
CC immune response such as a cytotoxic T cell response. The nucleic acid or  
CC vector encoding the chimeric polypeptide present in the composition is  
CC administered as naked DNA by gene gun or equivalent, or by liposomal  
CC formulation. These are thus useful for vaccinating a mammal against  
CC infection by inducing an immune response to a pathogen. Preferably they  
CC are useful for vaccinating a mammal against a tumour antigen. The  
CC compositions and methods are useful for stimulating or enhancing the  
CC immunogenicity of a selected antigen or stimulating or enhancing a  
CC cellular immune response specific for that antigen. The chimeric nucleic  
CC acid molecules and vaccination methods, yield potent antigen-specific  
CC immunotherapy. The polynucleotides and DNA vaccines can induce a cellular  
CC immune response that is at least 40 fold more potent than conventional  
CC DNA vaccines. The vaccines are safe and useful for administration to  
CC domesticated or agricultural animals, as well as humans, and have low  
CC immunogenicity  
XX  
SQ Sequence 98 AA;  
Query Match 99.0%; Score 512; DB 4; Length 98;  
Best Local Similarity 96.9%; Pred. No. 2.2e-57;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

RESULT 18  
AAU72607  
ID AAU72607 standard; protein; 98 AA.  
XX  
XX AAU72607;  
AC  
XX 06-AUG-2003 (revised)  
DT 26-FEB-2002 (first entry)  
XX  
DE Human papilloma virus (HPV) E7 fragment.  
XX  
XX Human papillomavirus; HPV; E7; cyclin B; cyclin A; viruside;  
XX E7-induced cyclin-dependent kinase-2; CDK2 kinase; HPV infection;  
XX adenoviral infection; simian virus 40 infection; SV40.  
XX  
OS Human papillomavirus.  
XX  
PN US2001029022-A1.  
XX  
PD 11-OCT-2001.  
XX  
XX 01-DEC-2000; 2000US-00728466.  
PF  
XX 25-AUG-1999; 99US-00382616.  
PR 25-AUG-2000; 2000US-00648215.  
XX  
XX (FISH/) FISHER C.  
PA (HEMW/) HE W.  
XX  
XX Fisher C, He W;  
XX WPI; 2001-647983/74.  
DR  
XX  
XX Identifying E7-induced cyclin-dependent kinase-2 activity inhibitor,  
PT comprises identifying test compounds which reduce cyclin-dependent kinase  
PT 2 substrate phosphorylation in presence of human papillomavirus E7 or  
PT its fragment.  
XX  
XX Claim 1; Page 12-13; 21pp; English.  
XX  
XX The invention relates to identifying inhibitor of E7-induced cyclin-  
CC dependent kinase-2 (CDK2) kinase (I) activity, comprising measuring (1)  
CC activity on CDK2 substrate in the presence of human papillomavirus (HPV)  
CC E7 or its fragment, and in the presence and absence of test compound. The  
CC test compound is identified as inhibitor of E7-induced (I) activity when  
CC decreased phosphorylation of CDK2 substrate is detected. The method is  
CC used for identifying inhibitor of E7-induced CDK2 kinase activity. This  
CC method is useful for identifying an antiviral agent which involves  
CC identifying an inhibitor of E7-induced increase in CDK2 kinase activity,  
CC measuring viral proliferation in the presence and absence of identified  
CC inhibitor and identifying the inhibitor as an antiviral agent when  
CC decreased proliferation is detected in the presence of the inhibitor  
CC compared to viral proliferation in the absence of the inhibitor. The  
CC identified inhibitors are useful for reducing HPV E7-induced kinase  
CC activity or for ameliorating HPV proliferation by inhibiting E7-induced  
CC proliferation in a HPV infected cell by inhibiting E7-binding to CDK2  
CC kinase complex. The inhibitors identified by the above method are useful  
CC for produced medicament for ameliorating viral infection e.g. HPV  
CC infection, adenoviral infection or simian virus 40 (SV40) infection. The  
CC present sequence represents the amino acid sequence of HPV E7 fragment as  
CC described in the method of the invention. (Updated on 06-AUG-2003 to  
CC correct OS field.)  
XX  
SQ Sequence 98 AA;  
Query Match 99.0%; Score 512; DB 4; Length 98;  
Best Local Similarity 96.9%; Pred. No. 2.2e-57;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 61 CDSTLRLCVQSTHVDIRTELDLMGTLGIYXPICSQKP 98  
 DB 61 CDSTLRLCVQSTHVDIRTELDLMGTLGIYXPICSQKP 98

## RESULT 19

AA867546  
 ID AA867546 standard; peptide; 98 AA.

AC AA867546;

DT 11-SEP-2003 (revised)

DT 29-MAY-2001 (first entry)

DE Amino acid sequence of a E7 fragment that activates CDK2.

KM E7-induced CDK2 kinase; CDK2 substrate; papillomavirus; E7;

KW viral infection.

OS Cottoncail rabbit papillomavirus.

PN W0200114584-A2.

PD 01-MAR-2001.

PF 25-AUG-2000; 2000WO-US023487.

PR 25-AUG-1999; 99US-00382616.

PA (PHAA ) PHARMACIA & UPJOHN.

PI Fisher C, He W;

PS WPI; 2001-226622/23.

PT Identifying inhibitors of human papilloma virus E7 protein-induced

PT increase in CDK2 kinase activity for use as antiviral agent, by measuring

PT kinase activity on CDK2 substrate in presence of E7 protein, test

PS compound.

PS Claim 2; Page 40; 49pp; English.

CC The specification describes a method for identifying inhibitors of E7-

CC induced CDK2 kinase activity. The method comprises measuring CDK2 kinase

CC activity on a CDK2 substrate in presence of human papillomavirus (HPV) E7

CC (or fragment), in presence and absence of a test compound and measuring

CC phosphorylation of substrate. The method is useful for identifying an

CC inhibitor of E7-induced CDK2 kinase activity. The identified inhibitor is

CC useful for reducing or inhibiting HPV proliferation in an individual.

CC Inhibitors of E7 binding to the CDK2 complex are useful in preparing

CC adenoviral or SV40 infection. The present sequence represents a

CC papillomavirus E7 fragment, which is used in the method of the invention.

CC (updated on 11-SEP-2003 to standardise OS field)

CC

DB

QY

AA866332

ID AA866332 standard; protein; 98 AA.

AC AA866332;

DT 18-SEP-2001 (first entry)

DE HPV 16 E7 peptide fragment.

KM Fusion protein; VP22; E7; cell import signal; cell export signal;

KW antigen; immunization; infection-induced auto-immune disease;

KW tumor disease.

OS Human papillomavirus.

PN W0200151516-A2.

PD 19-JUL-2001.

PF 15-JAN-2001; 2001WO-DE000134.

PR 13-JAN-2000; 2000DE-01001230.

PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

PI Mueller M, Michel N, Osen W, Giesmann L, Zentgraf H;

PS WPI; 2001-442135/47.

PT Identifying inhibitors and activators of eukaryotic potassium channels,

PT for use as therapeutic agents, comprises using a transformed yeast cell

PT that does not express endogenous channels.

PS Disclosure; Fig 4; 23pp; German.

CC This invention describes a fusion protein comprising cell import and/or

CC export signal sequences and an antigen which is suitable for immunizing

CC an individual against a disease, together with a DNA that codes for said

CC protein. The invention also relates to the use of the protein (II) and

CC its encoding DNA (I) for immunizing an individual against disease. In

CC particular against infection-induced auto-immune and tumor disease. This

CC sequence represents a fragment of the human papillomavirus E7 protein

CC used in the preparation of the fusion constructs described in the method

CC of the invention

CC

DB

QY

AAU77713

AAU77713 standard; protein; 98 AA.

AC AAU77713;

DT 05-JUN-2002 (first entry)

DE Human papillomavirus 16 (HPV16), E7 protein.

KW Calreticulin; CRT; endoplasmic reticulum chaperone polypeptide;

KW cytosolic; vaccine; human papillomavirus 16; HPV 16; E7; DNA vaccine;

KW enhanced antigen-specific immune response; cytotoxic T lymphocyte;

KW tumour; cancer; cervical cancer.

```

XX OS Human papillomavirus type 16.
XX PN WO200212281-A2.
XX PD 14-FEB-2002.
XX PF 02-AUG-2001; 2001WO-US024134.
XX PR 03-AUG-2000; 2000US-0222902P.
XX PA (UYJO ) UNIV JOHNS HOPKINS.
XX PI Wu T, Hung C;
XX DR WPI; 2002-257463/30.
XX PT New nucleic acids encoding a fusion polypeptide comprising an endoplasmic
XX PT reticulum chaperone polypeptide linked to an antigenic polypeptide,
XX PT useful as a vaccine for inducing antigen-specific immune responses.
XX PS Example 1; Page 32; 71pp; English.
XX CC The invention describes a nucleic acid molecule (I) encoding a fusion
XX CC polypeptide comprising a first polypeptide domain comprising an
XX CC endoplasmic reticulum chaperone polypeptide e.g. calreticulin (CRT) and a
XX CC second polypeptide domain comprising at least one antigenic peptide e.g.
XX CC Human papillomavirus 16 (HPV 16) E7. The nucleic acid is useful as a
XX CC vaccine (DNA vaccine) for inducing enhanced antigen-specific immune
XX CC responses, particularly those mediated by cytotoxic T lymphocytes. The
XX CC nucleic acid and compositions comprising the nucleic acid is also useful
XX CC for inhibiting the growth of tumours and cancers e.g. cervical cancer.
XX CC This is the amino acid sequence of the human papillomavirus type 16 (HPV
XX CC 16) early gene 7 (E7) used in the creation of a DNA vaccine
XX SQ Sequence 98 AA;
XX Query Match 99.0%; Score 512; DB 5; Length 98;
XX Best Local Similarity 96.9%; Pred. No. 2.2e-57;
XX Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 MGGDPTLHEXYMDLQPETTDLYXXYXQINDSSEDEIDGPAQAEPDRAHYNIIVTFCK 60
DB 1 MGGDPTLHEXYMDLQPETTDLYCCEQLNDSSEDEIDGPAQAEPDRAHYNIIVTFCK 60
QY 61 CDSTLRLCVOSTHVDIRLTEDLLMGTLGIVPICSQRP 98
DB 61 CDSTLRLCVOSTHVDIRLTEDLLMGTLGIVPICSQRP 98
RESULT 22
AAU10810
ID AAU10810 standard; protein; 98 AA.
XX AC AAU10810;
XX XX
XX DT 29-AUG-2003 (revised)
XX DT 14-FEB-2002 (first entry)
XX DE Human papillomavirus (HPV) 16, E7 coding region.
XX XX
XX XX Human papillomavirus 16; HPV 16; cancer; squamous cell carcinoma;
XX KM adenocarcinoma; kolloidcytosis; hyperkeratosis; intraepithelial neoplasia;
XX KM intraepithelial lesion; dysplasia; head cancer; neck cancer;
XX KM small cell lung cancer; melanoma; oncogene.
XX XX
XX OS Human papillomavirus type 16.
XX XX
XX FH Key Location/Qualifiers
XX FT 6..35
XX FT Peptide /label= E7_peptide_epitope_1
XX FT /note= "This region is specifically referred to in claim
XX FT 2"

```

```

FT FT Peptide 60..80
FT FT /label= E7_peptide_epitope_2
FT FT /note= "This region is specifically referred to in claim
FT FT 2"
XX XX WO200177142-A1.
XX XX 18-OCT-2001.
XX PD 05-APR-2001; 2001WO-US011233.
XX PF 05-APR-2001; 2001WO-US011233.
XX PR 05-APR-2000; 2000US-0194796P.
XX PA (IMPA-) IMPACT DIAGNOSTICS INC.
XX XX
XX PI Hu YX;
XX PT WPI; 2002-010888/01.
XX DR
XX XX The invention describes a novel peptide derived from the E2, E6 or E7
XX XX early coding region of human papillomavirus (HPV) 16 and 18, which is
XX XX soluble in aqueous solution and has a lysine or cysteine residue near the
XX XX amino terminus, very few tryptophan, methionine and cysteine residues,
XX XX and/or many glycine and asparagine residues. The peptides and diagnostic
XX XX method are used to diagnose HPV infection, especially infection with
XX XX oncogenic HPV by using peptides derived from the E2 region, since HPV 16
XX XX and 18 are the main HPV genetic types associated with cancers, and
XX XX presence of antibodies to E2 protein is known to provide evidence of HPV
XX XX infection. They are also useful to diagnose HPV associated malignancy or
XX XX premalignancy, especially carcinoma by using peptides derived from the E6
XX XX or E7 regions, since E6 and E7 are thought to be tumour-specific
XX XX antigens. The peptides and diagnostic method are especially useful to
XX XX diagnose cervical carcinoma (e.g. adenocarcinoma of the uterine cervix)
XX XX and any HPV associated epithelial cell abnormality including high grade
XX XX dysplasias, kolloidcytosis, hyperkeratosis, precancerous conditions
XX XX encompassing intraepithelial neoplasias or intraepithelial lesions, and
XX XX invasive or malignant cancers. They are also used to detect head and neck
XX XX cancers, small cell lung cancers, penai and anal squamous cell carcinomas
XX XX and melanoma. This is the amino acid sequence of the E7 early coding
XX XX region of HPV 16, an oncoprotein that destabilises cell cycle control
XX XX through its interaction with the cyclin-dependent kinase inhibitor
XX XX protein, p21, described in the method of the invention. (Updated on 29-
XX XX AUG-2003 to standardise OS field)
XX SQ Sequence 98 AA;
XX Query Match 99.0%; Score 512; DB 5; Length 98;
XX Best Local Similarity 96.9%; Pred. No. 2.2e-57;
XX Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 MGGDPTLHEXYMDLQPETTDLYXXYXQINDSSEDEIDGPAQAEPDRAHYNIIVTFCK 60
DB 1 MGGDPTLHEXYMDLQPETTDLYCCEQLNDSSEDEIDGPAQAEPDRAHYNIIVTFCK 60
QY 61 CDSTLRLCVOSTHVDIRLTEDLLMGTLGIVPICSQRP 98
DB 61 CDSTLRLCVOSTHVDIRLTEDLLMGTLGIVPICSQRP 98
RESULT 23
ABB82375
ID ABB82375 standard; protein; 98 AA.
XX AC ABB82375;
XX XX
XX DT 08-JAN-2003 (first entry)
XX FT

```

DE Wild-type HPV-E7 protein sequence.  
 XX Immunogenicity; cytostatic; virucide; protozoacide; antibacterial; CTL;  
 KW hepatocarcinogenic; anti-HIV; vaccine. cytotoxic T lymphocyte; tumour; HPV;  
 KM E7 protein.  
 XX  
 OS Human papillomavirus.  
 PN WO200274920-A2.  
 XX  
 PD 26-SEP-2002.  
 XX  
 PF 18-MAR-2002; 2002WO-US008033.  
 XX  
 PR 16-MAR-2001; 2001US-0276854P.  
 XX  
 PA (UWJO ) UNIV JOHNS HOPKINS.  
 XX  
 PI Wu T, Hung C;  
 DR WPI; 2002-740856/80.  
 XX  
 PT New nucleic acid molecule encoding an antigenic fusion polypeptide useful  
 PT as vaccines for enhancing or inducing immune responses, primarily  
 PT cytotoxic T lymphocytes (CTL) responses to specific antigens such as  
 PT tumor or viral antigens.  
 PS Disclosure; Page 19; 93pp; English.  
 XX  
 CC The invention relates to a nucleic acid molecule that encodes a fusion  
 CC polypeptide, comprising a first nucleic acid sequence encoding a fusion  
 CC polypeptide that comprises at least one immunogenically-potentiating  
 CC polypeptide, optionally, fused in frame with the nucleic acid, a linker  
 CC nucleic acid encoding a linker peptide, and a nucleic acid that is linked  
 CC in frame to them, and that encodes an antigenic peptide or polypeptide.  
 CC The nucleic acid molecule, polypeptides and vectors are useful as  
 CC vaccines for enhancing immune responses, primarily cytotoxic T  
 CC lymphocytes (CTL) responses to specific antigens such as tumour or viral  
 CC antigens, and for inhibiting growth or preventing re-growth of a tumour.  
 CC The packaging cell line is useful for generating alphavirus replicon  
 CC particles without contamination from replicon-competent virus. The  
 CC pathogenic organisms include viruses such as human papilloma virus (HPV),  
 CC hepatitis B virus, hepatitis C virus, human immunodeficiency virus,  
 CC Epstein Barr virus and herpes simplex virus, intracellular parasites such  
 CC as malaria, and bacteria that grow intracellularly such as mycobacteria  
 CC and listeria. The present sequence represents a wild-type HPV E-7 protein  
 XX  
 SQ Sequence 98 AA;  
 Query Match 99.0%; Score 512; DB 5; Length 98;  
 Best Local Similarity 96.9%; Pred. No. 2.2e-57;  
 Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 MHGDPPLHHEMYMDLPBETTDLYXXYXOLNDSSEDEIDGPAGQAEPPRAHYNIVTFCCK 60  
 DB 1 MHGDPPLHHEMYMDLPBETTDLYCYEQLNDSSEDEIDGPAGQAEPPRAHYNIVTFCCK 60  
 QY 61 CDSTLRLCVOSTHVDIRTLBDMGTGIVXPICSQRP 98  
 DB 61 CDSTLRLCVOSTHVDIRTLBDMGTGIVXPICSQRP 98  
 RESULT 24  
 ID AAO16630 standard; protein; 98 AA.  
 AC AAO16630;  
 DT 15-MAY-2003 (first entry)  
 XX Human papillomavirus E7 antigen.  
 DE Human papillomavirus E7 antigen.  
 XX Epitope; E7 antigen; CD4-positive T cell activation;

KW uterine cancer lesion.  
 XX  
 OS Human papillomavirus type 16.  
 XX  
 PN WO2002100889-A1.  
 XX  
 PD 19-DEC-2002.  
 XX  
 PF 10-JUN-2002; 2002WO-JP005747.  
 XX  
 PR 08-JUN-2001; 2001JP-00173803.  
 XX  
 PA (KIRI ) KIRIN BEER KK.  
 XX  
 PI Maeda H, Okubo M;  
 DR WPI; 2003-156946/15.  
 XX  
 PT Novel epitope of human papilloma virus E7 antigen capable of activating  
 PT CD4-positive T cells specific to (pre-)uterine cancer lesion, applicable  
 PT in drug compositions for preventing and treating uterine cancer.  
 PS Disclosure; Page 34; 40pp; Japanese.  
 XX  
 CC The invention comprises an epitope of the human papillomavirus E7 antigen  
 CC that is capable of activating CD4-positive T cells that are specific to  
 CC uterine cancer lesions. The epitope of the invention is useful for  
 CC preventing and treating uterine cancer. The present amino acid sequence  
 CC represents the human papillomavirus E7 antigen  
 XX  
 SQ Sequence 98 AA;  
 Query Match 99.0%; Score 512; DB 6; Length 98;  
 Best Local Similarity 96.9%; Pred. No. 2.2e-57;  
 Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 MHGDPPLHHEMYMDLPBETTDLYXXYXOLNDSSEDEIDGPAGQAEPPRAHYNIVTFCCK 60  
 DB 1 MHGDPPLHHEMYMDLPBETTDLYCYEQLNDSSEDEIDGPAGQAEPPRAHYNIVTFCCK 60  
 QY 61 CDSTLRLCVOSTHVDIRTLBDMGTGIVXPICSQRP 98  
 DB 61 CDSTLRLCVOSTHVDIRTLBDMGTGIVXPICSQRP 98  
 RESULT 25  
 ID ADF09516 standard; protein; 98 AA.  
 AC ADF09516;  
 DT 12-FEB-2004 (first entry)  
 XX Human papillomavirus 16 E7 SEQ ID NO:17.  
 DE Human papillomavirus 16 E7 SEQ ID NO:17.  
 XX  
 KW human, protein-protein interaction; virucide; cytostatic; vaccine;  
 KM human papilloma virus; HPV; cancer.  
 XX  
 OS Human papillomavirus.  
 PN WO2003066940-A2.  
 XX  
 PD 21-AUG-2003.  
 XX  
 PF 14-FEB-2003; 2003WO-US004594.  
 XX  
 PR 14-FEB-2002; 2002US-0356911P.  
 XX  
 PA (CURA-) CURAGEN CORP.  
 PA (HOFF ) HOFFMANN LA ROCHE INC.  
 XX  
 PI Jackson A, Ooi CE, Lewin DA, Cuthill S;

DR WPI: 2003-689668/65.  
DR N-PSDB; ADF09608.  
XX  
PT New purified complex comprising a first polypeptide and a second  
PT polypeptide, useful for identifying agents for treating/preventing a  
PT condition involving altered level of the complex e.g. human papilloma  
PT virus infection, or cancer.  
XX  
PS Example 3; SEQ ID NO 17, 156pp; English.  
XX  
CC The invention relates to a novel purified complex comprising a first  
CC polypeptide and a second polypeptide, where the polypeptides comprise  
CC defined amino acid sequences listed in the specification, and where the  
CC first polypeptide binds to the second polypeptide. A complex of the  
CC invention has virucide and cyrostatic activity, and may have a use as a  
CC vaccine. The complex is useful for identifying agents for treating or  
CC preventing a conditions involving altered level of the complex, e.g.  
CC human papilloma virus (HPV) infection, or cancer. The compositions,  
CC antibodies, vectors and methods are useful for treating such diseases.  
CC The sequences shown in ADF09500-ADF09583 represent proteins of the  
CC invention.  
XX  
SQ Sequence 98 AA;  
Query Match 99.0%; Score 512; DB 7; Length 98;  
Best Local Similarity 96.9%; Pred. No. 2.2e-57;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 MHGDTPTLHEYMLDLPETTDLYXXQLNDSSEEDSIDGPAQAEPDRAHNYITFCCK 60  
DB 1 MHGDTPTLHEYMLDLPETTDLYCYEQLNDSSEEDSIDGPAQAEPDRAHNYITFCCK 60  
QY 61 CDSTRLCVOSTHVDIRLTEDLLMGTIGIVXPCISQKP 98  
DB 61 CDSTRLCVOSTHVDIRLTEDLLMGTIGIVCPCISQKP 98  
RESULT 26  
ADFI8632  
ID ADFI8632 standard; protein; 98 AA.  
XX  
AC ADFI8632;  
XX  
DT 12-FEB-2004 (first entry)  
XX  
DE Human papilloma virus E7 oncoprotein.  
XX  
KW HPV; oncoprotein E7; cytoslatic; gene therapy; kinase; enzyme.  
XX  
OS Human papillomavirus.  
XX  
PN WO2003088922-A2.  
XX  
PD 30-OCT-2003.  
XX  
PF 21-APR-2003; 2003WO-US012667.  
XX  
PR 19-APR-2002; 2002US-0374245P.  
XX  
PA (UYRP ) UNIV ROCHESTER.  
XX  
PI Mccance D, Westbrook TF;  
XX  
DR WPI: 2003-845498/78.  
DR N-PSDB; ADFI8633; ADFI8634.  
XX  
PT Identifying a compound that inhibits E7 cellular proliferation activity  
PT by administering a compound to a system, where the system maintains Akt  
PT activity and selecting a compound that decreases the amount of Akt  
PT activity.  
XX  
PS Disclosure; SEQ ID NO 8; 119pp; English.

CC The present sequence is the protein sequence of human papillomavirus E7  
CC oncoprotein. E7 promotes oncogenesis through an inhibition of p21cip1  
CC transport into the nucleus. E7 abrogates Raf-associated arrest and  
CC prevents inhibition of cyclin E-CDK2 activity without disrupting Raf  
CC induction of p21cip1. E7 neither interacts with p21cip1 nor derepresses  
CC p21cip1-associated CDK2 activity, but instead reduces the association  
CC between p21cip1 and cyclin E-CDK2 complexes. Raf down-regulates steady-  
CC state levels of Akt, a regulator of p21cip1 localisation, leading to loss  
CC of p21cip1 phosphorylation and accumulation of p21cip1. E7 disrupts the  
CC effects of Raf on Akt activity and prevents p21cip1 nuclear accumulation.  
CC Maintenance of Akt activity is necessary and sufficient to bypass Raf  
CC arrest. The invention provides methods for identifying and using  
CC inhibitors of E7 cell proliferation activity, and for identifying and  
CC using compounds capable of promoting the nuclear localisation of p21cip1.  
CC The methods can be used to inhibit aberrant cellular proliferation for  
CC treatment of cancer.  
XX  
SQ Sequence 98 AA;  
Query Match 99.0%; Score 512; DB 7; Length 98;  
Best Local Similarity 96.9%; Pred. No. 2.2e-57;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 MHGDTPTLHEYMLDLPETTDLYXXQLNDSSEEDSIDGPAQAEPDRAHNYITFCCK 60  
DB 1 MHGDTPTLHEYMLDLPETTDLYCYEQLNDSSEEDSIDGPAQAEPDRAHNYITFCCK 60  
QY 61 CDSTRLCVOSTHVDIRLTEDLLMGTIGIVXPCISQKP 98  
DB 61 CDSTRLCVOSTHVDIRLTEDLLMGTIGIVCPCISQKP 98  
RESULT 27  
ADL90076  
ID ADL90076 standard; protein; 98 AA.  
XX  
AC ADL90076;  
XX  
DT 17-JUN-2004 (first entry)  
XX  
DE Human papillomavirus 16-E7 protein, SEQ ID 16.  
XX  
KW Immune response; immunoglobulin; Ig; E7.  
XX  
OS Human papillomavirus.  
XX  
PN WO2004027049-A2.  
XX  
PD 01-APR-2004.  
XX  
PF 18-SEP-2003; 2003WO-US030188.  
XX  
PR 20-SEP-2002; 2002US-0412219P.  
XX  
PR 14-MAR-2003; 2003WO-US007995.  
XX  
PA (ASTRAL-) ASTRAL INC.  
XX  
PI Bot A, Wang L, Smith D, Phillips B;  
XX  
DR WPI: 2004-295415/27.  
XX  
PT Generating an immune response to an antigen, useful for generating  
PT desired T cell responses comprises administering an immunoglobulin having  
PT one peptide epitope of the antigen attached to the immunoglobulin.  
XX  
PS Disclosure; Fig 1G; 154pp; English.  
XX  
CC The present invention relates to a method for generating an immune  
CC response to an antigen in a patient. The method comprises administering  
CC to the patient an immunoglobulin (Ig) or its portion where the Ig has at  
CC least one peptide epitope of the antigen attached to the Ig or its  
CC portion and administering the immunoglobulin or its portion in  
CC conjunction with a RNA segment. The present sequence is an antigen

CC sequence, used to illustrate the invention.

XX Sequence 98 AA;

Query Match 99.0%; Score 512; DB 8; Length 98;  
Best Local Similarity 96.9%; Pred. No. 2.2e-57;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGGDTPTLHEHYMLDLOPETTDLYXXYXQLNDSSEEDIDBPAGQAEPRRAHYNIIVTFCK 60  
DB 1 MGGDTPTLHEHYMLDLOPETTDLYCYEQNDSSSEEDIDBPAGQAEPRRAHYNIIVTFCK 60  
QY 61 CDSTLRLCVQSTHVDIRTLTDLMTGLGIYXPCISQKP 98  
DB 61 CDSTLRLCVQSTHVDIRTLTDLMTGLGIYXPCISQKP 98

# RESULT 28

ID ADM32916 standard; protein; 98 AA.

AC ADM32916;

DT 17-JUN-2004 (first entry)

DE Amino acid sequence of HPV16 E7 protein.

XX synonymous codon; translation efficiency; HPV16; E7 protein.

XX Human papillomavirus type 16.

XX W02004024915-A1.

XX 25-MAR-2004.

PF 15-SEP-2003; 2003WO-AU001200.

PR 13-SEP-2002; 2002US-0410410P.

PA (UYQU ) UNIV QUEENSLAND.

PI Frazer IH;

XX WPI; 2004-270043/25.

DR N-PSDB; ADM32915, ADM32917.

PT Constructing a synthetic polynucleotide, useful for producing a polypeptide at a higher level in a Chinese Hamster Ovary cell, comprises selecting a first codon of the parent polynucleotide for replacement with a synonymous codon.

XX Example 2; Fig 2; 82pp; English.

XX The specification describes a method for constructing a synthetic polynucleotide from which a polypeptide is producible at a different level in a Chinese Hamster Ovary (CHO) cell compared to when using a parent polynucleotide encoding the same polypeptide. The method comprises selecting a first codon of the parent polynucleotide for replacement with a synonymous codon, where the synonymous codon is selected on the basis that it exhibits a different translational efficiency in the CHO cell than the first codon in a comparison of translational efficiencies of codons in test CHO cells. The method is useful for constructing synthetic polynucleotides which are translated more efficiently, compared to the parent polynucleotide. The present sequence represents Human papillomavirus type 16 (HPV16) E7 protein. The E7 polynucleotide was codon-modified, to demonstrate the method of the invention.

XX Sequence 98 AA;

Query Match 99.0%; Score 512; DB 8; Length 98;  
Best Local Similarity 96.9%; Pred. No. 2.2e-57;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGGDTPTLHEHYMLDLOPETTDLYXXYXQLNDSSEEDIDBPAGQAEPRRAHYNIIVTFCK 60  
DB 1 MGGDTPTLHEHYMLDLOPETTDLYCYEQNDSSSEEDIDBPAGQAEPRRAHYNIIVTFCK 60

QY 61 CDSTLRLCVQSTHVDIRTLTDLMTGLGIYXPCISQKP 98  
DB 61 CDSTLRLCVQSTHVDIRTLTDLMTGLGIYXPCISQKP 98

# RESULT 29

ID ADO44073 standard; protein; 98 AA.

AC ADO44073;

DT 15-JUL-2004 (first entry)

DE Amino acid sequence of a wild type HPV16 E7 protein.

XX E6 protein; E7 protein; fusion protein; HPV16; HPV-associated cancer; cervical cancer; immune response; lower gastrointestinal tract cancer; anal cancer; reproductive system cancer; penile cancer; vulvar cancer.

XX Human papillomavirus type 16.

XX Synthetic.

XX W02004030636-A2.

PF 02-OCT-2003; 2003WO-US031726.

PR 03-OCT-2002; 2002US-0415929P.

PA (AMHP ) WYETH HOLDINGS CORP.

PI Smith L, Cassetti MC;

XX WPI; 2004-316328/29.

PT New polypeptide comprising human papillomavirus E6 and E7 polypeptides, useful for treating or preventing human papillomavirus (HPV)-associated cancers, e.g. cervical cancer.

XX Claim 1; Page 77; 101pp; English.

XX The present sequence represents a wild type E7 protein from human papillomavirus type 16 (HPV16), which is used to produce fusion proteins of the invention. The specification describes human papillomavirus E6 and E7 polypeptides, where the E7 polypeptide has mutations at any one or more of the amino acids corresponding to amino acids 24, 26 or 91 of the sequence given in ADO44073 and the E6 polypeptide has no mutations or has mutations at any one or more of the amino acids corresponding to amino acids 63 or 106 of the sequence given in ADO44072. The polypeptides of the invention are useful for treating or preventing human papillomavirus (HPV)-associated cancers, such as cervical cancer. The fusion proteins and nucleic acids encoding the fusion proteins are useful for generating immune responses against HPV. They are also useful for treating lower gastrointestinal tract cancers, e.g. anal cancer, and other cancers of the reproductive system, including penile and vulvar cancer.

XX Sequence 98 AA;

Query Match 99.0%; Score 512; DB 8; Length 98;  
Best Local Similarity 96.9%; Pred. No. 2.2e-57;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGGDTPTLHEHYMLDLOPETTDLYXXYXQLNDSSEEDIDBPAGQAEPRRAHYNIIVTFCK 60  
DB 1 MGGDTPTLHEHYMLDLOPETTDLYCYEQNDSSSEEDIDBPAGQAEPRRAHYNIIVTFCK 60  
QY 61 CDSTLRLCVQSTHVDIRTLTDLMTGLGIYXPCISQKP 98

Dh 61 CDSTLRLCVQSTHVDIRTELDLMLGTLGIVCPICSQKP 98

RESULT 30

ADN49005  
ID ADN49005 standard; protein; 98 AA.  
XX  
AC ADN49005;  
XX  
DT 15-JUL-2004 (first entry)  
XX  
DE Human papilloma virus (HPV) strain HPV16 E7 protein.  
XX  
KM Papilloma-virus specific protein; PVS; vaccine; infection;  
KM human papilloma virus; HPV; E7.  
XX  
OS Human papillomavirus.  
XX  
PN US2004081661-A1.  
XX  
PD 29-APR-2004.  
XX  
PP 04-SEP-2003; 2003US-00654129.  
XX  
PR 20-FEB-1998; 98US-00026896.  
PR 06-APR-1999; 99US-00284017.  
XX  
PA (MEDI-) MEDIGENE AG.  
XX  
PI Halilek M, Burger A;  
XX  
DR WPI; 2004-340126/31.  
DR N-PSDB; ADN49004.  
XX

PT New fusion proteins comprising an amino acid sequence from a first and a  
PT second papilloma-virus specific protein, useful in vaccines for treating  
PT or preventing a papilloma virus infection in an animal, particularly  
PT humans.  
XX  
XX  
PS Disclosure; SEQ ID NO 4; 20pp; English.  
XX  
CC The invention relates to papilloma-virus specific (PVS) protein and  
CC fusion protein constructs. The invention also relates to vaccine  
CC formulations comprising viral capsomeres and methods for their  
CC production. The fusion protein is useful for treating or preventing a  
CC papilloma virus infection in an animal, particularly humans and is also  
CC useful in the production of vaccines. The present sequence is human  
CC papilloma virus (HPV) strain HPV16 E7 protein.  
XX  
XX  
SQ Sequence 98 AA;

Query Match 99.0%; Score 512; DB 8; Length 98;  
Best Local Similarity 96.9%; Pred. No. 2.2e-57;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPTLHEMYLDLQPEPTDLYXXYXQLNDSSEEDIEDGPAQAEPPRAHYNIVTFCK 60  
Dh 1 MHGDTPTLHEMYLDLQPEPTDLYCYEQNLNDSSEEDIEDGPAQAEPPRAHYNIVTFCK 60

Qy 61 CDSTLRLCVQSTHVDIRTELDLMLGTLGIVCPICSQKP 98  
Dh 61 CDSTLRLCVQSTHVDIRTELDLMLGTLGIVCPICSQKP 98

RESULT 31

ADU66362  
ID ADU66362 standard; protein; 98 AA.  
XX  
AC ADU66362;  
XX  
DT 10-FEB-2005 (first entry)  
XX  
DE Human papillomavirus type 16 (HPV16) E7 protein - SEQ ID 3.

XX vaccine; MHC class I pathway; antigen specific immune response; tumor;  
KM E7 protein; E6 protein.  
XX  
OS Human papillomavirus type 16.  
XX  
PN WO2004098526-A2.  
XX  
PD 18-NOV-2004.  
XX  
PP 05-MAY-2004; 2004WO-US013756.  
XX  
PR 05-MAY-2003; 2003US-0467602P.  
XX  
PA (UYJO ) UNIV JOHNS HOPKINS.  
XX  
PI Wu T, Hung CF;  
XX  
DR WPI; 2004-813972/80.  
XX

PT New nucleic acid molecules encoding a fusion polypeptide comprising an  
PT antigen, a signal peptide, and a heat shock protein, useful as a vaccine  
PT for inducing or enhancing immune response or for inhibiting or preventing  
PT tumor growth.  
XX  
XX  
PS Disclosure; SEQ ID NO 3; 67pp; English.  
XX  
CC The invention comprises a nucleic acid molecule (DNA vaccine) that  
CC encodes a fusion polypeptide which is useful as a vaccine composition.  
CC The nucleic acid of the invention contains: a first nucleic acid encoding  
CC a polypeptide that promotes processing via the MHC class I pathway; a  
CC second sequence encoding a signal peptide; and a third sequence encoding  
CC an antigenic polypeptide. The DNA vaccine of the invention is useful for  
CC inducing or enhancing an antigen specific immune response, or to inhibit  
CC growth or prevent re-growth of a tumor expressing Human papillomavirus  
CC (HPV) E7 or E6 protein. The present amino acid sequence represents a  
CC human papillomavirus type 16 (HPV16) E7 protein.  
XX  
XX  
SQ Sequence 98 AA;

Query Match 99.0%; Score 512; DB 8; Length 98;  
Best Local Similarity 96.9%; Pred. No. 2.2e-57;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPTLHEMYLDLQPEPTDLYXXYXQLNDSSEEDIEDGPAQAEPPRAHYNIVTFCK 60  
Dh 1 MHGDTPTLHEMYLDLQPEPTDLYCYEQNLNDSSEEDIEDGPAQAEPPRAHYNIVTFCK 60

Qy 61 CDSTLRLCVQSTHVDIRTELDLMLGTLGIVCPICSQKP 98  
Dh 61 CDSTLRLCVQSTHVDIRTELDLMLGTLGIVCPICSQKP 98

RESULT 32

ADX15532  
ID ADX15532 standard; protein; 98 AA.  
XX  
AC ADX15532;  
XX  
DT 21-APR-2005 (first entry)  
XX  
DE Human papillomavirus E7 fragment, SEQ ID NO: 1.  
XX  
XX High throughput screening; pharmaceutical; antiviral.  
XX  
OS Human papillomavirus.  
XX  
PN US2005032038-A1.  
XX  
PD 10-FEB-2005.  
XX  
PP 08-SEP-2003; 2003US-00657399.  
XX

PR 25-AUG-1999; 99US-00382616.  
 PR 01-DEC-2000; 2000US-00728466.  
 XX  
 XX (FISH/) FISHER C.  
 PA (HEMW/) HE W.  
 XX  
 PI Fisher C, He W;  
 XX WPI, 2005-151661/16.  
 DR  
 XX Ameliorating human papillomavirus proliferation involves administering  
 PT inhibitor of E7-induced cyclin-dependent kinases 2 phosphorylation or  
 PT inhibitor of E7-binding cyclin-dependent kinases 2 kinase complex that  
 PT reduces kinase activity.  
 XX  
 PS Disclosure; SEQ ID NO 1; 20pp; English.  
 CC The present invention relates to a method of ameliorating human papilloma  
 CC virus (HPV) proliferation. The method involves administering an inhibitor  
 CC of E7-induced cyclin-dependent kinases (CDK2) phosphorylation or an  
 CC inhibitor of E7-binding CDK2 kinase complex that reduces HPV E7-induced  
 CC CDK2 kinase activity. The present sequence is the human papillomavirus E7  
 CC fragment.  
 XX  
 SQ Sequence 98 AA;  
 Query Match 99.0%; Score 512; DB 9; Length 98;  
 Best Local Similarity 96.9%; Pred. No. 2.2e-57;  
 Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 MHGDTPTLHEHYMDLOPETTDLYXXQINDSSEEDIDGPAGQAEPRRAHYNIIVTCCK 60  
 DB 1 MHGDTPTLHEHYMDLOPETTDLYCYEQINDSSEEDIDGPAGQAEPRRAHYNIIVTCCK 60  
 QY 61 CDSTLRACVQSTHYDRTLEDLMGTLGIYXPCISQKP 98  
 DB 61 CDSTLRACVQSTHYDRTLEDLMGTLGIYXPCISQKP 98  
 RESULT 33  
 ID ADY69083 standard; protein; 98 AA.  
 XX  
 AC ADY69083;  
 XX  
 DT 02-JUN-2005 (first entry)  
 XX  
 DE HPV 16 E7.  
 XX  
 KW Cytostatic; Gene Therapy; human papillomavirus; E7 protein;  
 KW immunohistological detection; Pap-smear; cervical; carcinoma; biopsy;  
 KW anogenital; mamma; head; neck; prostate; sexually transmitted disease;  
 KW cancer.  
 XX  
 OS Human papillomavirus.  
 XX  
 PN WO2005026731-A1.  
 PD 24-MAR-2005.  
 XX  
 PF 17-SEP-2004; 2004WO-EP010484.  
 XX  
 PR 17-SEP-2003; 2003EP-00020564.  
 XX  
 PA (AMYN-) AMYNON BIOTECH GMBH.  
 XX  
 PI Zwerschke WP, Jansen-Duerr P, Fiedler M, Latch A, Fitzky B;  
 XX WPI, 2005-242459/25.  
 DR N-PSDB; ADY69082.  
 XX  
 PT New combination of antibodies comprises an anti-HPV-16 E7 antibody and an  
 PT anti-HPV-18 E7 antibody, useful for preparing a diagnostic composition

PT for the (immuno-) histological detection of high risk HPV E7 protein.  
 XX  
 XX Example 2; SEQ ID NO 2; 146pp; English.  
 PS  
 CC This sequence represents human papillomavirus-16 (HPV-16) E7 protein. An  
 CC antibody raised against this protein may be used in a combination of  
 CC antibodies which comprises an anti-HPV-16 E7 antibody obtainable by  
 CC eliciting an in vivo humoral response against HPV-16 E7 protein or its  
 CC fragment in a goat, and affinity-purifying antibodies as obtained in the  
 CC eliciting step, and an anti-HPV-18 E7 antibody. The combination of  
 CC antibodies is useful for the preparation of a diagnostic composition for  
 CC the (immuno-) histological detection of high risk HPV E7 protein. The  
 CC (immuno-) histological detection is carried out on Pap-smears, cervical  
 CC (carcinoma) biopsies, anogenital biopsies, mamma biopsies, head- or neck  
 CC biopsies, or prostate biopsies. The diagnostic composition is used for  
 CC evaluating the risk of acquiring a sexually transmitted disease or  
 CC cancer, for measuring the status of an existing sexually transmitted  
 CC disease or cancer, or for screening therapy efficiency in the treatment  
 CC of a sexually transmitted disease or cancer. The sexually transmitted  
 CC disease is a high risk HPV infection or where the cancer is cervical  
 CC cancer, breast cancer/mamma cancer, prostate cancer, head and neck  
 CC cancer, penile cancer, and/or anogenital cancer/neoplasia (A1N). The  
 CC combination of antibodies or the diagnostic composition are useful in an  
 CC in vitro method for the detection of high risk HPV E7 protein. The  
 CC antibody is useful for detecting E7 protein of HPV-31, HPV-35,  
 CC HPV-39, HPV-45, HPV-52, HPV-56, HPV-58, and/or HPV-59. It is also useful  
 CC for the preparation of a diagnostic composition for detecting E7 protein  
 CC of HPV-16, HPV-18, HPV-31, HPV-33, HPV-35, HPV-39, HPV-45, HPV-52, HPV-  
 CC 56, HPV-58, and/or HPV-59.  
 XX  
 SQ Sequence 98 AA;  
 Query Match 99.0%; Score 512; DB 9; Length 98;  
 Best Local Similarity 96.9%; Pred. No. 2.2e-57;  
 Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 MHGDTPTLHEHYMDLOPETTDLYXXQINDSSEEDIDGPAGQAEPRRAHYNIIVTCCK 60  
 DB 1 MHGDTPTLHEHYMDLOPETTDLYCYEQINDSSEEDIDGPAGQAEPRRAHYNIIVTCCK 60  
 QY 61 CDSTLRACVQSTHYDRTLEDLMGTLGIYXPCISQKP 98  
 DB 61 CDSTLRACVQSTHYDRTLEDLMGTLGIYXPCISQKP 98  
 RESULT 34  
 ID AEA40816 standard; protein; 98 AA.  
 XX  
 AC AEA40816;  
 XX  
 DT 28-JUL-2005 (first entry)  
 XX  
 DE Anti-apoptotic vector HPV E7 antigenic protein, SEQ ID 6.  
 XX  
 KW immunogenicity; immunogenicity-potentiating polypeptide; ITP; T-cell;  
 KW vaccine; immune stimulation; tumor; cytostatic.  
 XX  
 OS Human papillomavirus - 16.  
 XX  
 PN WO2005047501-A1.  
 PD 26-MAY-2005.  
 XX  
 PF 24-FEB-2004; 2004WO-US005292.  
 XX  
 PR 24-FEB-2003; 2003US-0449429P.  
 XX  
 PR 18-JUL-2003; 2003US-0488527P.  
 XX  
 PR 31-DEC-2003; 2003US-0533752P.  
 XX  
 PA (UYJO ) UNIV JOHNS HOPKINS.  
 XX  
 PI Wu T, Hung CF, Kim T;

XX WPI: 2005-367009/37.  
DR GENBANK; NC\_001526.  
XX  
PT New nucleic acid composition comprising a first nucleic acid vector  
PT encoding an anti-apoptotic polypeptide and a second nucleic acid vector  
PT inhibiting the growth of a tumor.  
XX  
PS Disclosure; SEQ ID NO 6; 158bp; English.  
XX  
XX The invention relates to a novel nucleic acid composition useful as an  
CC immunogen. The composition comprises a combination of: a first nucleic  
CC acid vector comprising a first sequence encoding an antigenic polypeptide  
CC or peptide, and optionally, a second sequence linked to the first  
CC sequence and encoding an immunogenicity-potentiating polypeptide (IPP);  
CC and a second nucleic acid vector encoding an anti-apoptotic polypeptide.  
CC When the second vector is administered with the first vector to a  
CC subject, a T cell mediated immune response to the antigenic polypeptide  
CC or peptide is induced that is greater in magnitude and/or duration than  
CC an immune response induced by administration of the first vector alone.  
CC The invention further includes: a particle comprising a material that is  
CC suitable for introduction into a cell or an animal by particle  
CC bombardment, bound to which is the first and second vectors or  
CC composition; a pharmaceutical composition capable of inducing or  
CC enhancing an antigen specific immune response, comprising the particle  
CC and a carrier or an excipient; inducing or enhancing an antigen specific  
CC immune response in a subject; increasing the numbers of CD8+ CTLs  
CC specific for a selected desired antigen in a subject; and inhibiting the  
CC growth of a tumor in a subject. The nucleic acid composition is useful as  
CC an immunogen for inhibiting the growth of a tumor, hence it has  
CC cytostatic activity. This sequence represents an anti-apoptotic vector HPV  
CC E7 antigenic protein of the invention.  
SQ  
SQ Sequence 98 AA;  
Query Match 99.0%; Score 512; DB 9; Length 98;  
Best Local Similarity 96.9%; Pred. No. 2.2e-57;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 MHGPTLHEHYMLDLPETTDLYXXQNDSEDEIDSPAGQAEPRAHYNTVFCCK 60  
Db 1 MHGPTLHEHYMLDLPETTDLYCYEQNDSEDEIDSPAGQAEPRAHYNTVFCCK 60  
Qy 61 CDSTLRFCVOSTHYDRTLEDLMTGLGIYXPCISQKP 98  
Db 61 CDSTLRFCVOSTHYDRTLEDLMTGLGIYXPCISQKP 98  
RESULT 35  
AEB11989  
ID AEB11989 standard; protein; 98 AA.  
XX  
AC AEB11989;  
XX  
DT 08-SEP-2005 (first entry)  
XX  
DE HPV16 E7 protein.  
XX  
KW Tumor-associated antigen; vaccine; papilloma; cytostatic; neoplasm;  
KW cancer; HPV16 E7.  
XX  
OS Human papillomavirus type 16.  
XX  
PN WO2005060993-A1.  
XX  
PD 07-JUL-2005.  
XX  
PF 24-DEC-2003; 2003WO-NL000929.  
XX  
PR 24-DEC-2003; 2003WO-NL000929.  
XX  
PA (UYLE-) UNIV LEIDEN MEDICAL CENT.

XX  
PI Van Der Burg SH, Drifthout JW;  
XX WPI: 2005-497704/50.  
XX  
PT Producing a synthetic protein of a pathogen or tumor comprises chemically  
PT synthesizing two or more fragments of 2-80 continuous amino acids of  
PT sequence, the sequence of two or more fragments are neighboring and non-  
PT overlapping.  
XX  
PS Claim 11; SEQ ID NO 1; 53bp; English.  
XX  
XX The invention relates to a method of producing a synthetic protein  
CC comprising an amino acid sequence that is at least 80% identical to a  
CC naturally occurring antigenic protein of a pathogen or tumor comprising  
CC chemically synthesizing two or more fragments, chemically ligating the C-  
CC terminus of a fragment to the N-terminus of a neighboring fragment to  
CC produce the synthetic protein or its part and optionally repeating the  
CC second step to sequentially ligate a further neighboring fragment  
CC obtained from the second step. The invention also relates to a  
CC composition comprising the protein and a method for treating or  
CC preventing human papillomavirus (HPV) associated disease by administering  
CC to the subject the protein or composition in a therapeutically effective  
CC amount. In producing a synthetic protein, the neighboring non-overlapping  
CC fragments are selected to comprise N-terminal cysteine or glycine  
CC residues. The naturally occurring protein is an HPV protein, e.g. E2, E6  
CC or E7 protein from HPV16, HPV18, HPV31, HPV33 or HPV45. The composition  
CC further comprises an anti-CD40 antibody. The composition is useful as a  
CC vaccine for preventing or treating HPV associated disease, such as  
CC cancer. This sequence represents an HPV16 E7 protein used in the method  
CC of the invention.  
SQ  
SQ Sequence 98 AA;  
Query Match 99.0%; Score 512; DB 9; Length 98;  
Best Local Similarity 96.9%; Pred. No. 2.2e-57;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 MHGPTLHEHYMLDLPETTDLYXXQNDSEDEIDSPAGQAEPRAHYNTVFCCK 60  
Db 1 MHGPTLHEHYMLDLPETTDLYCYEQNDSEDEIDSPAGQAEPRAHYNTVFCCK 60  
Qy 61 CDSTLRFCVOSTHYDRTLEDLMTGLGIYXPCISQKP 98  
Db 61 CDSTLRFCVOSTHYDRTLEDLMTGLGIYXPCISQKP 98  
RESULT 36  
AEC96392  
ID AEC96392 standard; protein; 98 AA.  
XX  
AC AEC96392;  
XX  
DT 01-DEC-2005 (first entry)  
XX  
DE HPV protein E7 from HPV16.  
XX  
KW Human papilloma virus infection; virucide; cancer; cytostatic; vaccine;  
KW epitope mapping; immune stimulation; cytotoxic T-lymphocyte.  
XX  
OS Human papillomavirus type 16.  
XX  
PN WO2005089164-A2.  
XX  
PD 29-SEP-2005.  
XX  
PF 03-JAN-2005; 2005WO-US000077.  
XX  
PR 31-DEC-2003; 2003US-0533211P.  
XX  
PR 02-JUL-2004; 2004US-0584652P.  
XX  
PA (EPIM-) EPIMUNE INC.  
PA (INNO-) INNOGENETICS NV.

PA (CHES/) CHESNUT R.  
 PA (NEMM/) NEWMAN M J.  
 PA (MOTB/) MOTHE B.  
 PA (BAKE/) BAKER D.  
 PA (SOUT/) SOUTHWOOD S.  
 PA (BABE/) BABE L M.  
 PA (CHEN/) CHEN Y.  
 PA (DEYO/) DEYOUNG L M.  
 PA (HUAN/) HUANG M T F.  
 PA (POWE/) POWER S D.  
 PI Chesnut R, Newman MJ, Mothe B, Baker D, Southwood S, Babe LM;  
 PI Chen Y, Deyoung LM, Huang MTF, Power SD;  
 DR WPI; 2005-658982/67.  
 XX New polynucleotide comprises a multi-epitope construct comprising nucleic  
 PT acids encoding the human papillomavirus (HPV) cytotoxic T lymphocyte  
 PT (CTL) epitopes, useful in preparing a vaccine against HPV.  
 PS Disclosure; Page 56; 518pp; English.  
 XX The invention relates to a new polynucleotide comprising a multi-epitope  
 CC construct comprising nucleic acids encoding the human papillomavirus  
 CC (HPV) cytotoxic T lymphocyte (CTL) epitopes e.g., HPV16.E1.214, and that  
 CC are directly or indirectly joined to one another in the same reading  
 CC frame, a vaccine minigene. Also included are a vector comprising the  
 CC multi-epitope construct, a polypeptide comprising an amino acid sequence  
 CC encoded by the polynucleotide, a composition (comprising the  
 CC polynucleotide, vector and/or polypeptide and a carrier), a cell  
 CC (comprising the polynucleotide, vector or polypeptide), inducing an  
 CC immune response against human papillomavirus virus (HPV) and making the  
 CC polynucleotide, vector or polypeptide. The epitopes are derived from  
 CC different strains of HPV and are from the E1, E2, E6 and E7 proteins. The  
 CC epitopes may be linked via a GP-anchor/spacer peptide. The order of the  
 CC epitopes in the vaccine protein are disclosed in the tables referred to  
 CC in the claims of the specification. The polynucleotide, vector or  
 CC polypeptide is useful in preparing a composition for inducing an immune  
 CC response against human papillomavirus virus (HPV) and thus providing a  
 CC defense against HPV infection and HPV-related cancers. The present  
 CC sequence is an HPV protein used to derive epitopes for the vaccine of the  
 CC invention.  
 CC XX  
 SQ Sequence 98 AA;  
 Query Match 99.0%; Score 512; DB 9; Length 98;  
 Best Local Similarity 96.9%; Pred. No. 2.2e-57;  
 Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 MHGDTPTLHEVMDLQPEETDLYXXQLNDSSEEDSIDPAGAEPRRAHYNIIVTFCCK 60  
 DB 1 MHGDTPTLHEVMDLQPEETDLYCYEQUNSSSEEDSIDPAGAEPRRAHYNIIVTFCCK 60  
 QY 61 CDSTLRLCVOSTHVDIRTLBDMGTIGIYVPICSQKP 98  
 DB 61 CDSTLRLCVOSTHVDIRTLBDMGTIGIYVPICSQKP 98  
 RESULT 37  
 ID AEC98871 standard; protein; 98 AA.  
 AC AEC98871;  
 XX 01-DEC-2005 (first entry)  
 DT HPV\_16 Envelope protein E7.  
 DE  
 XX Human papilloma virus infection; virucide; cancer; cytostatic; vaccine;  
 KW epitope mapping; immune stimulation; cytotoxic T-lymphocyte.  
 XX Human papillomavirus type 16.  
 OS  
 XX

PN MO2005089164-A2.  
 XX 29-SEP-2005.  
 PD  
 XX 03-JAN-2005; 2005MO-US000077.  
 PF  
 XX 31-DEC-2003; 2003US-0533211P.  
 PR 02-JUL-2004; 2004US-0584652P.  
 XX  
 XX (BEIM-) EPIMUNE INC.  
 PA (INNO-) INNOGENETICS NV.  
 PA (CHES/) CHESNUT R.  
 PA (NEMM/) NEWMAN M J.  
 PA (MOTB/) MOTHE B.  
 PA (BAKE/) BAKER D.  
 PA (SOUT/) SOUTHWOOD S.  
 PA (BABE/) BABE L M.  
 PA (CHEN/) CHEN Y.  
 PA (DEYO/) DEYOUNG L M.  
 PA (HUAN/) HUANG M T F.  
 PA (POWE/) POWER S D.  
 PI Chesnut R, Newman MJ, Mothe B, Baker D, Southwood S, Babe LM;  
 PI Chen Y, Deyoung LM, Huang MTF, Power SD;  
 DR WPI; 2005-658982/67.  
 XX New polynucleotide comprises a multi-epitope construct comprising nucleic  
 PT acids encoding the human papillomavirus (HPV) cytotoxic T lymphocyte  
 PT (CTL) epitopes, useful in preparing a vaccine against HPV.  
 PS Example 10; Page 350; 518pp; English.  
 XX The invention relates to a new polynucleotide comprising a multi-epitope  
 CC construct comprising nucleic acids encoding the human papillomavirus  
 CC (HPV) cytotoxic T lymphocyte (CTL) epitopes e.g., HPV16.E1.214, and that  
 CC are directly or indirectly joined to one another in the same reading  
 CC frame, a vaccine minigene. Also included are a vector comprising the  
 CC multi-epitope construct, a polypeptide comprising an amino acid sequence  
 CC encoded by the polynucleotide, a composition (comprising the  
 CC polynucleotide, vector and/or polypeptide and a carrier), a cell  
 CC (comprising the polynucleotide, vector or polypeptide), inducing an  
 CC immune response against human papillomavirus virus (HPV) and making the  
 CC polynucleotide, vector or polypeptide. The epitopes are derived from  
 CC different strains of HPV and are from the E1, E2, E6 and E7 proteins. The  
 CC epitopes may be linked via a GP-anchor/spacer peptide. The order of the  
 CC epitopes in the vaccine protein are disclosed in the tables referred to  
 CC in the claims of the specification. The polynucleotide, vector or  
 CC polypeptide is useful in preparing a composition for inducing an immune  
 CC response against human papillomavirus virus (HPV) and thus providing a  
 CC defense against HPV infection and HPV-related cancers. The present  
 CC sequence is an HPV protein used to derive epitopes for the vaccine of the  
 CC invention.  
 CC XX  
 SQ Sequence 98 AA;  
 Query Match 99.0%; Score 512; DB 9; Length 98;  
 Best Local Similarity 96.9%; Pred. No. 2.2e-57;  
 Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 MHGDTPTLHEVMDLQPEETDLYXXQLNDSSEEDSIDPAGAEPRRAHYNIIVTFCCK 60  
 DB 1 MHGDTPTLHEVMDLQPEETDLYCYEQUNSSSEEDSIDPAGAEPRRAHYNIIVTFCCK 60  
 QY 61 CDSTLRLCVOSTHVDIRTLBDMGTIGIYVPICSQKP 98  
 DB 61 CDSTLRLCVOSTHVDIRTLBDMGTIGIYVPICSQKP 98  
 RESULT 38  
 ID AED13078 standard; protein; 98 AA.  
 XX

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AC AED13078;
XX
XX 15-DEC-2005 (first entry)
XX
XX HPV16 E7 wild-type protein sequence.
DE
XX mutagen; vaccine; antigen; virucide; antibacterial.
XX
XX Human papillomavirus type 16.
OS
XX FR2868781-A1.
PN
XX 14-OCT-2005.
PD
XX 13-APR-2004; 2004FR-00003848.
XX
XX 13-APR-2004; 2004FR-00003848.
PR
XX
XX (IMMU-) IMMUTEP.
PA
XX Triebel F;
PI
XX WPI: 2005-678227/70.
XX
XX N-PSDB; AED13076.
DR
XX
XX Therapeutic vaccine, for viral and bacterial conditions, comprises an
XX antigen protein and a viral or bacterial protein, coupled together by
XX PT steable hydrogen or covalence bonds in biological media.
XX
XX Diaclosure; Fig 1; 51pp; French.
PS
XX
XX The invention relates to a novel vaccine composed of an antigen protein
XX CC and a second protein as an s-(methyl mercury)-1-cysteine (CMH class II)
XX CC ligand. The second protein is taken from a group including human
XX CC lymphocyte Activation Gene (hLAG)-3. The first protein is a viral or
XX CC bacterial antigen, a tumor antigen, parasitic antigen, or their mixtures.
XX CC The viral antigens can be for hepatitis B (HBV), human papillomavirus
XX CC (HPV), hepatitis C (HCV), human immunodeficiency virus (HIV), Epstein-
XX CC Barr virus (EBV), cytomegalovirus (CMV), and their combinations. The
XX CC bacterial antigens can be intracellular bacteria of tuberculosis, leprosy
XX CC and listeria. A vaccine of the invention has virucide, and antibacterial
XX CC activity. The present sequence represents the HPV16 wild-type E7 protein
XX CC sequence.
XX
XX
XX Sequence 98 AA;
SQ
Query Match 99.0%; Score 512; DB 9; Length 98;
Best Local Similarity 96.9%; Pred. No. 2.2e-57;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 MHGDTPTLHEYMLDLPQETTDLYXXYXQLNDSSEBDEIDGPAGQAEPPRAHYNIVTFCK 60
DQ 1 MHGDTPTLHEYMLDLPQETTDLYCYEQLNDSSEBDEIDGPAGQAEPPRAHYNIVTFCK 60
Db 1 MHGDTPTLHEYMLDLPQETTDLYCYEQLNDSSEBDEIDGPAGQAEPPRAHYNIVTFCK 60
QY 61 CDSTLRUCVOSTHYDRTLEDLMLGTGIVXPICSOXP 98
DQ 61 CDSTLRUCVOSTHYDRTLEDLMLGTGIVXPICSOXP 98
Db 61 CDSTLRUCVOSTHYDRTLEDLMLGTGIVXPICSOXP 98

RESULT 39
AED64360
ID AED64360 standard; protein: 98 AA.
XX
XX AED64360;
XX
XX 12-JAN-2006 (first entry)
XX
XX Human papillomavirus type 16 E7 protein.
XX
XX Vaccine; therapeutic; papillomavirus infection; virucide; infection;
XX KM fusion protein; E7.
XX
XX Human papillomavirus type 16.
OS

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XX
XX US2005249745-A1.
XX
XX 10-NOV-2005.
XX
XX 13-JUL-2005; 2005US-00179478.
XX
XX 20-FEB-1998; 98US-00026896.
XX
XX 03-APR-2001; 2001US-00824017.
XX
XX 04-SEP-2003; 2003US-00654129.
XX
XX (MED1-) MEDIGENE AG.
XX
XX Halilek M, Burger A;
XX
XX WPI: 2005-746775/76.
XX
XX N-PSDB; AED64359.
DR
XX
XX New fusion protein comprising an amino acid sequence from a first or a
XX PT second papilloma virus-specific (PVS) protein, useful in preparing a
XX PT composition for treating or preventing papilloma virus infection.
XX
XX Example 1; SEQ ID NO 4; 20pp; English.
PS
XX
XX The present invention relates to fusion protein comprising papilloma
XX CC virus-specific (PVS) protein and their encoding polynucleotides. The
XX CC invention is useful in preparing a composition for treating and
XX CC preventing papilloma virus infection in humans. The present sequence is
XX CC the Human papillomavirus type 16 E7 protein.
XX
XX
XX Sequence 98 AA;
SQ
Query Match 99.0%; Score 512; DB 9; Length 98;
Best Local Similarity 96.9%; Pred. No. 2.2e-57;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 MHGDTPTLHEYMLDLPQETTDLYXXYXQLNDSSEBDEIDGPAGQAEPPRAHYNIVTFCK 60
DQ 1 MHGDTPTLHEYMLDLPQETTDLYCYEQLNDSSEBDEIDGPAGQAEPPRAHYNIVTFCK 60
Db 1 MHGDTPTLHEYMLDLPQETTDLYCYEQLNDSSEBDEIDGPAGQAEPPRAHYNIVTFCK 60
QY 61 CDSTLRUCVOSTHYDRTLEDLMLGTGIVXPICSOXP 98
DQ 61 CDSTLRUCVOSTHYDRTLEDLMLGTGIVXPICSOXP 98
Db 61 CDSTLRUCVOSTHYDRTLEDLMLGTGIVXPICSOXP 98

RESULT 40
AEE94089
ID AEE94089 standard; protein: 98 AA.
XX
XX AEE94089;
XX
XX 23-FEB-2006 (first entry)
XX
XX HPV16 E7 protein.
XX
XX Gene expression; therapeutic; immune stimulation; HIV infection;
XX KM acquired immune deficiency syndrome; E7 protein; anti-HIV; virucide;
XX KM infection; immune disorder.
XX
XX Human papillomavirus type 16.
XX
XX WO2005118874-A1.
XX
XX 15-DEC-2005.
XX
XX 06-JUN-2005; 2005MO-US019592.
XX
XX 04-JUN-2004; 2004US-0576819P.
XX
XX (AMHP ) WYETH.
XX
XX Smith LR, Shahabi V, Sidhu MK;
XX

```

DR WPI; 2006-047579/05.  
 DR N-PSDB; AEE94088.  
 XX Preparing a polynucleotide, useful for enhancing gene expression,  
 PT comprises assembling oligonucleotides comprising surrogate codons to form  
 PT a modified polynucleotide.  
 XX  
 XX Claim 149; SEQ ID NO 2; 13pp; English.  
 XX  
 CC The invention relates to a method of preparing a polynucleotide that  
 CC provides enhanced expression of a gene, comprising assembling  
 CC oligonucleotides comprising surrogate codons to form a modified  
 CC polynucleotide, comprising a predetermined nucleic acid sequence encoding  
 CC the same protein or polypeptide as a wild-type polynucleotide. The  
 CC invention also relates to a method for enhancing expression of a gene, a  
 CC method of preventing or treating a disease in a mammal, a composition  
 CC comprising a modified polynucleotide describe above and a pharmaceutical  
 CC vector. The method additionally comprises adding an immunoglobulin leader  
 CC sequence, such as an IGF leader sequence, to the modified polynucleotide.  
 CC The composition is useful for preparing a medicament for inducing an  
 CC immune response in a mammal or for treating an infection or condition,  
 CC e.g. HIV or AIDS in a mammal. The polynucleotide and methods are useful  
 CC for enhancing gene expression. This sequence represents the HPV16 E7  
 CC protein used in the scope of the invention.  
 CC  
 XX  
 SQ Sequence 98 AA;  
 XX  
 Query Match 99.0%; Score 512; DB 10; Length 98;  
 Best Local Similarity 96.9%; Pred. No. 2.2e-57;  
 Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 MHGDTPLHRYMDLQPEETDLYXXQLNDSSEEDIDGPAQAEPDRAHYNIVTCCK 60  
 DB 1 MHGDTPLHRYMDLQPEETDLYCYEQLNDSSEEDIDGPAQAEPDRAHYNIVTCCK 60  
 QY 61 CDSTLRVCVOSTHYDRTLEDLMGTIGIYXPCISQKP 98  
 DB 61 CDSTLRVCVOSTHYDRTLEDLMGTIGIYXPCISQKP 98  
 RESULT 41  
 ADQ88451  
 ID ADQ88451 standard; protein; 99 AA.  
 XX  
 AC ADQ88451;  
 XX  
 DT 23-SEP-2004 (first entry)  
 XX  
 DE HPV16 E7 protein.  
 XX  
 KW HPV 16; E7 gene; cyostatic; vaccine; tumour.  
 XX  
 OS Human papillomavirus; HPV16.  
 XX  
 PN RU2229307-C1.  
 XX  
 PD 27-MAY-2004.  
 XX  
 PF 22-OCT-2002; 2002RU-00128131.  
 XX  
 PR 22-OCT-2002; 2002RU-00128131.  
 XX  
 PA (BIOM-) BIOMEDINVEST STOCK CO.  
 XX  
 PI Paltsev MA, Severin ES, Kiselev OI, Kiselev VI, Sveshnikov PG;  
 XX  
 DR WPI; 2004-446846/42.  
 DR N-PSDB; ADQ88450.  
 XX  
 XX Recombinant protein composition, useful in immunotherapy and prophylactic  
 PT vaccination of tumor diseases in anus-genital sphere.  
 XX  
 PS Disclosure; Page 7; 10pp; Russian.

XX  
 CC The invention involves hybrid proteins consisting of amino acid sequences  
 CC of oncoprotein E7 of human papilloma virus of 16 and 18 types that are  
 CC bound covalently with amino acid sequence of heat shock protein with  
 CC molecular mass 70 kDa (Hsp70) from M. tuberculosis - E716-Hsp70 and E718-  
 CC Hsp70, respectively. The invention relates to composition of recombinant  
 CC proteins, method for preparing the composition, pharmaceutical kit of  
 CC reagents used in immunotherapy and prophylactic vaccination of tumour  
 CC diseases in anal-genital region and methods for immunotherapy and  
 CC prophylactic vaccination. The fusion proteins are used in immunotherapy  
 CC and prophylactic vaccination of tumour diseases in anal-genital sphere.  
 CC The present sequence is the HPV16 E7 protein.  
 XX  
 SQ Sequence 99 AA;  
 XX  
 Query Match 99.0%; Score 512; DB 8; Length 99;  
 Best Local Similarity 96.9%; Pred. No. 2.2e-57;  
 Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 MHGDTPLHRYMDLQPEETDLYXXQLNDSSEEDIDGPAQAEPDRAHYNIVTCCK 60  
 DB 2 MHGDTPLHRYMDLQPEETDLYCYEQLNDSSEEDIDGPAQAEPDRAHYNIVTCCK 61  
 QY 61 CDSTLRVCVOSTHYDRTLEDLMGTIGIYXPCISQKP 98  
 DB 62 CDSTLRVCVOSTHYDRTLEDLMGTIGIYXPCISQKP 99  
 RESULT 42  
 ADY92615  
 ID ADY92615 standard; protein; 99 AA.  
 XX  
 AC ADY92615;  
 XX  
 DT 16-JUN-2005 (first entry)  
 XX  
 DE HPV16 E7 oncoprotein protein sequence.  
 XX  
 KW Antibody; monoclonal antibody; antibody production; hybridoma; screening;  
 KW E7 oncoprotein; immuno-diagnosis; diagnostic; immunocombinate;  
 KW immunoassay; radioimmunoassay; enzyme-linked immunosorbent assay;  
 KW transmissible spongiform encephalopathy; cerebroprotective;  
 KW cervical intraepithelial neoplasia; cyostatic; immunoglobulin.  
 XX  
 OS Human papillomavirus type 16.  
 XX  
 PN W02005028510-A2.  
 XX  
 PD 31-MAR-2005.  
 XX  
 PF 24-SEP-2004; 2004WO-RU000373.  
 XX  
 PR 25-SEP-2003; 2003RU-00128660.  
 XX  
 PA (KISEV/) KISELEV V I.  
 PA (SVES/) SVESHNIKOV P G.  
 XX  
 PI Kiselev VI, Sveshnikov PG;  
 XX  
 DR WPI; 2005-273121/28.  
 DR N-PSDB; ADY92614.  
 XX  
 XX Producing monoclonal antibodies specific to an antigen of low  
 PT immunogenicity by immunizing an animal with the chemically conjugated  
 PT antigen, useful for detecting cervical intraepithelial neoplasia.  
 XX  
 PS Disclosure; SEQ ID NO 2; 72pp; English.  
 XX  
 CC The new invention relates to methods and compositions that allow  
 CC production of antigen specific antibodies to antigens that have  
 CC traditionally been unable to elicit an adequate and specific immune  
 CC response. The method comprises producing monoclonal antibodies specific  
 CC to an antigen of low immunogenicity by chemically conjugating the antigen

CC to a carrier molecule, immunizing an animal with the conjugated antigen,  
CC harvesting B cells from the animal, creating a hybridoma from the  
CC harvested B cells, and screening the hybridomas for specificity to the  
CC native antigen. The antigens can be E7 oncoprotein, P10n protein  
CC peptide, hyaluronic acid or matrix metalloproteinase 3. The carrier  
CC molecule is HSP70. The chemical conjugation comprises creating a plasmid  
CC with a nucleotide sequence encoding the antigen, such as E7 oncoprotein  
CC and a nucleotide sequence encoding HSP70 and transfecting a host cell  
CC with the plasmid. The nucleotide sequence encoding E7 oncoprotein  
CC comprises ADY92614 or ADY92616. The nucleotide sequence encoding HSP70  
CC comprises ADY92618. Alternatively, the conjugating is performed  
CC chemically using glutaraldehyde. Screening for specificity is done by  
CC various assays such as radioimmunoassay, enzyme-linked immunosorbent  
CC assay, or sandwich immunoassay. The antibodies are useful for determining  
CC if a subject is at risk of developing spongiform encephalopathy  
CC comprising an antibody that specifically detects Prion protein. The Prion  
CC protein peptide comprises ADY92619, ADY92620 or ADY92622. Antibodies  
CC specific to E7 oncoprotein are useful for detecting cervical  
CC intraepithelial neoplasia by obtaining a specimen of cervical epithelial  
CC cells and screening the specimen for the presence of E7 oncoprotein. The  
CC monoclonal antibodies comprise at least two immunoglobulin isotypes. The  
CC immunoglobulin isotype is IgG2a or IgG2b. The immunoglobulin isotype has  
CC specificity for a different antigenic determinant than the second  
CC immunoglobulin isotype. The present sequence HPV16 E7 oncoprotein  
CC sequence.

XX Sequence 99 AA;

Query Match 99.0%; Score 512; DB 9; Length 99;  
Best Local Similarity 96.9%; Pred. No. 2.2e-57;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDPPTLHEXYMLDLPETTDLYXXYXQLNDSSEEDIDGPAQAEPDRAHNYIVTFCK 60  
Db 2 MHGDPPTLHEXYMLDLPETTDLYCYEQLNDSSEEDIDGPAQAEPDRAHNYIVTFCK 61  
61 CDSTLRFCVQSTHVDIRTLIEDLGMGTIGIYXPICSQKP 98  
62 CDSTLRFCVQSTHVDIRTLIEDLGMGTIGIYCPICQKP 99

RESULT 43

AAB31608  
ID AAB31608 standard; proteoin; 121 AA.

XX AAB31608;

AC 30-APR-2001 (first entry)

XX Amino acid sequence of a His-tagged HPV16 E7 protein.

XX Heat shock protein; Hsp; Th1 response; Th1 cell; CD4+ T lymphocyte cell;

XX lymphocyte; Hsp65; Hsp40; Hsp10; Hsp60; Hsp71; microbial pathogen;

XX E7 protein.

XX Synthetic.

OS Human papillomavirus.

XX WO200104344-A2.

XX 18-JAN-2001.

XX 10-JUL-2000; 2000WO-US018828.

XX 08-JUL-1999; 99US-0143757P.

XX (STRE-) STRESSGEN BIOTECHNOLOGIES CORP.

XX Siegel M, Chu NR, Mitzzen LA;

XX WPI; 2001-138361/14.

XX N-PSDB; AAF25008.

PT Screening for compounds that stimulate Th1-like responses in CD4+ T  
PT lymphocyte cells.

XX Example 4; Fig 3; 88pp; English.

XX The present sequence represents a HPV16 E7 protein. HPV16 E7 was fused to  
CC a heat shock protein (Hsp), and used used in the method of the invention.  
CC The specification describes a method of determining whether a compound  
CC stimulates a Th1-like response. Th1 cells are a subset of CD4+ T  
CC lymphocyte cells. The method comprises contacting naive lymphocytes in  
CC vitro with a fusion protein comprising at least a fragment of Hsp, and  
CC then detecting the Th1-like response exhibited by the cell sample. The  
CC proteins which may be used in the method of the invention are Hsp65,  
CC Hsp40, Hsp10, Hsp60, and Hsp71. The method may be used to identify  
CC compounds that stimulate Th1-like responses in response to microbial  
CC pathogens

XX Sequence 121 AA;

Query Match 99.0%; Score 512; DB 4; Length 121;  
Best Local Similarity 96.9%; Pred. No. 2.8e-57;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDPPTLHEXYMLDLPETTDLYXXYXQLNDSSEEDIDGPAQAEPDRAHNYIVTFCK 60  
Db 24 MHGDPPTLHEXYMLDLPETTDLYCYEQLNDSSEEDIDGPAQAEPDRAHNYIVTFCK 83  
61 CDSTLRFCVQSTHVDIRTLIEDLGMGTIGIYXPICSQKP 98  
84 CDSTLRFCVQSTHVDIRTLIEDLGMGTIGIYCPICQKP 121

RESULT 44

AAB31616  
ID AAB31616 standard; proteoin; 198 AA.

XX AAB31616;

AC 30-APR-2001 (first entry)

XX Amino acid sequence of Hsp10-E7 fusion protein.

XX Heat shock protein; Hsp; Th1 response; Th1 cell; CD4+ T lymphocyte cell;

XX lymphocyte; Hsp65; Hsp40; Hsp10; Hsp60; Hsp71; microbial pathogen;

XX E7 protein.

XX Synthetic.

OS Mycobacterium tuberculosis.

XX Human papillomavirus.

XX WO200104344-A2.

XX 18-JAN-2001.

XX 10-JUL-2000; 2000WO-US018828.

XX 08-JUL-1999; 99US-0143757P.

XX (STRE-) STRESSGEN BIOTECHNOLOGIES CORP.

XX Siegel M, Chu NR, Mitzzen LA;

XX WPI; 2001-138361/14.

XX N-PSDB; AAF25023.

XX Screening for compounds that stimulate Th1-like responses in CD4+ T  
XX lymphocyte cells.

XX Example 13; Fig 12; 88pp; English.  
CC The present sequence represents a fusion protein comprising Mycobacterium  
CC tuberculosis heat shock protein (Hsp) 10 fused at its 3' end to HPV16 E7  
CC protein. The fusion protein is used in the method of the invention. The

CC specification describes a method of determining whether a compound  
 CC stimulates a Th1-like response. Th1 cells are a subset of CD4+ T  
 CC lymphocyte cells. The method comprises contacting native lymphocytes in  
 CC vitro with a fusion protein comprising at least a fragment of Hsp, and  
 CC then detecting the Th1-like response exhibited by the cell sample. The  
 CC proteins which may be used in the method of the invention are Hsp65,  
 CC Hsp40, Hsp10, Hsp60, and Hsp71. The method may be used to identify  
 CC compounds that stimulate Th1-like responses in response to microbial  
 CC pathogens

XX Sequence 198 AA:

Query Match 99.0%; Score 512; DB 4; Length 198;  
 Best Local Similarity 96.9%; Pred. No. 5.3e-57;  
 Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MGGDPTLHERYMDLOPETDLDYXXYXQINDSSEEDIDDPAGQAEPRRAHYNIVTFCK 60  
 Db 101 MGGDPTLHERYMDLOPETDLDYCYEQINDSSEEDIDDPAGQAEPRRAHYNIVTFCK 160

Qy 61 CDSTLRRCVOSTHYDRTLEDLMTGLGIYXPCISQKP 98  
 Db 161 CDSTLRRCVOSTHYDRTLEDLMTGLGIYXPCISQKP 198

RESULT 45

ADT75831  
 ID ADT75831 standard; protein; 212 AA.

XX ADT75831;

XX 13-JAN-2005 (first entry)

XX Novel Fve fusion protein mutant sequence #48.

XX Fve polypeptide; anti-allergic; anti-inflammatory; antiaschematic;  
 KW cytostatic; respiratory-Gen; antiaschematic; vaccine; immunomodulator;  
 KW immune response; atopic disease; allergy; seasonal respiratory allergy;  
 KW perennial respiratory allergy; allergic rhinitis; hayfever;  
 KW nonallergic rhinitis; vasomotor rhinitis; irritant rhinitis;  
 KW grass pollen allergy; weed pollen; tree pollen; animal danders;  
 KW allergic asthma; food allergy; house dust mite allergy; fungal spore;  
 KW cancer; tumour progression; T cell lymphoma; melanoma; lung cancer;  
 KW colon cancer; breast cancer; prostate cancer.

XX Plasmidina velutipes.  
 OS Human papillomavirus.  
 OS Chimeric.

PN WO2004092210-A2.

PD 28-OCT-2004.

PF 16-APR-2004; 2004WO-SG000098.

PR 17-APR-2003; 2003GB-00008988.

PA (UYNA-) UNIV NAT SINGAPORE.  
 (SCTE-) AGENCY SCI TECHNOLOGY & RES.

PI Chua KY, Seow SV, Kolatkar PR;  
 XX

XX WPI; 2004-758336/74.

DR N-PSDB; ADT75832.

PT New Fve polypeptide that is a fragment, homologue, variant or derivative  
 of Fve protein and that comprises a biological activity of native Fve  
 protein, useful for preventing and treating allergy or cancer.

XX Claim 6; Page 166; 286pp; English.

CC This invention relates to a novel Fve (Plasmidina velutipes) polypeptide  
 comprising at least one biological activity of native Fve protein, and

CC being its fragment, homologue, variant or derivative. The invention may  
 CC be useful for the production of compounds with an anti-allergic,  
 CC anti-inflammatory, antiaschematic, cytostatic, respiratory-Gen or  
 CC antiaschematic activity or for the development of a vaccine. The  
 CC composition (including the native Fve polypeptide, or an Fve polypeptide,  
 CC nucleic acid, vector, DNA vaccine, host cell or transgenic organism) is  
 CC useful as an immunomodulator or to enhance an immune response in a  
 CC mammal, as an adjuvant for a vaccine, in a method of treatment or  
 CC prophylaxis of a disease, for the preparation of a pharmaceutical  
 CC composition for the treatment of a disease, such as an atopic disease or  
 CC an allergy (for example seasonal respiratory allergy, perennial  
 CC respiratory allergy, allergic rhinitis, hayfever, nonallergic rhinitis,  
 CC vasomotor rhinitis, irritant rhinitis, an allergy against grass pollen,  
 CC weed pollen, tree pollen or animal danders, an allergy associated with  
 CC allergic asthma, food allergy or an allergy to a house dust mite from  
 CC Family Glyphagidae, preferably Blomia tropicalis or from Family  
 CC Pyroglyphidae, preferably Dermatophagoides pteronyssinus or  
 CC Dermatophagoides farinae, or to fungi or fungal spores, preferably  
 CC Aspergillus fumigatus). These may also be used for treating or preventing  
 CC cancer or in suppressing tumour progression, where the cancer comprises a  
 CC T cell lymphoma, melanoma, lung cancer, colon cancer, breast cancer or  
 CC prostate cancer. The present sequence is that of a gene which encodes a  
 CC novel Fve-derived protein of the invention.

XX Sequence 212 AA:

Query Match 99.0%; Score 512; DB 8; Length 212;  
 Best Local Similarity 96.9%; Pred. No. 5.8e-57;  
 Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MGGDPTLHERYMDLOPETDLDYXXYXQINDSSEEDIDDPAGQAEPRRAHYNIVTFCK 60  
 Db 1 MGGDPTLHERYMDLOPETDLDYCYEQINDSSEEDIDDPAGQAEPRRAHYNIVTFCK 60

Qy 61 CDSTLRRCVOSTHYDRTLEDLMTGLGIYXPCISQKP 98  
 Db 61 CDSTLRRCVOSTHYDRTLEDLMTGLGIYXPCISQKP 98

RESULT 46

AAV25375  
 ID AAV25375 standard; protein; 220 AA.

XX AAV25375;

XX 06-SEP-1999 (first entry)

XX HPV fusion protein D1/3-E7-His (HPV16).

XX Fusion protein; E6 protein; E7 protein; E6/E7; immunomodulator; tumour;  
 KW immunological fusion partner; CpG oligonucleotide; immune response;  
 KW HPV antigen; prevention; treatment.

XX Synthetic.  
 OS Human papillomavirus.

PN WO9933868-A2.

PD 08-JUL-1999.

PF 18-DEC-1998; 98WO-EP008563.

PR 24-DEC-1997; 97GB-00027262.

PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.

PI Dalemans WJ, Gerard CMG;

XX WPI; 1999-405485/34.

DR N-PSDB; AAV25375.

PT Composition comprising an E6, E7 or E6/E7 fusion protein from HPV to  
 induce immune response to HPV.

XX Example 1; Page 46-47; 62pp; English.

XX  
PS  
CC AAX78791-X78801 represent nucleic acid sequences which encode novel  
CC constructs comprising an E6 or E7 protein or E6/E7 fusion protein from  
CC HPV (represented in AAY25375-Y25386). These constructs are optionally  
CC linked to an immunological fusion partner and an immunomodulatory Cpg  
CC oligonucleotide. The products of the invention can be used to induce an  
CC immune response in a patient to an HPV antigen. They can also be used for  
CC preventing or treating HPV induced tumours

XX  
SQ Sequence 220 AA;

Query Match 99.0%; Score 512; DB 2; Length 220;  
Best Local Similarity 96.9%; Pred. No. 6.1e-57;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MGGDPTLHEYMDLQPETTDLYXXYQNDSSSEEDIDGPAGQAEPPRAHYNIITFCCK 60  
Db 114 MGGDPTLHEYMDLQPETTDLYCYEQNDSSSEEDIDGPAGQAEPPRAHYNIITFCCK 173

Qy 61 CDSTLRVCVOSTHVDIRLTEDLMGTIGIYXPCISQKP 98  
Db 174 CDSTLRVCVOSTHVDIRLTEDLMGTIGIYXPCISQKP 211

RESULT 47

AA02631  
ID AA02631 standard; protein; 220 AA.

XX  
AC AAY02631;

XX  
DT 17-OCT-2003 (revised)  
DT 22-JUN-1999 (first entry)

XX  
DE Protdchr126-E7-His tail protein.

XX  
KW Chimeric; E6; E7; fusion protein; protein D; vaccine; immunotherapy;  
KW tumour; lesion; benign; malignant; virus; infection.

XX  
OS Human papillomavirus.  
OS Haemophilus influenzae.  
OS Chimeric.

XX  
PN MO9910375-A2.

XX  
PD 04-MAR-1999.

XX  
PF 17-AUG-1998; 98WO-EP005285.

XX  
PR 22-AUG-1997; 97GB-00017953.

XX  
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.

XX  
PI Bruck C, Cabezon Silva T, Delisse AEF, Gerard CMG;  
PI Lombardo-Bencheikh A;

XX  
DR WPI: 1999-190587/16.  
DR N-PSDB: AAX29780.

XX  
PT Human Papilloma Virus (HPV) fusion proteins - useful in vaccines for  
PT treatment or prophylaxis of HPV induced lesions.

XX  
PS Disclosure; Fig 1; 95pp; English.

XX  
CC This sequence represents a chimeric E6 or E7 protein or E6/E7 fusion  
CC protein from Human papillomavirus (HPV) linked to an immunological fusion  
CC partner, in this case, a fragment of the Haemophilus influenzae B protein  
CC D. The sequence also contains a histidine tag at the C-terminus of the  
CC encoded protein. The protein can be used in a vaccine, for immuno-  
CC therapeutically creating HPV induced tumour lesions (benign or malignant)  
CC and preventing HPV viral infection. (Updated on 17-OCT-2003 to  
CC standardise OS field)

XX  
SQ Sequence 220 AA;

XX  
PS  
CC Query Match 99.0%; Score 512; DB 2; Length 220;  
CC Best Local Similarity 96.9%; Pred. No. 6.1e-57;  
CC Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MGGDPTLHEYMDLQPETTDLYXXYQNDSSSEEDIDGPAGQAEPPRAHYNIITFCCK 60  
Db 114 MGGDPTLHEYMDLQPETTDLYCYEQNDSSSEEDIDGPAGQAEPPRAHYNIITFCCK 173

Qy 61 CDSTLRVCVOSTHVDIRLTEDLMGTIGIYXPCISQKP 98  
Db 174 CDSTLRVCVOSTHVDIRLTEDLMGTIGIYXPCISQKP 211

RESULT 48

AED52631  
ID AED52631 standard; protein; 220 AA.

XX  
AC AED52631;

XX  
DT 29-DEC-2005 (first entry)

XX  
DE Fusion protein D1/3-E7-His (HPV16).

XX  
KW Fusion protein; vaccine; papilloma; cytostatic; papillomavirus infection;  
KW virucide; uterine cervix tumor; E7; D protein.

XX  
OS Haemophilus influenzae; strain 772.  
OS Human papillomavirus type 16.  
OS Synthetic.  
OS Chimeric.

XX  
PN IN9801903-I4.

XX  
PD 04-MAR-2005.

XX  
PF 24-AUG-1998; 98IN-CH001903.

XX  
PR 22-AUG-1997; 97EP-00179535.

XX  
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.

XX  
PI Tyrrell AMR;

XX  
DR WPI: 2005-557648/57.  
DR N-PSDB: AED52632.

XX  
PT Vaccine.

XX  
PS Example 1; Fig 1; 96pp; English.

XX  
CC The invention relates to human Papilloma virus (HPV) fusion proteins,  
CC linked to an immunological fusion partner that provides T helper epitopes  
CC to the HPV antigen. Vaccine formulations comprising the fusion proteins  
CC are useful in the treatment or prophylaxis of HPV induced lesions  
CC (papillomas, warts and cervical cancer). HPV 16 (and HPV 18) E6 and E7  
CC proteins (singly, as an E6-E7 fusion or mutated) were fused to either  
CC Haemophilus influenzae D protein (20-127), the C-terminus of  
CC Streptococcus pneumoniae Lyta protein (cLyta) or chloroixin. The present  
CC sequence represents an HPV-H. influenzae D protein, fusion protein of the  
CC invention.

XX  
SQ Sequence 220 AA;

Query Match 99.0%; Score 512; DB 9; Length 220;  
Best Local Similarity 96.9%; Pred. No. 6.1e-57;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MGGDPTLHEYMDLQPETTDLYXXYQNDSSSEEDIDGPAGQAEPPRAHYNIITFCCK 60  
Db 114 MGGDPTLHEYMDLQPETTDLYCYEQNDSSSEEDIDGPAGQAEPPRAHYNIITFCCK 173

QY 61 CDSTLRICVOSTHVDIRTTLEDLMGTIGIYXPICSOXP 98  
 |||||  
 DB 174 CDSTLRICVOSTHVDIRTTLEDLMGTIGIYXPICSOXP 211  
 |||||

RESULT 49  
 AAY25380  
 ID AAY25380 standard; protein, 239 AA.  
 XX  
 AC AAY25380;  
 XX  
 DT 06-SEP-1999 (first entry)  
 XX  
 DE HPV fusion protein CLYTA-E7-His/HPV16.  
 XX  
 KM Fusion protein; E6 protein; E7 protein; E6/E7; immunomodulator; tumour;  
 KM immunological fusion partner; Cpg oligonucleotide; immune response;  
 KM HPV antigen; prevention; treatment.  
 XX  
 OS Synthetic.  
 OS Human papillomavirus.  
 XX  
 PN WO933868-A2.  
 XX  
 PD 08-JUL-1999.  
 XX  
 PF 18-DEC-1998; 98WO-EP008563.  
 XX  
 PR 24-DEC-1997; 97GB-00027262.  
 XX  
 PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
 XX  
 PI Dalemans WJ, Gerard CMG;  
 XX  
 DR WPI: 1999-405485/34.  
 XX  
 DR N-PSDB; AAX78796.  
 XX  
 PT Composition comprising an E6, E7 or E6/E7 fusion protein from HPV to  
 PT induce immune response to HPV.  
 XX  
 PS Example VII; Page 53; 62pp; English.  
 XX  
 CC AAX78791-X78801 represent nucleic acid sequences which encode novel  
 CC constructs comprising an E6 or E7 protein or E6/E7 fusion protein from  
 CC HPV (represented in AAY25375-Y25386). These constructs are optionally  
 CC linked to an immunological fusion partner and an immunomodulatory Cpg  
 CC oligonucleotide. The products of the invention can be used to induce an  
 CC immune response in a patient to an HPV antigen. They can also be used for  
 CC preventing or treating HPV induced tumours  
 CC  
 SQ Sequence 239 AA;  
 XX

Query Match 99.0%; Score 512; DB 2; Length 239;  
 Best Local Similarity 96.9%; Pred. No. 6.8e-57;  
 Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDTPTLHEHYMDLQPEETDLYXXYXQNDSSSEDEIDGPAGAEPPDRAHYNIVTFCK 60  
 |||||  
 DB 133 MHGDTPTLHEHYMDLQPEETDLYCYEQNDSSSEDEIDGPAGAEPPDRAHYNIVTFCK 192  
 |||||

QY 61 CDSTLRICVOSTHVDIRTTLEDLMGTIGIYXPICSOXP 98  
 |||||  
 DB 193 CDSTLRICVOSTHVDIRTTLEDLMGTIGIYXPICSOXP 230  
 |||||

RESULT 50  
 AAY02636  
 ID AAY02636 standard; protein, 239 AA.  
 XX  
 AC AAY02636;  
 XX  
 DT 17-OCT-2003 (revised)

DT 22-JUN-1999 (first entry)  
 XX  
 DE CLYTA-E7-His protein.  
 XX  
 KM Chimeric; E6; E7; fusion protein; CLYTA; vaccine; immunotherapy; tumour;  
 KM lesion; benign; malignant; virus; infection.  
 XX  
 OS Human papillomavirus.  
 OS Streptococcus pneumoniae.  
 OS Chimeric.  
 XX  
 PN WO910375-A2.  
 XX  
 PD 04-MAR-1999.  
 XX  
 PF 17-AUG-1998; 98WO-EP005285.  
 XX  
 PR 22-AUG-1997; 97GB-00017953.  
 XX  
 PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
 XX  
 PI Bruck C, Cabezon Silva T, Delisse AEF, Gerard CMG;  
 PI Lombardo-Bencheikh A;  
 XX  
 DR WPI: 1999-190587/16.  
 DR N-PSDB; AAX29785.  
 XX  
 PT Human Papilloma Virus (HPV) fusion proteins - useful in vaccines for  
 PT treatment or prophylaxis of HPV induced lesions.  
 XX  
 PS Disclosure; Fig 12; 95pp; English.  
 XX  
 CC This sequence represents a chimeric E6 or E7 protein or E6/E7 fusion  
 CC protein from Human papillomavirus (HPV) linked to an immunological fusion  
 CC partner, in this case, a fragment of the Streptococcus pneumoniae CLYTA  
 CC protein of the encoded protein. The protein can be used in a vaccine, for  
 CC immuno-therapeutically treating HPV induced tumour lesions (benign or  
 CC malignant) and preventing HPV viral infection. (Updated on 17-OCT-2003 to  
 CC standardise OS field)  
 CC  
 SQ Sequence 239 AA;  
 XX

Query Match 99.0%; Score 512; DB 2; Length 239;  
 Best Local Similarity 96.9%; Pred. No. 6.8e-57;  
 Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDTPTLHEHYMDLQPEETDLYXXYXQNDSSSEDEIDGPAGAEPPDRAHYNIVTFCK 60  
 |||||  
 DB 133 MHGDTPTLHEHYMDLQPEETDLYCYEQNDSSSEDEIDGPAGAEPPDRAHYNIVTFCK 192  
 |||||

QY 61 CDSTLRICVOSTHVDIRTTLEDLMGTIGIYXPICSOXP 98  
 |||||  
 DB 193 CDSTLRICVOSTHVDIRTTLEDLMGTIGIYXPICSOXP 230  
 |||||

RESULT 51  
 AED52644  
 ID AED52644 standard; protein, 239 AA.  
 XX  
 AC AED52644;  
 XX  
 DT 29-DEC-2005 (first entry)  
 XX  
 DE Fusion protein cLYTA-E7-His/HPV16.  
 XX  
 KM Fusion protein; vaccine; papilloma; cytostatic; papillomavirus infection;  
 KM virucide; uterine cervix tumor; E7; LyCA.  
 XX  
 OS Streptococcus pneumoniae.  
 OS Human papillomavirus type 16.  
 OS Synthetic.  
 OS Chimeric.

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PN IN9801903-14.
XX
XX 04-MAR-2005.
XX
XX 24-AUG-1998; 98IN-CH001903.
XX
XX 22-AUG-1997; 97EP-00179535.
XX
XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
XX Tyrrell AMR;
XX
XX WPI; 2005-557648/57.
XX
XX N-PSDB; AED52643.
XX
XX Vaccine.
XX
XX Example 11; Fig 12; 96pp; English.
XX
XX The invention relates to human Papilloma virus (HPV) fusion proteins,
XX linked to an immunological fusion partner that provides T helper epitopes
XX to the HPV antigen. Vaccine formulations comprising the fusion proteins
XX are useful in the treatment or prophylaxis of HPV induced lesions
XX (papillomas, warts and cervical cancer). HPV 16 (and HPV 18) E6 and E7
XX proteins (singly, as an E6-E7 fusion or mutated) were fused to either
XX Haemophilus influenzae D protein (20-127), the C-terminus of
XX Streptococcus pneumoniae LytA protein (clyfA) or chloredoxin. The present
XX sequence represents an HPV-LyftA, fusion protein of the invention.
XX
XX Sequence 239 AA:
SQ
Query Match 99.0%; Score 512; DB 9; Length 239;
Beat Local Similarity 96.9%; Pred. No. 6.8e-57;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 MHGDPPTLHEHYMLDLPQETTDLYXXQLNDSSEEDIEDPAGQAEPRRAHYNIVTFCK 60
Db 133 MHGDPPTLHEHYMLDLPQETTDLYCYEQLNDSSEEDIEDPAGQAEPRRAHYNIVTFCK 192
Qy 61 CDSTLRICVOSTHVDIRTLEDLMGTGIVYPCISQKP 98
Db 193 CDSTLRICVOSTHVDIRTLEDLMGTGIVCPCISQKP 230

```

RESULT 52

ADO44066 standard; protein; 248 AA.

XX ADO44066;

XX 15-JUN-2004 (first entry)

XX Amino acid sequence of an E7E6 fusion protein.

XX E6 protein; E7 protein; fusion protein; HPV16; HPV-associated cancer;

XX cervical cancer; immune response; lower gastrointestinal tract cancer;

XX anal cancer; reproductive system cancer; penile cancer; vulvar cancer.

XX Human papillomavirus type 16.

XX Synthetic.

XX WO2004030636-A2.

XX 15-APR-2004.

XX 02-OCT-2003; 2003WO-US031726.

XX 03-OCT-2002; 2002US-0415929P.

XX (AMHP ) WYETH HOLDINGS CORP.

XX Smith L, Caesetti MC;

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DR WPI; 2004-316328/29.
DR N-PSDB; ADO44067.
XX
XX New polypeptide comprising human papillomavirus E6 and E7 polypeptides,
XX useful for treating or preventing human papillomavirus (HPV)-associated
XX cancers, e.g. cervical cancer.
XX
XX Example 1; Page 72-73; 101pp; English.
XX
XX The present sequence represents an E7E6 fusion protein, comprising wild
XX type E7 and E6 polypeptides from human papillomavirus type 16 (HPV16).
XX The specification describes human papillomavirus E6 and E7 polypeptides,
XX where the E7 polypeptide has mutations at any one or more of the amino
XX acids corresponding to amino acids 24, 26 or 91 of the sequence given in
XX ADO44073 and the E6 polypeptide has no mutations or has mutations at any
XX one or more of the amino acids corresponding to amino acids 63 or 106 of
XX the sequence given in ADO44072. The polypeptides of the invention are
XX useful for treating or preventing human papillomavirus (HPV)-associated
XX cancers, such as cervical cancer. The fusion proteins and nucleic acids
XX encoding the fusion proteins are useful for generating immune responses
XX against HPV. They are also useful for treating lower gastrointestinal
XX tract cancers, e.g. anal cancer, and other cancers of the reproductive
XX system, including penile and vulvar cancer.
XX
XX Sequence 248 AA:
SQ
Query Match 99.0%; Score 512; DB 8; Length 248;
Beat Local Similarity 96.9%; Pred. No. 7.1e-57;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 MHGDPPTLHEHYMLDLPQETTDLYXXQLNDSSEEDIEDPAGQAEPRRAHYNIVTFCK 60
Db 1 MHGDPPTLHEHYMLDLPQETTDLYCYEQLNDSSEEDIEDPAGQAEPRRAHYNIVTFCK 60
Qy 61 CDSTLRICVOSTHVDIRTLEDLMGTGIVYPCISQKP 98
Db 61 CDSTLRICVOSTHVDIRTLEDLMGTGIVCPCISQKP 98

```

RESULT 53

AA43480 standard; protein; 253 AA.

XX AA43480;

XX 17-OCT-2003 (revised)

XX 27-AUG-2003 (revised)

XX 26-JAN-2000 (first entry)

XX Amino acid sequence of a CTLA4-E7 fusion protein.

XX CTLA4; E7; fusion protein; B7 receptor positive B cell;

XX CTLA4 receptor positive T cell interaction; immune system; suppression;

XX autoimmune disease; lupus erythematosus; host-graft;

XX transplant rejection; chimera.

XX Homo sapiens.

XX Papillomavirus.

XX Chimeric.

XX Key Location/Qualifiers

XX Peptide 1..26

XX Protein /note="leader sequence"

XX Protein /note="CTLA4 sequence"

XX Protein /note="E7 sequence"

XX US5968510-A.

XX 19-OCT-1999.

XX 04-OCT-1996; 96US-00725776.

```

XX 27-JUN-1991; 91US-00723617.
PR 22-JAN-1993; 93US-00008898.
PR 15-APR-1994; 94US-00228208.
PR 18-JAN-1995; 95US-00375390.
PR 05-JUN-1995; 95US-00465078.
XX (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX Ledbetter JA, Damle NK, Brady W, Kiener PA, Linsley PS;
XX WPI; 1999-600811/51.
XX
XX Regulating CTLA4 positive T cell interactions.
XX
XX Disclosure; Fig 37; 75pp; English.
XX
XX The present sequence represents a soluble CTLA4 fusion protein, for use
XX in the method of the invention. The specification describes a method for
XX regulating CTLA4 receptor positive T cell interactions with B7 receptor
XX positive B cells. The method comprises contacting the CTLA4-positive T
XX cells with monoclonal antibody fragments reacting with CTLA4. This
XX inhibits (and therefore regulates) interactions between CTLA4-positive T
XX cells and B7 positive B cells. The method may be used for regulating
XX CTLA4 receptor positive T cell interactions with B7 receptor positive B
XX cells. In this way the immune system of an individual can be manipulated
XX (especially suppressed) for the treatment of autoimmune diseases
XX (especially lupus erythematosus) and to prevent host-graft and transplant
XX rejection. (Updated on 27-AUG-2003 to correct OS field.) (Updated on 17-
XX OCT-2003 to standardize OS field)
XX
XX Sequence 253 AA:
SQ
XX
XX Query Match 99.0%; Score 512; DB 2; Length 253;
XX Best Local Similarity 96.9%; Pred. No. 7.3e-57;
XX Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 1 MHGDPPTLHRYM.DLQETTDLYXXQLNDSSEDEIDGPAGAEPRDAHYNIIVTFCK 60
XX 156 MHGDPPTLHRYM.DLQETTDLYCYEQNDSSSEDEIDGPAGAEPRDAHYNIIVTFCK 215
XX
XX DB 61 CDSTLRLCVQSTHYDRTITLEDLMGTGIYXPCSQKP 98
XX 216 CDSTLRLCVQSTHYDRTITLEDLMGTGIYXPCSQKP 253
XX
XX
XX RESULT 54
XX AAY01502
XX ID AAY01502 standard; protein; 253 AA.
XX
XX AC AAY01502;
XX
XX DT 26-MAY-1999 (first entry)
XX
XX DE Amino terminal CTLA4-carboxy terminal E7 fusion protein.
XX
XX CTLA4 receptor; immunoglobulin; Ig; fusion protein; B7 antigen;
XX soluble CTLA4; T cell interaction; B7 positive cell; immune disorder;
XX immune system disease; graft versus host disease; psoriasis;
XX graft transplant rejection; T cell lymphoma; benign lymphocytic angitis;
XX autoimmune disease; lupus erythematosus; Grave's disease;
XX Addison's disease; Crohn's disease; multiple sclerosis;
XX ulcerative colitis; Sjogren's syndrome; mixed connective tissue disease;
XX viral proliferation; T cell activation; AIDS; HTLV1.
XX
XX OS Synthetic.
XX XX Homo sapiens.
XX
XX PN US5885579-A.
XX
XX PD 23-MAR-1999.
XX
XX PF 08-JUL-1997; 97US-00889666.

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XX 27-JUN-1991; 91US-00723617.
PR 22-JAN-1993; 93US-00008898.
PR 15-APR-1994; 94US-00228208.
PR 18-JAN-1995; 95US-00375390.
XX (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX Damle NK, Kiener PA, Brady W, Ledbetter JA, Linsley PS;
XX WPI; 1999-228484/19.
XX
XX Human CTLA4 receptor protein - used to regulate T-cell interactions with
XX B7 positive cells.
XX
XX Disclosure; Fig 37; 75pp; English.
XX
XX The specification describes a CTLA4 receptor/immunoglobulin (Ig) fusion
XX protein which is reactive with the B7 antigen. DNA encoding the CTLA4
XX protein can be used in a vector in a host vector system for producing
XX soluble CTLA4. The CTLA4 fusion protein can be used for regulating T cell
XX interactions with B7 positive cells. The CTLA4 fusion protein can be
XX used for treating immune system diseases mediated by T cell interactions
XX with B7 positive cells. The immune system diseases include graft versus
XX host disease, psoriasis, immune disorders associated with graft
XX transplant rejection, T cell lymphoma, benign lymphocytic angitis, and
XX autoimmune diseases such as lupus erythematosus, Grave's disease,
XX Addison's disease, Crohn's disease, multiple sclerosis, ulcerative
XX colitis, Sjogren's syndrome, and mixed connective tissue disease. The
XX fusion protein may also be used to block the proliferation of viruses
XX dependent on T cell activation, such as the virus that causes AIDS,
XX HTLV1. The present sequence was created in the course of the invention
XX
XX Sequence 253 AA:
SQ
XX
XX Query Match 99.0%; Score 512; DB 2; Length 253;
XX Best Local Similarity 96.9%; Pred. No. 7.3e-57;
XX Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 1 MHGDPPTLHRYM.DLQETTDLYXXQLNDSSEDEIDGPAGAEPRDAHYNIIVTFCK 60
XX 156 MHGDPPTLHRYM.DLQETTDLYCYEQNDSSSEDEIDGPAGAEPRDAHYNIIVTFCK 215
XX
XX DB 61 CDSTLRLCVQSTHYDRTITLEDLMGTGIYXPCSQKP 98
XX 216 CDSTLRLCVQSTHYDRTITLEDLMGTGIYXPCSQKP 253
XX
XX
XX RESULT 55
XX AAW97612
XX ID AAW97612 standard; protein; 253 AA.
XX
XX AC AAW97612;
XX
XX DT 26-MAY-1999 (first entry)
XX
XX DE Amino terminal CTLA4-carboxy terminal E7 fusion protein.
XX
XX CTLA4 receptor; immunoglobulin; Ig; fusion protein; B7 antigen;
XX soluble CTLA4; T cell interaction; B7 positive cell; immune disorder;
XX immune system disease; graft versus host disease; psoriasis;
XX graft transplant rejection; T cell lymphoma; benign lymphocytic angitis;
XX autoimmune disease; lupus erythematosus; Grave's disease;
XX Addison's disease; Crohn's disease; multiple sclerosis;
XX ulcerative colitis; Sjogren's syndrome; mixed connective tissue disease;
XX viral proliferation; T cell activation; AIDS; HTLV1.
XX
XX OS Synthetic.
XX XX Homo sapiens.
XX
XX PN US5885796-A.
XX
XX PD 23-MAR-1999.

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XX 05-JUN-1995; 95US-00465078.
XX
PF 27-JUN-1991; 91US-00723617.
XX 22-JAN-1993; 93US-00008898.
PR 22-JAN-1993; 93US-00008898.
PR 15-APR-1994; 94US-00228208.
PR 18-JAN-1995; 95US-00375390.
XX
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
PI Danle NK, Brady W, Ledbetter JA, Linsley PS;
XX WPI; 1999-228535/19.
XX
PT CTLA4 receptor protein for use in treatment of immune system diseases.
XX
PS Discloure; Fig 37; 75pp; English.
XX
XX The specification describes a CTLA4 receptor/immunoglobulin (Ig) fusion
CC protein which is reactive with the B7 antigen. DNA encoding the CTLA4
CC protein can be used in a vector in a host vector system for producing
CC soluble CTLA4. The CTLA4 fusion protein can be used for regulating T cell
CC interactions with B7 positive cells. The CTLA4Ig fusion protein can be
CC used for treating immune system diseases mediated by T cell interactions
CC with B7 positive cells. The immune system diseases include graft versus
CC host disease, psoriasis, immune disorders associated with graft
CC transplant rejection, T cell lymphoma, benign lymphocytic angitis, and
CC autoimmune diseases such as lupus erythematosus, Grave's disease, and
CC Addison's disease, Crohn's disease, multiple sclerosis, ulcerative
CC colitis, Sjogren's syndrome, and mixed connective tissue disease. The
CC fusion protein may also be used to block the proliferation of viruses
CC dependent on T cell activation, such as the virus that causes AIDS,
CC HTLV1. The present sequence was created in the course of the invention
XX
SQ Sequence 253 AA;
Query Match 99.0%; Score 512; DB 2; Length 253;
Best Local Similarity 96.9%; Pred. No. 7.3e-57;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDTPTLHEYMLDLPQETTDLYXXOLNDSSEEDRIDGPAQAEPDRAHYNIVTFCK 60
DB 156 MHGDTPTLHEYMLDLPQETTDLYCYEQLNDSSEEDRIDGPAQAEPDRAHYNIVTFCK 215

QY 61 CDSTLRFCVOSTHVDIRTELDLMGTIGIVXPICQKP 98
DB 216 CDSTLRFCVOSTHVDIRTELDLMGTIGIVPICQKP 253

RESULT 56
AAV41132
ID AAV41132 standard; protein; 253 AA.
XX
AC AAV41132;
XX
DT 24-JAN-2000 (first entry)
XX
DE CTLA4/E7 fusion protein.
XX
XX Monoclonal antibody; Mab; extracellular domain; CTLA4; B7 antigen;
KM T cell interaction; inflammation; autoimmunity; transplantation; GCHD;
KM neoplasia; infectious disease; graft versus host disease; psoriasis;
KM immune disorder; lymphoma; leukemia; autoimmune disease; arthritis;
KM diabetes mellitus; oncostatin M; fusion protein; E7.
XX
OS Synthetic.
XX Homo sapiens.
XX
PN US977318-A.
XX
PD 02-NOV-1999.
XX
PF 07-JUN-1995; 95US-00488062.

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XX 27-JUN-1991; 91US-00723617.
PR 22-JAN-1993; 93US-00008898.
PR 15-APR-1994; 94US-00228208.
PR 18-JAN-1995; 95US-00375390.
XX
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
PI Kleiner PA, Brady W, Danle NK, Linsley PS, Ledbetter JA;
XX WPI; 1999-619712/53.
XX
XX New anti-CTLA4 monoclonal antibodies, used for treating e.g.
PT inflammation, autoimmunity, transplant rejection, infectious diseases or
PT neoplasia.
XX
XX Example; Fig 37; 74pp; English.
XX
XX The invention provides new monoclonal antibodies (Mabs) which bind the
CC extracellular domain of CTLA4 and prevent the binding of CTLA4 to B7
CC antigen. The Mabs can be used for regulating T cell interactions with B7
CC positive cells. They can also be used for preventing or reversing
CC inflammation and for treating autoimmunity, transplantation, infectious
CC diseases and neoplasia. They can be used for treating diseases e.g. graft
CC versus host disease (GCHD), psoriasis, immune disorders associated with
CC graft transplantation rejection, T cell lymphoma, T cell acute
CC lymphoblastic leukemia, testicular angiosarcoma, R cell lymphoma, benign
CC lymphocytic angitis, autoimmune diseases such as lupus erythematosus,
CC Hashimoto's thyroiditis, primary myxedema, Graves disease, pernicious
CC anemia, autoimmune atrophic gastritis, Addison's disease, insulin
CC dependent diabetes mellitus, Goodpasture's syndrome, myasthenia gravis,
CC pemphigus, Crohn's disease, sympathetic ophthalmia, autoimmune uveitis,
CC multiple sclerosis, autoimmune hemolytic anemia, primary biliary
CC cirrhosis, idiopathic thrombocytopenia, chronic action hepatitis,
CC ulcerative colitis, Sjogren's syndrome, rheumatoid arthritis,
CC polyomyelitis, scleroderma, and mixed connective tissue disease. They can
CC also be used for detection, diagnosis, prognosis and monitoring of
CC diseases. The present sequence represents the CTLA4/E7 fusion protein
CC containing an amino terminal CTLA4 domain and a E7 carboxy-terminal
CC domain
XX
SQ Sequence 253 AA;
Query Match 99.0%; Score 512; DB 2; Length 253;
Best Local Similarity 96.9%; Pred. No. 7.3e-57;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDTPTLHEYMLDLPQETTDLYXXOLNDSSEEDRIDGPAQAEPDRAHYNIVTFCK 60
DB 156 MHGDTPTLHEYMLDLPQETTDLYCYEQLNDSSEEDRIDGPAQAEPDRAHYNIVTFCK 215

QY 61 CDSTLRFCVOSTHVDIRTELDLMGTIGIVXPICQKP 98
DB 216 CDSTLRFCVOSTHVDIRTELDLMGTIGIVPICQKP 253

RESULT 57
AAW81586
ID AAW81586 standard; protein; 253 AA.
XX
AC AAW81586;
XX
DT 05-FEB-1999 (first entry)
XX
DE CTLA4/E7 fusion protein sequence.
XX
XX CTLA4 receptor; CTLA4-Ig; fusion protein; B7 antigen; hinge; CH2; CH3;
KM extracellular domain; human; immunoglobulin; T cell; immune system;
KM autoimmune disease; cancer; viral infection; E7.
XX
OS Homo sapiens.
XX Human papillomavirus.
XX

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FH Key Location/Qualifiers
FT Peptide 1..26
FT /note= "leader sequence"
FT Protein 27..154
FT /note= "CTLA4 partial sequence"
FT Domain 27..154
FT /note= "CTLA4 amino terminal domain"
FT Protein 155..253
FT /note= "E7 partial sequence"
FT Domain 155..253
FT /note= "E7 carboxy terminal domain"
XX
XX US844095-A.
XX
XX 01-DEC-1998.
XX
XX 18-JAN-1995; 95US-00375390.
XX
XX 27-JUN-1991; 91US-00723617.
XX 22-JAN-1993; 93US-00008898.
XX 28-MAY-1993; 93US-00069693.
XX 15-APR-1994; 94US-00228208.
XX
XX (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
XX Brady W, Linsley PS, Damlle NK, Ledbetter JA;
XX WPI; 1999-044666/04.
XX
XX Fusion protein of CTLA4 and immunoglobulin fragment - for treating immune
XX system disorders.
XX
XX Example 8; Fig 37; 75pp; English.
XX
XX This represents a CTLA4/E7 fusion protein. The invention provides a CTLA4
XX -Ig fusion protein that binds the B7 antigen and has a first amino acid
XX sequence consisting of the extracellular domain of CTLA4 and a second
XX amino acid sequence consisting of the hinge, CH2 and CH3 regions of a
XX human immunoglobulin molecule. The fusion protein inhibits interaction of
XX T cells with B7-positive cells and may be useful for treating immune
XX system diseases, e.g. autoimmune diseases, cancer or viral infections.
XX The present sequence is an example of such a fusion protein and contains
XX an amino-terminal CTLA4 domain and an E7 carboxy-terminal domain
XX
XX Sequence 253 AA;
SQ
Query Match 99.0%; Score 512; DB 2; Length 253;
Best Local Similarity 96.9%; Pred. No. 7.3e-57;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 MHGDTPTLHRYMDLQPEETDLYXXYQNDSSSEEDIDGPAGQAEPPRAHYNIIVTFCK 60
DB 156 MHGDTPTLHRYMDLQPEETDLYCYEQLNDSSSEEDIDGPAGQAEPPRAHYNIIVTFCK 215
QY 61 CDSTLRLCVOSTHYDRTLTEDLTMGTIGIYXPICSQKP 98
DB 216 CDSTLRLCVOSTHYDRTLTEDLTMGTIGIYXPICSQKP 253

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OS Synthetic.
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1..15
XX /note= "signal peptide"
XX Protein 16..155
XX /note= "CTLA4 protein"
XX Protein 155..253
XX /note= "E7 protein"
XX
XX US851795-A.
XX
XX 22-DEC-1998.
XX
XX 02-JUN-1995; 95US-00459818.
XX
XX 27-JUN-1991; 91US-00723617.
XX 22-JAN-1993; 93US-00008898.
XX 15-APR-1994; 94US-00228208.
XX 18-JAN-1995; 95US-00375390.
XX
XX (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
XX Ledbetter JA, Brady W, Damlle NK, Kiener PA, Linsley PS;
XX WPI; 1999-080402/07.
XX
XX Soluble CTLA4 protein that binds B7 antigen of activated B cells - and
XX fusion proteins useful for regulating T-cell interactions with B cells.
XX
XX Claim 18; Fig 37; 75pp; English.
XX
XX The present sequence represents a CTLA4-E7 fusion protein. CTLA4 is a
XX receptor protein having a high degree of homology with CD28. The CTLA4
XX receptor is identified as a ligand for the B7 antigen. The CTLA4 protein
XX can also be used to construct a fusion protein of CTLA4 and human
XX immunoglobulin (Ig-gamma1). The CTLA4 protein was fused to the hinge CH2
XX and CH3 regions of human IgG-gamma1. Soluble CTLA4-Ig fusion proteins can
XX be used to regulate T-cell interactions with B7-positive cells and to
XX treat immune system diseases mediated by such interactions
XX
XX Sequence 253 AA;
SQ
Query Match 99.0%; Score 512; DB 2; Length 253;
Best Local Similarity 96.9%; Pred. No. 7.3e-57;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 MHGDTPTLHRYMDLQPEETDLYXXYQNDSSSEEDIDGPAGQAEPPRAHYNIIVTFCK 60
DB 156 MHGDTPTLHRYMDLQPEETDLYCYEQLNDSSSEEDIDGPAGQAEPPRAHYNIIVTFCK 215
QY 61 CDSTLRLCVOSTHYDRTLTEDLTMGTIGIYXPICSQKP 98
DB 216 CDSTLRLCVOSTHYDRTLTEDLTMGTIGIYXPICSQKP 253

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RESULT 58
AAW87562
ID AAW87562 standard; protein; 253 AA.
XX
XX AAW87562;
XX
XX 01-MAR-1999 (first entry)
XX
XX CTLA4-E7 fusion protein.
XX
XX CD28; B7; fusion protein; hinge CH2; CH3; human IgG-gamma1; CTLA4;
XX CTLA4 receptor; ligand; regulation; T-cell interaction; B7-positive cell;
XX immune system disease.
XX
XX

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RESULT 59
ADRA47005
ID ADRA47005 standard; protein; 256 AA.
XX
XX ADRA47005;
XX
XX 18-NOV-2004 (first entry)
XX
XX Human papillomavirus type 16 E7 protein for Dengue virus vaccine.
XX
XX cytostatic; virucide; dengue virus; recombinant replicon; deletion;
XX piem protein; C protein; NS1 protein signal; vaccine; cervical cancer;
XX viral disease; antigen; dendritic cell; immune response;
XX human papillomavirus.
XX
XX Human papillomavirus type 16.
XX

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XX      WO2004072274-A1.
PN      26-AUG-2004.
XX      30-JAN-2004; 2004WO-CN000088.
PD      30-JAN-2003; 2003CN-00115272.
XX      30-JAN-2003; 2003CN-00115273.
XX      (SHAN-) SHANGHAI TENGGEN BIOMEDICAL CO LTD.
PA      (TENG-) TENGGEN BIOMEDICAL CO.
PA      (BEIJ-) BEIJING ORIENTAL TENGGEN TECHNOLOGY DEV C.
XX      Pang X;
PI      WPI; 2004-625870/60.
XX      N-PSDB; ADRA47004.
DR      Virus-like particle vaccines containing dengue virus recombinant replicon
XX      as core for carrier, applicable in preventives or/and remedies for tumors
PT      like cervical cancer and viral diseases.
XX      Example 2; SEQ ID NO 2; 38pp; Chinese.
PS      A dengue virus recombinant replicon has a deletion of the complete coding
XX      sequence for prem protein of dengue virus and also includes elements of
CC      e.g. the non-coding region in the whole of the 5'-end, the coding region
CC      of the front 20 amino acids in the C protein, and the coding region of
CC      NS1 protein signal; coding regions of all non-structural proteins. The
CC      obtained vaccines are useful in producing preventives or/and remedies for
CC      cancer like cervical cancer and viral diseases. Such vaccines can
CC      efficiently express antigen in infected cells, which is because dengue
CC      virus can infect dendritic cells, and can effectively present antigen to
CC      provide immunity effect. Different types of dengue virus can be used to
CC      repeatedly produce efficient immune response thereby strengthening the
CC      body's immune system against the pathogen that contains such antigen.
CC      Human papillomavirus (HPV) vaccines were prepared by using a gene-
CC      expressing system using of the full-length dengue virus cDNA clone
CC      (pBS/FLU2). The recombinant virus vectors were transfected into baby
CC      hamster kidney (BHK) cells to enable the screening of BHK-21 Tet-off cell
CC      lines. This sequence corresponds to the HPV type 16 E7 protein whose
CC      encoding gene is used as the gene of interest in the recombinant replicon
CC      of the invention.
XX      SQ      Sequence 256 AA;
Query Match      99.0%; Score 512; DB 8; Length 256;
Best Local Similarity 96.9%; Pred. No. 7.4e-57;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY      1 MHGDPPTLHEXYMLDLPETTDLYXXYXQUNDSEDEIDGPAGQAEPPRAHNYIVTFCK 60
DB      1 MHGDPPTLHEXYMLDLPETTDLYCYEQUNDSEDEIDGPAGQAEPPRAHNYIVTFCK 60
QY      61 CDSTLRLCVQSTHVDIRTLIEDLIMGTLGIVXPICQKP 98
DB      61 CDSTLRLCVQSTHVDIRTLIEDLIMGTLGIVCPICQKP 98
RESULT 60
AEF40157 ID AEF40157 standard; protein; 256 AA.
XX
AC      AEF40157;
XX
DT      23-MAR-2006 (first entry)
XX
DE      Human papillomavirus 16 (HPV-16) E7-E6 oncoprotein.
XX
KW      Vaccine, virus-like particle; replicon; therapeutic; cancer; cytostatic;
KM      neoplasm; viral infection; virucide; infection; oncoprotein.
XX

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OS      Human papillomavirus type 16.
XX      US2006018928-A1.
XX      26-JAN-2006.
XX      29-JUL-2005; 2005US-00192923.
XX      30-JAN-2003; 2003CN-00115272.
XX      30-JAN-2003; 2003CN-00115273.
XX      30-JAN-2004; 2004WO-00072274.
XX      (PANG/) PANG X.
XX      Pang X;
PI      WPI; 2006-109169/11.
XX      N-PSDB; AEF40156.
DR      New recombinant DEN replicons with a deletion of prem, useful for
XX      producing a drug for the prophylaxis and treatment of cancer or viral
PT      infection.
XX      Example 2; SEQ ID NO 2; 24pp; English.
PS      The present invention provides a virus-like particle (VLP) vaccine which
XX      contains dengue virus (DENV) recombinant replicon as its core. The DEN
CC      replicon contains exogenous nucleotide sequences such as human
CC      papillomavirus (HPV) antigen proteins, immune regulators or combination
CC      of HPV antigen and immune regulators. The invention is useful for
CC      producing a drug for the prophylaxis and treatment of cancer or viral
CC      infection. The present sequence is a human papillomavirus oncoprotein.
XX      SQ      Sequence 256 AA;
Query Match      99.0%; Score 512; DB 10; Length 256;
Best Local Similarity 96.9%; Pred. No. 7.4e-57;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY      1 MHGDPPTLHEXYMLDLPETTDLYXXYXQUNDSEDEIDGPAGQAEPPRAHNYIVTFCK 60
DB      1 MHGDPPTLHEXYMLDLPETTDLYCYEQUNDSEDEIDGPAGQAEPPRAHNYIVTFCK 60
QY      61 CDSTLRLCVQSTHVDIRTLIEDLIMGTLGIVXPICQKP 98
DB      61 CDSTLRLCVQSTHVDIRTLIEDLIMGTLGIVCPICQKP 98
RESULT 61
AAR97561 ID AAR97561 standard; protein; 266 AA.
XX
AC      AAR97561;
XX
DT      27-AUG-2003 (revised)
DT      11-JAN-1997 (first entry)
XX
DE      Human papilloma virus E6/E7 protein variant.
XX
KW      Human papilloma virus; E6; E7; deletion mutant; HPV; immune response;
KM      humoral immune response; cellular immune response; vaccine.
XX
OS      Human papillomavirus.
XX      WO9619496-A1.
XX
PD      27-JUN-1996.
XX
PF      20-DEC-1995; 95WO-AU000868.
XX
PR      20-DEC-1994; 94AU-00000157.
XX      (CSLC-) CSL LTD.
PA

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PA (UYOU ) UNIV QUEENSLAND.  
 XX Edwards SJ, Cox J, Webb EA, Frazer I;  
 PT WPI; 1996-309518/31.  
 DR N-PSDB; AAT31833.  
 XX  
 PT Vaccine variants of human papilloma virus antigens - contain variants of  
 PT E6 and/or E7 protein, pref. deletion mutants, and are used to treat or  
 PT prevent HPV infection.  
 PS Example 1; Page 15-16; 37pp; English.  
 XX  
 CC A variant of the human papilloma virus (HPV) E6 or E7 protein which  
 CC elicits a humoral and/or cellular immune response against HPV can be used  
 CC in vaccines against HPV or to treat HPV infection. The variant is  
 CC preferably a deletion mutant comprising at least half, and preferably two  
 CC thirds of full length E6 or E7 protein starting from the N- or C-  
 CC terminal, or is a full length E6 moiety fused to a full length E7 moiety.  
 CC The variant optionally has a linkage moiety and a foreign protein or  
 CC peptide which facilitates the purification of, and enhances the  
 CC immunogenicity of, the fusion protein. This sequence is a full length  
 CC E6/E7 fusion protein. (Updated on 27-AUG-2003 to correct OS field.)  
 CC  
 XX Sequence 266 AA:  
 SQ  
 Query Match 99.0%; Score 512; DB 2; Length 266;  
 Best Local Similarity 96.9%; Pred. No. 7.8e-57;  
 Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 MHGGPTLHXYMIDLQPEETDLYXXYXOLNDSSEEDIDGPAQAEPRAHYNIIVTFCK 60  
 DB 161 MHGGPTLHXYMIDLQPEETDLYCYEQLNDSSEEDIDGPAQAEPRAHYNIIVTFCK 220  
 QY 61 CDSTLRLCVOSTHYDITRLDLMGTIGIYXPICQKP 98  
 DB 221 CDSTLRLCVOSTHYDITRLDLMGTIGIYXPICQKP 258  
 RESULT 62  
 AAU02129  
 ID AAU02129 standard; protein; 288 AA.  
 XX  
 AC AAU02129;  
 XX  
 DT 29-AUG-2001 (first entry)  
 XX  
 DE Flt-3 ligand (FL) used to make chimeric immunogenic polypeptide.  
 XX  
 KW Mouse; granulocyte-macrophage-colony stimulating factor; GM-CSF;  
 KW chimeric; heat shock protein; HSP; Flt-3 ligand; FL; exotoxin A; ETA dII;  
 KW antigenic; immunogenic; cytotoxic T cell response; tumour; vaccine;  
 KW immunotherapy.  
 XX  
 OS Unidentified.  
 XX  
 PN W0200129233-A2.  
 XX  
 PD 26-APR-2001.  
 XX  
 PF 20-OCT-2000; 2000WO-US041422.  
 XX  
 PR 20-OCT-1999; 99US-00421608.  
 XX  
 PR 09-FEB-2000; 2000US-00501097.  
 XX  
 PA (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.  
 XX  
 PI Wu T, Hung C;  
 XX  
 DR WPI; 2001-290921/30.  
 XX  
 PT New chimeric polypeptide, useful as anti-tumor vaccines, comprises  
 PT carboxy terminal fragment of heat shock protein, Flt-3 ligand or

PT cytoplasmic translocation domain of Pseudomonas exotoxin A and antigenic  
 PT polypeptide.  
 XX  
 XX Claim 9; Fig 19; 110pp; English.  
 XX  
 CC The sequence represents the amino acid sequence of Flt-3 ligand (FL) used  
 CC in construction of a chimeric polypeptide comprising: (a) a first  
 CC polypeptide domain containing a carboxy terminal fragment of a heat shock  
 CC protein (HSP), an Flt-3 ligand (FL), a cytoplasmic translocation domain  
 CC of a Pseudomonas exotoxin A (ETA dII), or a granulocyte-macrophage colony  
 CC stimulating factor (GM-CSF); and (b) a second polypeptide domain  
 CC containing an antigenic polypeptide. A composition comprising the  
 CC chimeric polypeptide is useful for inducing an immune response such as a  
 CC cytotoxic T cell response. The nucleic acid or vector encoding the  
 CC chimeric polypeptide present in the composition is administered as naked  
 CC DNA by gene gun or equivalent, or by liposomal formulation. These are  
 CC thus useful for vaccinating a mammal against infection by inducing an  
 CC immune response to a pathogen. Preferably they are useful for vaccinating  
 CC a mammal against a tumour antigen. The compositions and methods are  
 CC useful for stimulating or enhancing the immunogenicity of a selected  
 CC antigen or stimulating or enhancing a cellular immune response specific  
 CC for that antigen. The chimeric nucleic acid molecules and vaccination  
 CC methods, yield potent antigen-specific immunotherapy. The polynucleotides  
 CC and DNA vaccines can induce a cellular immune response that is at least  
 CC 40 fold more potent than conventional DNA vaccines. The vaccines are safe  
 CC and useful for administration to domesticated or agricultural animals, as  
 CC well as humans, and have low immunogenicity  
 CC  
 XX Sequence 288 AA:  
 SQ  
 Query Match 99.0%; Score 512; DB 4; Length 288;  
 Best Local Similarity 96.9%; Pred. No. 8.7e-57;  
 Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 MHGGPTLHXYMIDLQPEETDLYXXYXOLNDSSEEDIDGPAQAEPRAHYNIIVTFCK 60  
 DB 190 MHGGPTLHXYMIDLQPEETDLYCYEQLNDSSEEDIDGPAQAEPRAHYNIIVTFCK 249  
 QY 61 CDSTLRLCVOSTHYDITRLDLMGTIGIYXPICQKP 98  
 DB 250 CDSTLRLCVOSTHYDITRLDLMGTIGIYXPICQKP 287  
 RESULT 63  
 AAB31615  
 ID AAB31615 standard; protein; 295 AA.  
 XX  
 AC AAB31615;  
 XX  
 DT 30-APR-2001 (first entry)  
 XX  
 DE Amino acid sequence of Hsp65-E7 fusion protein.  
 XX  
 KW Heat shock protein; Hsp; Th1 response; Th1 cell; CD4+ T lymphocyte cell;  
 KW lymphocyte; Hsp65; Hsp40; Hsp10; Hsp60; Hsp71; microbial pathogen;  
 KW E7 protein.  
 XX  
 OS Synthetic.  
 OS Mycobacterium bovis.  
 OS Human papillomavirus.  
 XX  
 PN W0200104344-A2.  
 XX  
 PD 18-JAN-2001.  
 XX  
 PF 10-JUL-2000; 2000WO-US018828.  
 XX  
 PR 08-JUL-1999; 99US-0143757P.  
 XX  
 PA (STRE-) STRESSGEN BIOTECHNOLOGIES CORP.  
 XX  
 PI Siegel M, Chu NR, Mitzzen LA;  
 XX

DR WPI: 2001-138361/14.  
DR N-PSDB: AAF25022.  
XX Screening for compounds that stimulate Th1-like responses in CD4+ T  
PT lymphocyte cells.  
XX  
PS Example 12; Fig 11; 88pp; English.  
XX  
CC The present sequence represents a fusion protein comprising Mycobacterium  
CC bovis heat shock protein (Hsp) 65 fused at its C terminal to a HPV16 E7  
CC protein. The fusion protein is used in the method of the invention. The  
CC specification describes a method of determining whether a compound  
CC stimulates a Th1-like response. Th1 cells are a subset of CD4+ T  
CC lymphocyte cells. The method comprises contacting naive lymphocytes in  
CC vitro with a fusion protein comprising at least a fragment of Hsp, and  
CC then detecting the Th1-like response exhibited by the cell sample. The  
CC proteins which may be used in the method of the invention are Hsp65,  
CC Hsp40, Hsp10, Hsp60, and Hsp71. The method may be used to identify  
CC compounds that stimulate Th1-like responses in response to microbial  
CC pathogens  
XX  
SQ Sequence 295 AA:  
Query Match 99.0%; Score 512; DB 4; Length 295;  
Best Local Similarity 96.9%; Pred. No. 8.9e-57;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
OY 1 MHGDTPLHEYMLDLOPETTDLYXXQLNDSSEEDIDGPAGQAEPRRAHYNIVTFCK 60  
DB 198 MHGDTPLHEYMLDLOPETTDLYCYEQLNDSSEEDIDGPAGQAEPRRAHYNIVTFCK 257  
OY 61 CDSTLRFCVOSTHYDIRTLEDLMGTIGIYXPCISQKP 98  
DB 258 CDSTLRFCVOSTHYDIRTLEDLMGTIGIYCPICISQKP 295  
RESULT 64  
AAB31613  
ID AAB31613 standard; protein; 324 AA.  
XX  
AC AAB31613;  
XX  
DT 30-APR-2001 (first entry)  
XX  
DE Amino acid sequence of glutathion-S-transferase (GST) -E7 protein.  
XX  
KM Heat shock protein; Hsp; Th1 response; Th1 cell; CD4+ T lymphocyte cell;  
KM lymphocyte; Hsp65; Hsp40; Hsp10; Hsp60; Hsp71; microbial pathogen;  
KM glutathion-S-transferase; GST; E7 protein.  
XX  
XX Synthetic.  
OS Human papillomavirus.  
OS Unidentified.  
OS  
XX MO200104344-A2.  
XX  
PN 18-JAN-2001.  
XX  
PD 10-JUL-2000; 2000WO-US018828.  
XX  
PR 08-JUL-1999; 99US-0143757P.  
XX  
PA (STRE-) STRESSGEN BIOTECHNOLOGIES CORP.  
XX  
PI Siegel M, Chu NR, Mizzzen LA;  
XX  
DR WPI: 2001-138361/14.  
DR N-PSDB: AAF25016.  
XX  
XX Screening for compounds that stimulate Th1-like responses in CD4+ T  
PT lymphocyte cells.  
XX  
PS Example 10; Fig 9; 88pp; English.

XX  
CC The present sequence represents a glutathion-S-transferase (GST) linked  
CC to HPV16 E7 protein, for purification purposes. The E7 protein was used  
CC to construct a fusion protein with Mycobacterium bovis heat shock  
CC proteins (Hsp). The fusion proteins are used in the method of the  
CC invention. The specification describes a method of determining whether a  
CC compound stimulates a Th1-like response. Th1 cells are a subset of CD4+ T  
CC lymphocyte cells. The method comprises contacting naive lymphocytes in  
CC vitro with a fusion protein comprising at least a fragment of Hsp, and  
CC then detecting the Th1-like response exhibited by the cell sample. The  
CC proteins which may be used in the method of the invention are Hsp65,  
CC Hsp40, Hsp10, Hsp60, and Hsp71. The method may be used to identify  
CC compounds that stimulate Th1-like responses in response to microbial  
CC pathogens  
XX  
SQ Sequence 324 AA:  
Query Match 99.0%; Score 512; DB 4; Length 324;  
Best Local Similarity 96.9%; Pred. No. 1e-56;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
OY 1 MHGDTPLHEYMLDLOPETTDLYXXQLNDSSEEDIDGPAGQAEPRRAHYNIVTFCK 60  
DB 227 MHGDTPLHEYMLDLOPETTDLYCYEQLNDSSEEDIDGPAGQAEPRRAHYNIVTFCK 286  
OY 61 CDSTLRFCVOSTHYDIRTLEDLMGTIGIYXPCISQKP 98  
DB 287 CDSTLRFCVOSTHYDIRTLEDLMGTIGIYCPICISQKP 324  
RESULT 65  
AAO22926  
ID AAO22926 standard; protein; 334 AA.  
XX  
AC AAO22926;  
XX  
DT 12-DEC-2002 (first entry)  
XX  
DE HbsAg-EB7 fusion protein sequence.  
XX  
KM Virucide; cytosratic; E6; E7 fusion protein; HPV; immunogenic; vaccine;  
KM fusion partner; immunogenicity; HPV infection; neoplasm; HbsAg-EB7;  
KM chimeric.  
XX  
OS Unidentified.  
OS Chimeric.  
XX  
XX EPI243655-A1.  
XX  
PD 25-SEP-2002.  
XX  
PF 23-MAR-2001; 2001EP-00107271.  
XX  
PR 23-MAR-2001; 2001EP-00107271.  
XX  
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
XX  
PI Cid-Arregui A, Zur Hausen H;  
XX  
DR WPI: 2002-724952/79.  
DR N-PSDB: AAL53424.  
XX  
XX A new DNA sequence encoding a fusion protein comprising a mutagenized HPV  
PT (human papillomavirus) E6 or E7 coding sequence and a sequence encoding a  
PT highly immunogenic fusion partner is useful to vaccinate against HPV  
PT infection.  
XX  
PS Disclosure; Fig 5; 34pp; English.  
XX  
CC The invention relates to a new DNA sequence encodes an E6 or E7 fusion  
CC protein of HPV, where at least 20% of the original codons are replaced by  
CC codons which lead to enhanced translation in a mammalian cell, containing  
CC a mutation which results in production of a truncated non-functional

CC protein, and encoding a highly immunogenic polypeptide fusion partner  
 CC capable of enhancing immunogenicity of the B6 or E7 protein in the  
 CC mammalian host. The invention is used as a vaccine for the prevention or  
 CC treatment of an HPV infection or a neoplasm associated with HPV  
 CC infection. This sequence represents the HbsAg-E67 fusion protein  
 CC sequence of the invention  
 XX

SO Sequence 334 AA;

Query Match 99.0%; Score 512; DB 5; Length 334;  
 Best Local Similarity 96.9%; Pred. No. 1e-56;  
 Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Dy 1 MGGPTPLHEYMDLOPETTDLYXXQLNDSSEEDSIDGPAQAEPRRAHYNIVTFCCK 60  
 |||||||  
 Db 229 MGGPTPLHEYMDLOPETTDLYCYEQLNDSSEEDSIDGPAQAEPRRAHYNIVTFCCK 288  
 |||||||

Oy 61 CDSTLRFCVOSTHVDIRTEEDLMGTGIVXPICSOXP 98  
 |||||||  
 Db 289 CDSTLRFCVOSTHVDIRTEEDLMGTGIVXPICSOXP 326  
 |||||||

#### RESULT 66

AEA40828  
 ID AEA40828 standard; protein; 349 AA.

AC AEA40828;

DT 28-JUL-2005 (first entry)

XX Anti-apoptotic vector E7-BCL-XL protein.

DE immunogenicity; immunogenicity-potentiating polypeptide; IPP; T-cell;  
 KM vaccine; immune stimulation; tumor; cytostatic.

XX Human papillomavirus.

OS Synthetic.

OS Undifferentiated.

PN WO2005047501-A1.

XX 26-MAY-2005.

XX 24-FEB-2004; 2004WO-US005292.

XX 24-FEB-2003; 2003US-0449429P.

PR 18-JUL-2003; 2003US-0488527P.

PR 31-DEC-2003; 2003US-0533792P.

XX (UYJO ) UNIV JOHNS HOPKINS.

PI Wu T, Hung CF, Kim T;

XX WPI; 2005-367009/37.

DR N-PSDB; AEA40827.

XX New nucleic acid composition comprising a first nucleic acid vector  
 PT encoding an anti-apoptotic polypeptide and a second nucleic acid vector  
 PT inhibiting the growth of a tumor.

XX Disclosure; SEQ ID NO 18; 158pp; English.

CC The invention relates to a novel nucleic acid composition useful as an  
 CC immunogen. The composition comprises a combination of: a first nucleic  
 CC acid vector comprising a first sequence encoding an antigenic polypeptide  
 CC or peptide, and optionally, a second sequence linked to the first  
 CC sequence and encoding an immunogenicity-potentiating polypeptide (IPP);  
 CC and a second nucleic acid vector encoding an anti-apoptotic polypeptide.  
 CC When the second vector is administered with the first vector to a  
 CC subject, a T cell mediated immune response to the antigenic polypeptide  
 CC or peptide is induced that is greater in magnitude and/or duration than  
 CC an immune response induced by administration of the first vector alone.

CC The invention further includes: a particle comprising a material that is  
 CC suitable for introduction into a cell or an animal by particle  
 CC bombardment, bound to which is the first and second vectors or  
 CC composition; a pharmaceutical composition capable of inducing or  
 CC enhancing an antigen specific immune response, comprising the particle  
 CC and a carrier or an excipient; inducing or enhancing an antigen specific  
 CC immune response in a subject; increasing the numbers of CD8+ CTLs  
 CC specific for a selected desired antigen in a subject; and inhibiting the  
 CC growth of a tumor in a subject. The nucleic acid composition is useful as  
 CC an immunogen for inhibiting the growth of a tumor, hence it has  
 CC cytostatic activity. This sequence represents an anti-apoptotic vector E7-  
 CC BCL-XL protein of the invention.

SO Sequence 349 AA;

Query Match 99.0%; Score 512; DB 9; Length 349;  
 Best Local Similarity 96.9%; Pred. No. 1.e-56;  
 Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Dy 1 MGGPTPLHEYMDLOPETTDLYXXQLNDSSEEDSIDGPAQAEPRRAHYNIVTFCCK 60  
 |||||||  
 Db 1 MGGPTPLHEYMDLOPETTDLYCYEQLNDSSEEDSIDGPAQAEPRRAHYNIVTFCCK 60  
 |||||||

Oy 61 CDSTLRFCVOSTHVDIRTEEDLMGTGIVXPICSOXP 98  
 |||||||  
 Db 61 CDSTLRFCVOSTHVDIRTEEDLMGTGIVXPICSOXP 98  
 |||||||

#### RESULT 67

AEA40831  
 ID AEA40831 standard; protein; 349 AA.

AC AEA40831;

DT 28-JUL-2005 (first entry)

XX Anti-apoptotic vector E7-mtBCL-XL fusion protein.

DE immunogenicity; immunogenicity-potentiating polypeptide; IPP; T-cell;  
 KM vaccine; immune stimulation; tumor; cytostatic.

XX Human papillomavirus.

OS Synthetic.

OS Undifferentiated.

PN WO2005047501-A1.

XX 26-MAY-2005.

XX 24-FEB-2004; 2004WO-US005292.

XX 24-FEB-2003; 2003US-0449429P.

PR 18-JUL-2003; 2003US-0488527P.

PR 31-DEC-2003; 2003US-0533792P.

XX (UYJO ) UNIV JOHNS HOPKINS.

PI Wu T, Hung CF, Kim T;

XX WPI; 2005-367009/37.

DR New nucleic acid composition comprising a first nucleic acid vector  
 PT encoding an anti-apoptotic polypeptide and a second nucleic acid vector  
 PT inhibiting the growth of a tumor.

XX Disclosure; SEQ ID NO 21; 158pp; English.

CC The invention relates to a novel nucleic acid composition useful as an  
 CC immunogen. The composition comprises a combination of: a first nucleic  
 CC acid vector comprising a first sequence encoding an antigenic polypeptide  
 CC or peptide, and optionally, a second sequence linked to the first  
 CC sequence and encoding an immunogenicity-potentiating polypeptide (IPP);



QY 1 MGGDTPLHEHYMDLQEPETDLYXXQLNDSSEDEIDGPAQAEPDRAHYNIVTFCK 60  
 DB 265 MGGDTPLHEHYMDLQEPETDLYCYEQNDSSSEDEIDGPAQAEPDRAHYNIVTFCK 324  
 QY 61 CDSTLRLCVOSTHVDIRLTEDLGMGTGIVXPICSOXP 98  
 DB 325 CDSTLRLCVOSTHVDIRLTEDLGMGTGIVXPICSOXP 362

## RESULT 70

AED52638

ID AED52638 standard; protein: 371 AA.

XX AED52638;

DT 29-DEC-2005 (first entry)

DE Fusion protein D1/3-E6-E7-His/HPV16.

XX Fusion protein; vaccine; papilloma; cytostatic; papillomavirus infection;

KM viricide; uterine cervix tumor; E7; D protein.

XX Haemophilus influenzae; strain 772.

OS Human papillomavirus type 16.

OS Synthetic.

OS Chimeric.

PN IN9801903-I4.

PD 04-MAR-2005.

PP 24-AUG-1998; 98IN-CH001903.

PR 22-AUG-1997; 97EP-00179535.

XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.

PA Tyrell AMR;

PI WPI; 2005-557648/57.

DR N-PSDB; AED52637.

XX Vaccine.

PT Example 6; Fig 6; 96pp; English.

XX The invention relates to human Papilloma virus (HPV) fusion proteins,  
 CC linked to an immunological fusion partner that provides T helper epitopes  
 CC to the HPV antigen. Vaccine formulations comprising the fusion proteins  
 CC are useful in the treatment or prophylaxis of HPV induced lesions  
 CC (papillomas, warts and cervical cancer). HPV 16 (and HPV 18) E6 and E7  
 CC proteins (singly, as an E6-E7 fusion or mutated) were fused to either  
 CC Hemophilus influenzae D protein (20-127), the C-terminus of  
 CC Streptococcus pneumoniae Lyta protein (cLYTA) or thiodoxin. The present  
 CC sequence represents an HPV-H. Influenzae D protein, fusion protein of the  
 CC invention.  
 CC  
 SQ Sequence 371 AA;

Query Match 99.0%; Score 512; DB 9; Length 371;  
 Best Local Similarity 96.9%; Pred. No. 1.2e-56;  
 Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGGDTPLHEHYMDLQEPETDLYXXQLNDSSEDEIDGPAQAEPDRAHYNIVTFCK 60  
 DB 265 MGGDTPLHEHYMDLQEPETDLYCYEQNDSSSEDEIDGPAQAEPDRAHYNIVTFCK 324  
 QY 61 CDSTLRLCVOSTHVDIRLTEDLGMGTGIVXPICSOXP 98  
 DB 325 CDSTLRLCVOSTHVDIRLTEDLGMGTGIVXPICSOXP 362

## RESULT 71

AAV25381

ID AAV25381 standard; protein: 390 AA.

XX AAV25381;

DT 06-SEP-1999 (first entry)

DE HPV fusion protein CLYTA-E6E7-His/HPV16.

XX Fusion protein; E6 protein; E7 protein; E6/E7; immunomodulator; tumour;

KM immunological fusion partner; CpG oligonucleotide; immune response;

XX HPV antigen; prevention; treatment.

OS Synthetic.

OS Human papillomavirus.

PN WO933868-A2.

PD 08-JUL-1999.

PP 18-DEC-1998; 98WO-EP008563.

PR 24-DEC-1997; 97GB-00027262.

XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.

PA Dalemans WLJ, Gerard CMG;

PI WPI; 1999-405485/34.

DR N-PSDB; AAX78797.

XX Composition comprising an E6, E7 or E6/E7 fusion protein from HPV to

PT induce immune response to HPV.

XX Example VIII; Page 55-56; 62pp; English.

XX AAX78791-X78801 represent nucleic acid sequences which encode novel  
 CC constructs comprising an E6 or E7 protein or E6/E7 fusion protein from  
 CC HPV (represented in AAY25375-125386). These constructs are optionally  
 CC linked to an immunological fusion partner and an immunomodulatory CpG  
 CC oligonucleotide. The products of the invention can be used to induce an  
 CC immune response in a patient to an HPV antigen. They can also be used for  
 CC preventing or treating HPV induced tumours  
 CC  
 SQ Sequence 390 AA;

Query Match 99.0%; Score 512; DB 2; Length 390;  
 Best Local Similarity 96.9%; Pred. No. 1.3e-56;  
 Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGGDTPLHEHYMDLQEPETDLYXXQLNDSSEDEIDGPAQAEPDRAHYNIVTFCK 60  
 DB 284 MGGDTPLHEHYMDLQEPETDLYCYEQNDSSSEDEIDGPAQAEPDRAHYNIVTFCK 343  
 QY 61 CDSTLRLCVOSTHVDIRLTEDLGMGTGIVXPICSOXP 98  
 DB 344 CDSTLRLCVOSTHVDIRLTEDLGMGTGIVXPICSOXP 381

## RESULT 72

AAV02637

ID AAV02637 standard; protein: 390 AA.

XX AAV02637;

DT 17-OCT-2003 (revised)

DT 22-JUN-1999 (first entry)

DE CLYTA-E6E7-His protein.

XX Chimeric; E6; E7; fusion protein; CLYTA; vaccine; immunotherapy; tumour;  
 KM lesion; benign; malignant; virus; infection.

```
XX OS Human Papillomavirus.
XX OS Streptococcus pneumoniae.
XX OS Chimeric.
XX PN MO9910375-A2.
XX PD 04-MAR-1999.
XX PF 17-AUG-1998; 98MO-EP005285.
XX PR 22-AUG-1997; 97GB-00017953.
XX PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX PI Bruck C, Cabezon Silva T, Delisse ABF, Gerard CMG,
XX P1 Lombardo-Benichalk A;
XX DR WPI; 1999-190587/16.
XX DR N-PSDB; AAX29786.
XX PT Human Papilloma Virus (HPV) fusion proteins - useful in vaccines for
XX PT treatment or prophylaxis of HPV induced lesions.
XX PS Disclosure; Fig 14; 95pp; English.
XX CC This sequence represents a chimeric E6 or E7 protein or E6/E7 fusion
XX CC protein from Human papillomavirus (HPV) linked to an immunological fusion
XX CC partner, in this case, a fragment of the Streptococcus pneumoniae CLYTA
XX CC protein in the encoded protein. The protein can be used in a vaccine, for
XX CC immuno-therapeutically treating HPV induced tumour lesions (benign or
XX CC malignant) and preventing HPV viral infection. (Updated on 17-OCT-2003 to
XX CC standardise OS field)
XX SQ Sequence 390 AA;

Query Match 99.0%; Score 512; DB 2; Length 390;
Best Local Similarity 96.9%; Pred. No. 1.3e-56;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDTPTLHEYMLDLOPETTDLYXXQLNDSSEDEIDGPAGAEPRRAHYNIYTFCK 60
DB 284 MHGDTPTLHEYMLDLOPETTDLYCYEQLNDSSEDEIDGPAGAEPRRAHYNIYTFCK 343
QY 61 CDSTLRLCVOSTHVDIRTELDLMTGLGIVXPICSQKP 98
DB 344 CDSTLRLCVOSTHVDIRTELDLMTGLGIVCPICSQKP 381

RESULT 73
AED52646
ID AED52646 standard; protein; 390 AA.
XX AC AED52646;
XX DT 29-DEC-2005 (first entry)
XX DE Fusion protein clyta-E6-E7-His/HPV16.
XX KM Fusion protein; vaccine; papilloma; cytostatic; papillomavirus infection;
XX KM virucide; uterine cervix tumor; E7; LYTA.
XX OS Streptococcus pneumoniae.
XX OS Human Papillomavirus type 16.
XX OS Synthetic.
XX OS Chimeric.
XX PN IN9801903-14.
XX PD 04-MAR-2005.
XX PF 24-AUG-1998; 98IN-CH001903.
XX
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PR 22-AUG-1997; 97EP-00179535.
XX PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX PI Tyrell AMR;
XX DR WPI; 2005-557648/57.
XX DR N-PSDB; AED52645.
XX PT Vaccine.
XX PS Example 12; Fig 14; 96pp; English.
XX CC The invention relates to human Papilloma virus (HPV) fusion proteins,
XX CC linked to an immunological fusion partner that provides T helper epitopes
XX CC to the HPV antigen. Vaccine formulations comprising the fusion proteins
XX CC are useful in the treatment or prophylaxis of HPV induced lesions
XX CC (papillomas, warts and cervical cancer). HPV 16 (and HPV 18) E6 and E7
XX CC proteins (singly, as an E6-E7 fusion or mutated) were fused to either
XX CC Haemophilus influenzae D protein (20-127), the C-terminus of
XX CC Streptococcus pneumoniae Lyta protein (clyta) or thioredoxin. The present
XX CC sequence represents an HPV-LyTA, fusion protein of the invention.
XX SQ Sequence 390 AA;

Query Match 99.0%; Score 512; DB 9; Length 390;
Best Local Similarity 96.9%; Pred. No. 1.3e-56;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDTPTLHEYMLDLOPETTDLYXXQLNDSSEDEIDGPAGAEPRRAHYNIYTFCK 60
DB 284 MHGDTPTLHEYMLDLOPETTDLYCYEQLNDSSEDEIDGPAGAEPRRAHYNIYTFCK 343
QY 61 CDSTLRLCVOSTHVDIRTELDLMTGLGIVXPICSQKP 98
DB 344 CDSTLRLCVOSTHVDIRTELDLMTGLGIVCPICSQKP 381

RESULT 74
AAM50663
ID AAM50663 standard; protein; 421 AA.
XX AC AAM50663;
XX DT 29-AUG-2003 (revised)
XX DT 08-APR-2002 (first entry)
XX DE Thioredoxin-ubiquitin-ProteinD1/3 E7-His triple fusion protein.
XX KM Thioredoxin; ubiquitin; proteinD1/3 E7; tumour; antigen; cancer; vaccine;
XX KM therapy; human.
XX OS Homo sapiens.
XX OS Escherichia coli.
XX OS Chimeric.
XX FH Key
XX FT Protein 1..109
XX FT Peptide /label= Thioredoxin
XX FT Protein /label= linker
XX FT Protein 126..199
XX FT Cleavage-site /label= Ubiquitin
XX FT 201..202
XX FT Protein /label= UbP1_cleavage_site
XX FT Peptide 203..412
XX FT Peptide /label= ProteinD1/3-E7
XX FT 413..421
XX FT /label= Histidine_tail
XX PN MO200200892-A1.
XX PD 03-JAN-2002.
XX
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XX PF 19-JUN-2001; 2001WO-EP006952.
XX PR 26-JUN-2000; 2000GB-00015619.
XX PR 30-OCT-2000; 2000GB-00026484.
XX PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX PI Cabezon Silva TEV, Delisse AEF;
XX DR WPI; 2002-14788/19.
XX N-PSDB; ABA91285.
XX PT Novel DNA sequence encoding triple fusion protein comprising ubiquitin
XX PT fused between thiorodoxin and polypeptide of interest, useful for
XX PT producing recombinant polypeptide of interest suitable for medicinal use.
XX PS Example 12; Fig 19a; 87pp; English.
XX CC The present sequence is that of a triple fusion protein comprising, from
XX CC the N-terminal end, Escherichia coli thiorodoxin, human ubiquitin and
XX CC human papillomavirus Protein1/3 E7, followed by a histidine affinity
XX CC tail. The triple fusion protein was produced in E. coli G1724 host cells
XX CC transformed by an expression vector comprising DNA (see ABA91285)
XX CC encoding the fusion. This is an example of the production of triple
XX CC fusion proteins of the invention that comprise ubiquitin fused between
XX CC thiorodoxin and a protein of interest, in this case Protein1/3 E7. A
XX CC claimed method of producing a recombinant protein of interest involves:
XX CC culturing a host cell (preferably E. coli) under conditions which allow
XX CC co-expression of the triple fusion and a ubiquitin-specific endoprotease
XX CC (especially UBP1 from Saccharomyces cerevisiae); and recovering the
XX CC recombinant protein directly from the bacterial cells after it has been
XX CC subjected to the action of the ubiquitin-specific endoprotease in vivo.
XX CC In the present case, expression is controlled by the addition of
XX CC tryptophan. The recombinant protein can be used as a vaccine for cancer
XX CC therapy. (Updated on 29-AUG-2003 to standardise OS field)
XX SQ Sequence 421 AA;

Query Match 99.0%; Score 512; DB 5; Length 421;
Best Local Similarity 96.9%; Pred. No. 1.4e-56;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDTPTLHEMYMDLOPETHDLYXXYXQNDSSSEDEIDPAGQAEPRAHYNIIVTFCK 60
DB 315 MHGDTPTLHEMYMDLOPETHDLYCYEQNDSSSEDEIDPAGQAEPRAHYNIIVTFCK 374
QY 61 CDSTLRFCVOSTHYDRTLEDLMGTIGIYXPICSQRP 98
DB 375 CDSTLRFCVOSTHYDRTLEDLMGTIGIYVPICSQRP 412

RESULT 75
AAB31610
ID AAB31610 standard; protein; 493 AA.
XX AC AAB31610;
XX DT 30-APR-2001 (first entry)
XX DE Amino acid sequence of Hsp40-E7 fusion protein.
XX KW Heat shock protein; Hsp; Th1 response; Th1 cell; CD4+ T lymphocyte cell;
XX KW lymphocyte; Hsp5; Hsp40; Hsp10; Hsp60; Hsp71; microbial pathogen;
XX KW E7 protein.
XX OS Synthetic.
XX OS Mycobacterium tuberculosis.
XX OS Human papillomavirus.
XX PN WO200104344-A2.
XX PD 18-JAN-2001.

```

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XX PF 10-JUL-2000; 2000WO-US018828.
XX PR 08-JUL-1999; 99US-0143757P.
XX PA (STRE-) STRESSGEN BIOTECHNOLOGIES CORP.
XX PI Siegel M, Chu NR, Mizen LA;
XX DR WPI; 2001-138361/14.
XX N-PSDB; AAF25013.
XX PT Screening for compounds that stimulate Th1-like responses in CD4+ T
XX PT lymphocyte cells.
XX PS Example 6; Fig 5A-B; 88pp; English.
XX CC The present sequence represents a fusion protein comprising a
XX CC Mycobacterium tuberculosis heat shock protein (Hsp) 40 fused at its 3'
XX CC end to a Hsp16 E7 protein. The fusion protein is used in the method of
XX CC the invention. The specification describes a method of determining
XX CC whether a compound stimulates a Th1-like response. Th1 cells are a subset
XX CC of CD4+ T lymphocyte cells. The method comprises contacting native
XX CC lymphocytes in vitro with a fusion protein comprising at least a fragment
XX CC of Hsp, and then detecting the Th1-like response exhibited by the cell
XX CC sample. The proteins which may be used in the method of the invention are
XX CC Hsp65, Hsp40, Hsp10, Hsp60, and Hsp71. The method may be used to identify
XX CC compounds that stimulate Th1-like responses in response to microbial
XX CC pathogens
XX SQ Sequence 493 AA;

Query Match 99.0%; Score 512; DB 4; Length 493;
Best Local Similarity 96.9%; Pred. No. 1.7e-56;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDTPTLHEMYMDLOPETHDLYXXYXQNDSSSEDEIDPAGQAEPRAHYNIIVTFCK 60
DB 396 MHGDTPTLHEMYMDLOPETHDLYCYEQNDSSSEDEIDPAGQAEPRAHYNIIVTFCK 455
QY 61 CDSTLRFCVOSTHYDRTLEDLMGTIGIYXPICSQRP 98
DB 456 CDSTLRFCVOSTHYDRTLEDLMGTIGIYVPICSQRP 493

RESULT 76
AAB03790
ID AAB03790 standard; protein; 638 AA.
XX AC AAB03790;
XX DT 12-SEP-2003 (revised)
XX DT 06-AUG-2003 (revised)
XX DT 13-OCT-2000 (first entry)
XX DE Heat shock protein and tumour specific antigen fusion protein sequence.
XX KW Heat shock protein; tumour specific antigen; colibacillus; microzyme;
XX KW plant; immune response; tumour; cancer; human papillomavirus;
XX KW pointed condyloma.
XX OS Mycobacterium bovis.
XX OS Human papillomavirus.
XX OS Chimeric.
XX PN CN1248631-A.
XX PD 29-MAR-2000.
XX PF 24-SEP-1998; 98CN-00112264.
XX PR 24-SEP-1998; 98CN-00112264.
XX PD 24-SEP-1998; 98CN-00112264.

```

PA (ZHOU/) ZHOU G.  
 XX  
 PI Zhou G;  
 XX  
 DR WPI; 2000-431995/38.  
 XX  
 PT New fusion protein for immunotherapy of venereal disease and cancer - is  
 XX a heat shock protein of Mycobacterium bovis.  
 PS Claim 9; Fig 1; 5pp; Chinese.  
 XX  
 CC The present sequence represents a fusion protein, consisting of a heat  
 CC shock protein of mycobacterium bovis (var. BCG) fused to a tumour  
 CC specific antigen of human papillomavirus (HPV). The fusion protein can be  
 CC expressed in colibacillus, microzymes and plants. The fusion protein is  
 CC used to make immunostimulant injections, as it can produce specific cell  
 CC immune and humoral immune responses. It possesses prophylaxis and  
 CC therapeutic capacity for preventing human papillomavirus (HPV) infection,  
 CC but also can be used for immunotherapy of pointed condyloma, tumours and  
 CC cancer caused by HPV. (Updated on 06-AUG-2003 to correct OS field.)  
 CC (Updated on 12-SEP-2003 to standardise OS field)  
 CC  
 XX  
 SQ Sequence 638 AA;  
 Query Match 99.0%; Score 512; DB 3; Length 638;  
 Best Local Similarity 96.9%; Pred. No. 2.4e-56;  
 Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 MHGPTLHEHYMLDLPETTDLYXXQLNDSSEDEIDGPAGQAEPRAHYNIYTFCK 60  
 DB 541 MHGPTLHEHYMLDLPETTDLYCYEQLNDSSEDEIDGPAGQAEPRAHYNIYTFCK 600  
 QY 61 CDSTLRFCVOSTHVDIRTLIEDLMGTGIVXPCISQKP 98  
 DB 601 CDSTLRFCVOSTHVDIRTLIEDLMGTGIVCPCISQKP 638  
 Db  
 RESULT 77  
 AAB31609  
 ID AAB31609 standard; protein; 639 AA.  
 XX  
 AC AAB31609;  
 XX  
 DT 30-APR-2001 (first entry)  
 XX  
 DE Amino acid sequence of Hsp65-E7 fusion protein.  
 XX  
 KM Heat shock protein; Hsp; Th1 response; Th1 cell; CD4+ T lymphocyte cell;  
 KM lymphocyte; Hsp65; Hsp40; Hsp10; Hsp60; Hsp71; microbial pathogen;  
 KM E7 protein.  
 XX  
 OS Synthetic.  
 OS Mycobacterium bovis.  
 OS Human papillomavirus.  
 XX  
 PN WO200104344-A2.  
 PD 18-JAN-2001.  
 XX  
 PF 10-JUL-2000; 2000WO-US018828.  
 XX  
 PR 08-JUL-1999; 99US-0143757P.  
 XX  
 PA (STRE-) STRESSGEN BIOTECHNOLOGIES CORP.  
 XX  
 PI Siegel M, Chu NR, Mizzen LA;  
 XX  
 DR WPI; 2001-138361/14.  
 DR N-PSDB; AAF25012.  
 XX  
 PT Screening for compounds that stimulate Th1-like responses in CD4+ T  
 XX lymphocyte cells.

PS Example 5; Fig 4A-B; 8pp; English.  
 XX  
 CC The present sequence represents a fusion protein comprising a  
 CC Mycobacterium bovis heat shock protein (Hsp) 65 fused to its C terminal  
 CC to a HPV16 E7 protein. The fusion protein is used in the method of the  
 CC invention. The specification describes a method of determining whether a  
 CC compound stimulates a Th1-like response. Th1 cells are a subset of CD4+ T  
 CC lymphocyte cells. The method comprises contacting naive lymphocytes in  
 CC vitro with a fusion protein comprising at least a fragment of Hsp, and  
 CC then detecting the Th1-like response exhibited by the cell sample. The  
 CC proteins which may be used in the method of the invention are Hsp65,  
 CC Hsp40, Hsp10, Hsp60, and Hsp71. The method may be used to identify  
 CC compounds that stimulate Th1-like responses in response to microbial  
 CC pathogens  
 CC  
 XX  
 SQ Sequence 639 AA;  
 Query Match 99.0%; Score 512; DB 4; Length 639;  
 Best Local Similarity 96.9%; Pred. No. 2.4e-56;  
 Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 MHGPTLHEHYMLDLPETTDLYXXQLNDSSEDEIDGPAGQAEPRAHYNIYTFCK 60  
 DB 542 MHGPTLHEHYMLDLPETTDLYCYEQLNDSSEDEIDGPAGQAEPRAHYNIYTFCK 601  
 QY 61 CDSTLRFCVOSTHVDIRTLIEDLMGTGIVXPCISQKP 98  
 DB 602 CDSTLRFCVOSTHVDIRTLIEDLMGTGIVCPCISQKP 639  
 Db  
 RESULT 78  
 AAB31619  
 ID AAB31619 standard; protein; 641 AA.  
 XX  
 AC AAB31619;  
 XX  
 DT 30-APR-2001 (first entry)  
 XX  
 DE Amino acid sequence of Hsp65-E7 fusion protein.  
 XX  
 KM Heat shock protein; Hsp; Th1 response; Th1 cell; CD4+ T lymphocyte cell;  
 KM lymphocyte; Hsp65; Hsp40; Hsp10; Hsp60; Hsp71; microbial pathogen;  
 KM E7 protein.  
 XX  
 OS Synthetic.  
 OS Streptococcus pneumoniae.  
 OS Human papillomavirus.  
 XX  
 PN WO200104344-A2.  
 PD 18-JAN-2001.  
 XX  
 PF 10-JUL-2000; 2000WO-US018828.  
 XX  
 PR 08-JUL-1999; 99US-0143757P.  
 XX  
 PA (STRE-) STRESSGEN BIOTECHNOLOGIES CORP.  
 XX  
 PI Siegel M, Chu NR, Mizzen LA;  
 XX  
 DR WPI; 2001-138361/14.  
 DR N-PSDB; AAF25036.  
 XX  
 PT Screening for compounds that stimulate Th1-like responses in CD4+ T  
 XX lymphocyte cells.  
 XX  
 PS Example 15; Fig 15A-B; 8pp; English.  
 XX  
 CC The present sequence represents a fusion protein comprising a  
 CC Streptococcus pneumoniae heat shock protein (Hsp) 65 fused to a HPV16 E7  
 CC protein. The fusion protein is used in the method of the invention. The  
 CC specification describes a method of determining whether a compound  
 CC stimulates a Th1-like response. Th1 cells are a subset of CD4+ T

CC lymphocyte cells. The method comprises contacting naive lymphocytes in  
 CC vitro with a fusion protein comprising at least a fragment of Hsp, and  
 CC then detecting the Th1-like response exhibited by the cell sample. The  
 CC proteins which may be used in the method of the invention are Hsp65,  
 CC Hsp40, Hsp10, Hsp60, and Hsp71. The method may be used to identify  
 CC compounds that stimulate Th1-like responses in response to microbial  
 CC pathogens  
 CC  
 SQ Sequence 641 AA;  
 Query Match 99.0%; Score 512; DB 4; Length 641;  
 Best Local Similarity 96.9%; Pred. No. 2.4e-56;  
 Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 MHGDTPLHEHYMDLQPEETDLYXXQLNDSSEDEIDDPAGQAEPRRAHYNIVTFCK 60  
 DB 544 MHGDTPLHEHYMDLQPEETDLYCYEQLNDSSEDEIDDPAGQAEPRRAHYNIVTFCK 603  
 QY 61 CDSTLRKCVOSTHVDIRTELDLMGTIGIYXPICSQKP 98  
 DB 604 CDSTLRKCVOSTHVDIRTELDLMGTIGIYXPICSQKP 641  
 RESULT 79  
 AAB31620  
 ID AAB31620 standard; protein; 647 AA.  
 AC AAB31620;  
 XX  
 DT 30-APR-2001 (first entry)  
 XX  
 DE Amino acid sequence of Hsp60-E7 fusion protein.  
 XX  
 KM Heat shock protein; Hsp; Th1 response; Th1 cell; CD4+ T lymphocyte cell;  
 KM lymphocyte; Hsp65; Hsp40; Hsp10; Hsp60; Hsp71; microbial pathogen;  
 KM E7 protein.  
 XX  
 OS Synthetic.  
 OS Aspergillus fumigatus.  
 OS Human papillomavirus.  
 XX  
 PN WO200104344-A2.  
 XX  
 PD 18-JAN-2001.  
 XX  
 PF 10-JUL-2000; 2000WO-US018828.  
 XX  
 PR 08-JUL-1999; 99US-0143757P.  
 XX  
 PA (STRE-) STRESSGEN BIOTECHNOLOGIES CORP.  
 XX  
 PI Siegel M, Chu NR, Mlazen LA;  
 XX  
 DR WPI; 2001-138361/14.  
 DR N-PSDB; AAF25037.  
 XX  
 PT Screening for compounds that stimulate Th1-like responses in CD4+ T  
 PT lymphocyte cells.  
 XX  
 PS Example 16; Fig 16A-B; 88pp; English.  
 XX  
 CC The present sequence represents a fusion protein comprising a Aspergillus  
 CC fumigatus heat shock protein (Hsp) 60 fused to a HPV16 E7 protein. The  
 CC fusion protein is used in the method of the invention. The specification  
 CC describes a method of determining whether a compound stimulates a Th1-  
 CC like response. Th1 cells are a subset of CD4+ T lymphocyte cells. The  
 CC method comprises contacting naive lymphocytes in vitro with a fusion  
 CC protein comprising at least a fragment of Hsp, and then detecting the Th1  
 CC like response exhibited by the cell sample. The proteins which may be  
 CC used in the method of the invention are Hsp65, Hsp40, Hsp10, Hsp60, and  
 CC Hsp71. The method may be used to identify compounds that stimulate Th1-  
 CC like responses in response to microbial pathogens

SQ Sequence 647 AA;  
 Query Match 99.0%; Score 512; DB 4; Length 647;  
 Best Local Similarity 96.9%; Pred. No. 2.5e-56;  
 Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 MHGDTPLHEHYMDLQPEETDLYXXQLNDSSEDEIDDPAGQAEPRRAHYNIVTFCK 60  
 DB 550 MHGDTPLHEHYMDLQPEETDLYCYEQLNDSSEDEIDDPAGQAEPRRAHYNIVTFCK 609  
 QY 61 CDSTLRKCVOSTHVDIRTELDLMGTIGIYXPICSQKP 98  
 DB 610 CDSTLRKCVOSTHVDIRTELDLMGTIGIYXPICSQKP 647  
 RESULT 80  
 ADF18635  
 ID ADF18635 standard; protein; 98 AA.  
 AC ADF18635;  
 XX  
 DT 12-FEB-2004 (first entry)  
 XX  
 DE Human papilloma virus E7 oncoprotein.  
 XX  
 KM HPV; oncoprotein E7; cytosolic; gene therapy; kinase; enzyme.  
 XX  
 OS Human papillomavirus.  
 OS WO2003088922-A2.  
 XX  
 PN 30-OCT-2003.  
 XX  
 PD 21-APR-2003; 2003WO-US012667.  
 XX  
 PF 19-APR-2002; 2002US-0374245P.  
 XX  
 PR (UTR ) UNIV ROCHESTER.  
 XX  
 PA Mccance D, Westbrook TF;  
 XX  
 PI WPI; 2003-845498/78.  
 XX  
 DR N-PSDB; ADF18636, ADF18637.  
 XX  
 PT Identifying a compound that inhibits E7 cellular proliferation activity  
 PT by administering a compound to a system, where the system maintains Akt  
 PT activity and selecting a compound that decreases the amount of Akt  
 XX  
 PS Disclosure; SEQ ID NO 11; 119pp; English.  
 XX  
 CC The present sequence is the protein sequence of human papillomavirus E7  
 CC oncoprotein. E7 promotes oncogenesis through an inhibition of p21cip1  
 CC transport into the nucleus. E7 abrogates Raf-associated arrest and  
 CC prevents inhibition of cyclin E-CDK2 activity without disrupting Raf  
 CC induction of p21cip1. E7 neither interacts with p21cip1 nor derepresses  
 CC p21cip1-associated CDK2 activity, but instead reduces the association  
 CC between p21cip1 and cyclin E-CDK2 complexes. Raf down-regulates steady-  
 CC state levels of Akt, a regulator of p21cip1 localisation, leading to loss  
 CC of p21cip1 phosphorylation and accumulation of p21cip1. E7 disrupts the  
 CC effects of Raf on Akt activity and prevents p21cip1 nuclear accumulation.  
 CC Maintenance of Akt activity is necessary and sufficient to bypass Raf  
 CC arrest. The invention provides methods for identifying and using  
 CC inhibitors of E7 cell proliferation activity, and for identifying and  
 CC using compounds capable of promoting the nuclear localisation of p21cip1.  
 CC The methods can be used to inhibit aberrant cellular proliferation for  
 CC treatment of cancer.  
 XX  
 SQ Sequence 98 AA;  
 Query Match 98.8%; Score 511; DB 7; Length 98;  
 Best Local Similarity 95.9%; Pred. No. 2.9e-57;  
 Matches 94; Conservative 1; Mismatches 3; Indels 0; Gaps 0;



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Db      151 LHGGPTLHRYMDLPETTDLYGYQLNDSSEEDIDGPAGAEPPRAHYNIVTFCK 210
      :|||||
Oy      61 CDSTLRCLVOSTHVDIRTLIEDLGMGTIGIYVPICSQKP 98
      |||||
Db      211 CDSTLRCLVOSTHVDIRTLIEDLGMGTIGIYVPICSQKP 248

RESULT 83
ADO44060 ID ADO44060 standard; protein; 248 AA.
XX
XX ADO44060;
XX
XX 15-JUL-2004 (first entry)
XX
XX Amino acid sequence of an E6E7 fusion protein.
XX
XX E6 protein; E7 protein; fusion protein; HPV16; HPV-associated cancer;
XX cervical cancer; immune response; lower gastrointestinal tract cancer;
XX anal cancer; reproductive system cancer; penile cancer; vulvar cancer.
XX
XX Human papillomavirus type 16.
XX Synthetic.
XX
XX WO2004030636-A2.
XX
XX 15-APR-2004.
XX
XX 02-OCT-2003; 2003WO-US031726.
XX
XX 03-OCT-2002; 2002US-0415929P.
XX
XX (AMHP ) WYETH HOLDINGS CORP.
XX
XX PI Smith L, Casasetti MC;
XX
XX WPI; 2004-316328/29.
XX
XX N-PSDB; ADO44061.
XX
XX New polypeptide comprising human papillomavirus E6 and E7 polypeptides,
XX PT useful for treating or preventing human papillomavirus (HPV)-associated
XX PT cancers, e.g. cervical cancer.
XX
XX Example 1; Page 67-68; 101pp; English.
XX
XX
XX The present sequence represents an E6E7 fusion protein, comprising wild
XX CC type E6 and E7 polypeptides from human papillomavirus type 16 (HPV16).
XX CC The specification describes human papillomavirus E6 and E7 polypeptides,
XX CC where the E7 polypeptide has mutations at any one or more of the amino
XX CC acids corresponding to amino acids 24, 26 or 91 of the sequence given in
XX CC ADO44073 and the E6 polypeptide has no mutations or has mutations at any
XX CC one or more of the amino acids corresponding to amino acids 63 or 106 of
XX CC there sequence given in ADO44072. The polypeptides of the invention are
XX CC useful for treating or preventing human papillomavirus (HPV)-associated
XX CC cancers, such as cervical cancer. The fusion proteins and nucleic acids
XX CC encoding the fusion proteins are useful for generating immune responses
XX CC against HPV. They are also useful for treating lower gastrointestinal
XX CC tract cancer, e.g. anal cancer, and other cancers of the reproductive
XX CC system, including penile and vulvar cancer.
XX
XX Sequence 248 AA;
SQ
Query Match 98.5%; Score 509; DB 8; Length 248;
Best Local Similarity 95.9%; Pred. No. 1.7e-56;
Matches 94; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Oy      1 MHGDTPLHRYMDLPETTDLYXXQLNDSSEEDIDGPAGAEPPRAHYNIVTFCK 60
      :|||||
Db      151 LHGGPTLHRYMDLPETTDLYCYEQLNDSSEEDIDGPAGAEPPRAHYNIVTFCK 210
      :|||||
Oy      61 CDSTLRCLVOSTHVDIRTLIEDLGMGTIGIYVPICSQKP 98
      |||||

```

```

Db      211 CDSTLRCLVOSTHVDIRTLIEDLGMGTIGIYVPICSQKP 248
      :|||||
      :
RESULT 84
AAV50703 ID AAV50703 standard; protein; 98 AA.
XX
XX AAV50703;
XX
XX 04-FEB-2000 (first entry)
XX
XX HPV16 E7 protein.
XX
XX E7 protein; immunogenic; active immunization.
XX
XX Human papillomavirus.
XX
XX WO955876-A2.
XX
XX 04-NOV-1999.
XX
XX 30-APR-1999; 99WO-DE001331.
XX
XX 30-APR-1998; 98DE-01019476.
XX
XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX
XX Glasmann I, Jochmus I;
XX
XX WPI; 2000-023362/02.
XX
XX N-PSDB; AA224129.
XX
XX Immunogenic protein with altered biological function, useful for active
XX PT immunization.
XX
XX Example 1; Page 25; 33pp; German.
XX
XX
XX This invention describes the construction of a novel polypeptide with
XX CC immunogenic and altered biological function of a protein, where the
XX CC polypeptide has regions of the protein of about 10-40 amino acids in a
XX CC different order. The polypeptide, or its DNA, is useful for active
XX CC immunization without cross-reactivity and problems associated with the
XX CC biological function of the protein. This sequence represents the human
XX CC papillomavirus type 16 E7 protein which is used to illustrate the method
XX CC of the invention
XX
XX Sequence 98 AA;
SQ
Query Match 98.1%; Score 507; DB 3; Length 98;
Best Local Similarity 95.9%; Pred. No. 9.5e-57;
Matches 94; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Oy      1 MHGDTPLHRYMDLPETTDLYXXQLNDSSEEDIDGPAGAEPPRAHYNIVTFCK 60
      :|||||
Db      1 MHGDTPLHRYMDLPETTDLYCYEQLNDSSEEDIDGPAGAEPPRAHYNIVTFCK 60
      :|||||
Oy      61 CDSTLRCLVOSTHVDIRTLIEDLGMGTIGIYVPICSQKP 98
      |||||
Db      61 CDSTLRCLVOSTHVDIRTLIEDLGMGTIGIYVPICSQKP 98
      |||||

RESULT 85
AAB49453 ID AAB49453 standard; protein; 98 AA.
XX
XX AAB49453;
XX
XX 06-AUG-2003 (revised)
XX
XX 07-MAR-2001 (first entry)
XX
XX HPV 16E7.
XX
XX Immune response; gene therapy; antigen presentation; vaccine; cancer;
XX

```

```

KM infection; autoimmune disease.
XX
OS Hepatitis B virus.
XX
PN MO20067761-A1.
XX
PD 16-NOV-2000.
XX
PE 05-MAY-2000; 2000MO-US012177.
XX
PR 06-MAY-1999; 99US-0132750P.
XX
PR 06-MAY-1999; 99US-0132752P.
XX
PA (UTWA-) UNIV WAKE FOREST.
XX
PI Chen S, You Z;
XX
DR WPI; 2001-007312/01.
XX
PT Novel vector expressing secreted antigen fused to cell binding element,
PT useful in vaccines for treatment of e.g. cancer and infection, also
PT identification of epitopes.
XX
PS Disclosure; Fig 17; 163pp; English.
XX
* The present invention relates to an expression vector comprising a
CC promoter, signal sequences, an antigen, a cell-binding element, and a
CC polyadenylation sequence. The expression vector can be used directly or
CC after transduction of antigen-presenting cells, in vaccines for treatment
CC and prevention of cancer, infections and autoimmune diseases. Vectors
CC similar to the expression vector of the present invention, but expressing
CC a test sequence rather than an antigen, are used to identify polypeptides
CC that contain MHC-II restricted epitopes for activation of CD4+ cells or
CC elicitation of an immune response in vivo. The identified polypeptides
CC (in APC) or vector containing DNA that expresses the polypeptides are
CC useful for treating the above conditions. The present sequence is HPV
CC 1657. E7 is a cytosolic protein, which has a string of charged residues
CC which hamper the secretion of the protein. Elimination of these residues
CC to result in the present protein, stabilises the protein and facilitates
CC secretion. The coding sequence for the present protein was used to
CC construct the expression vector of the present invention. (updated on 06-
CC AUG-2003 to correct OS field.)
XX
SQ Sequence 98 AA;
XX
Query Match 98.1%; Score 507; DB 4; Length 98;
Best Local Similarity 95.9%; Pred. No. 9.5e-57;
Matches 94; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
XX
OY 1 MHGDPPTLHEYMLDLQPEPTDLYXXYXQLNDSSEDEIDGPAGQAEPRAHYNIIVTFCK 60
Db 1 MHGDPPTLHEYMLDLQPEPTDLYCYEQLSDSSEDEIDGPAGQAEPRAHYNIIVTFCK 60
OY 61 CDSTLRLCVOSTHVDIRLTEDLMGTGIVXPCSQKP 98
Db 61 CDSTLRLCVOSTHVDIRLTEDLMGTGIVCPCSQKP 98
XX
RESULT 86
AAO22639
ID AAO22639 standard; protein; 98 AA.
XX
AC AAO22639;
XX
DT 15-MAY-2003 (first entry)
XX
DE HPV-16 protein sequence, SEQ ID No 26.
XX
KM Cytostatic; peptide therapy; immunotherapy; pre-; cancerous growth;
KM cancer; human papilloma virus; cervix; cell-mediated immune response;
KM HPV; HPV-16.
XX
OS Human papilloma virus.

```

```

XX
PN MO2003006649-A1.
XX
PD 30-JAN-2003.
XX
PE 19-JUN-2002; 2002MO-US023198.
XX
PR 20-JUL-2001; 2001US-0306809P.
XX
PA (TEXA ) UNIV TEXAS SYSTEM.
XX
PI Sastry KJ, Tortolero-Luna G, Folien M,
XX
DR WPI; 2003-239363/23.
XX
PT Determining a possible recurrence of a (pre-)cancerous growth in a
PT patient infected with human papilloma virus (HPV), comprises incubating
PT the sample with an HPV E6 or E7 peptide and detecting a cell-mediated
PT immune response.
XX
PS Disclosure; Page 129-130; 133pp; English.
XX
* The invention relates to a novel method for determining the possibility
CC of recurrence of a (pre-)cancerous growth in a patient infected with
CC human papilloma virus (HPV) or suspected of being infected with HPV, and
CC has or had a (pre-)cancerous growth on or around the cervix. The novel
CC method comprises incubating an E6 or E7 peptide of HPV with a sample from
CC the patient, and assaying the sample for a cell-mediated immune response
CC against the peptide. The method is useful for determining the possibility
CC and preventing the recurrence of a (pre-)cancerous growth in a patient
CC infected with HPV or suspected of being infected with HPV. The HPV E6 or
CC E7 peptides are useful in immunotherapy for the preventing or reducing
CC the risk of development of (pre-)cancerous growths. This sequence
CC represents an HPV-16 protein of the invention
XX
SQ Sequence 98 AA;
XX
Query Match 98.1%; Score 507; DB 6; Length 98;
Best Local Similarity 95.9%; Pred. No. 9.5e-57;
Matches 94; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
XX
OY 1 MHGDPPTLHEYMLDLQPEPTDLYXXYXQLNDSSEDEIDGPAGQAEPRAHYNIIVTFCK 60
Db 1 MHGDPPTLHEYMLDLQPEPTDLYCYEQLSDSSEDEIDGPAGQAEPRAHYNIIVTFCK 60
OY 61 CDSTLRLCVOSTHVDIRLTEDLMGTGIVXPCSQKP 98
Db 61 CDSTLRLCVOSTHVDIRLTEDLMGTGIVCPCSQKP 98
XX
RESULT 87
AAO22923
ID AAO22923 standard; protein; 111 AA.
XX
AC AAO22923;
XX
DT 12-DEC-2002 (first entry)
XX
DE Human papillomavirus-16 (HPV16) E7T-protein sequence.
XX
KM Virucide; cytostatic; E6; E7 fusion protein; HPV; immunogenic; vaccine;
KM fusion partner; immunogenicity; HPV infection; neoplasm; HPV16;
KM human papillomavirus-16; E7T-sequence.
XX
OS Human papillomavirus.
XX
PN EPI243655-A1.
XX
PD 25-SEP-2002.
XX
PR 23-MAR-2001; 2001EP-00107271.
XX
PR 23-MAR-2001; 2001EP-00107271.

```

XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
 XX Cld-Arregui A, Zur Hausen H;  
 XX WPI; 2002-724952/79.  
 DR N-PSDB; AAL53421.  
 XX  
 PT A new DNA sequence encoding a fusion protein comprising a mutagenized HPV  
 PT (human papillomavirus) E6 or E7 coding sequence and a sequence encoding a  
 PT highly immunogenic fusion partner is useful to vaccinate against HPV  
 PT infection.  
 XX Disclosure; Fig 1; 34pp; English.  
 XX  
 CC The invention relates to a new DNA sequence encodes an E6 or E7 fusion  
 CC protein of HPV, where at least 20% of the original codons are replaced by  
 CC codons which lead to enhanced translation in a mammalian cell, containing  
 CC a mutation which results in production of a truncated non-functional  
 CC protein, and encoding a highly immunogenic polypeptide fusion partner  
 CC capable of enhancing immunogenicity of the E6 or E7 protein in the  
 CC mammalian host. The invention is used as a vaccine for the prevention or  
 CC treatment of an HPV infection or a neoplasm associated with HPV  
 CC infection. This sequence represents the human papillomavirus-16 (HPV16)  
 CC E6/E7-protein sequence of the invention  
 CC  
 SQ Sequence 111 AA;  
 XX  
 Query Match 98.1%; Score 507; DB 5; Length 111;  
 Best Local Similarity 96.9%; Pred. No. 1.1e-56;  
 Matches 94; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 Qy 2 HGDPTLHEHYMLDLOPETTDLYXXYXQNDSSSEDEIDGPAGAEPPRAHYNIYTFCKC 61  
 Db 7 HGDPTLHEHYMLDLOPETTDLYXXYXQNDSSSEDEIDGPAGAEPPRAHYNIYTFCKC 66  
 Qy 62 DSTLRCLCVOSTHVDIRITLEDLMGTIGIYXPCSQKP 98  
 Db 67 DSTLRCLCVOSTHVDIRITLEDLMGTIGIYXPCSQKP 103  
 RESULT 88  
 AAR27724  
 ID AAR27724 standard; protein; 262 AA.  
 XX  
 AC AAR27724;  
 XX  
 DT 24-OCT-2003 (revised)  
 DT 25-MAR-2003 (revised)  
 DT 09-MAR-1993 (first entry)  
 XX  
 DE HPV 16 E7 protein fragment.  
 XX  
 KW Virus vector; vaccinia virus; papillomavirus; HPV; human; amplification;  
 KW immunotherapeutic.  
 XX  
 OS Human papillomavirus type 16.  
 XX  
 FH Key location/Qualifiers  
 FT Peptide 162..259  
 FT /note="start of HPV-16 E7 protein"  
 XX  
 XX WO9216636-A1.  
 XX  
 PD 01-OCT-1992.  
 XX  
 PD 10-MAR-1992; 92WO-GB000424.  
 XX  
 PR 14-MAR-1991; 91GB-00005383.  
 XX  
 PA (IMMU ) IMMUNOLOGY LTD.  
 XX  
 PI Bournefell MEG, Inglis SC, Munro AJ;

XX WPI; 1992-349219/42.  
 DR N-PSDB; AAQ29389.  
 XX  
 PT Recombinant virus vectors encoding human papillomavirus proteins - for  
 PT treating and vaccinating against HPV infections and conditions caused by  
 PT them, such as cervical cancer.  
 XX  
 XX Disclosure; Fig 1a; 83pp; English.  
 XX  
 CC The fragment of DNA contg. the HPV-16 E6/E7 coding region was prep'd. by  
 CC PCR from plasmid pBR322/HPV16 (Durst et al., PNAS, 80: 3812 (1983)) using  
 CC oligonucleotides S05 and S06. The prod. of the second reading frame is  
 CC the HPV-16 E7 protein whereas the third reading frame encodes HPV-16 E6.  
 CC The E6 and E7 ORFs are fused together to form a single continuous ORF via  
 CC site directed mutagenesis and the immortalising potential of E7 is  
 CC removed by altering two key codons of the HPV E7 sequence. The single ORF  
 CC of HPV-16 E6/E7 may be inserted into vaccinia virus DNA at neutral sites  
 CC (pref. by inserting two sets of the DNA in opposite orientations to  
 CC overcome the problem of intertypic recombination) to make a recombinant  
 CC virus vector for use immunotherapeutically to activate cells of the  
 CC immune system against HPV. See also AAR27723-43. (Updated on 25-MAR-2003  
 CC to correct PW field.) (Updated on 24-OCT-2003 to standardise OS field)  
 CC  
 SQ Sequence 262 AA;  
 XX  
 Query Match 97.7%; Score 505; DB 2; Length 262;  
 Best Local Similarity 95.9%; Pred. No. 6.1e-56;  
 Matches 94; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 Qy 1 MHGDTPLHEHYMLDLOPETTDLYXXYXQNDSSSEDEIDGPAGAEPPRAHYNIYTFCKC 60  
 Db 162 MHGDTPLHEHYMLDLOPETTDLYXXYXQNDSSSEDEIDGPAGAEPPRAHYNIYTFCKC 221  
 Qy 61 CDSTLRCLCVOSTHVDIRITLEDLMGTIGIYXPCSQKP 98  
 Db 222 CDSTLRCLCVOSTHVDIRITLEDLMGTIGIYXPCSQKP 259  
 RESULT 89  
 AAY08020  
 ID AAY08020 standard; protein; 98 AA.  
 XX  
 AC AAY08020;  
 XX  
 DT 27-AUG-2003 (revised)  
 DT 08-JUL-1999 (first entry)  
 XX  
 DE Human papilloma virus E7 protein.  
 XX  
 XX L1 protein; capsomer; virus; vaccine; infection; treatment; prevention;  
 KW cervical carcinoma; fusion protein; anti-capsid; antibody; E7 protein;  
 KW antigenicity.  
 XX  
 OS Human papillomavirus.  
 XX  
 XX WO9918220-A1.  
 XX  
 PD 15-APR-1999.  
 XX  
 PD 06-OCT-1998; 98WO-US020965.  
 XX  
 PR 06-OCT-1997; 97US-00944368.  
 XX  
 PA (LOYO ) UNIV LOYOLA CHICAGO.  
 XX  
 PI Giesmann L, Mueller M;  
 XX  
 DR WPI; 1999-264026/22.  
 DR N-PSDB; AAX37567.  
 XX  
 PT Human papilloma virus (HPV) L1 fusion protein capsomers, used in vaccines  
 PT against HPV infection.

XX Disclosure; Page 33; 48pp; English.  
XX  
CC This invention describes novel vaccines comprising a human papilloma  
CC virus (HPV) capsomer, composed of a HPV L1 fusion protein or a HPV L1  
CC truncated protein. The vaccines can prevent or treat human papilloma  
CC virus infection. Such therapeutic vaccinations can be used for relief  
CC against, e.g. cervical carcinoma. Construction of chimeric proteins  
CC comprising amino acid residues from L1 protein, and e.g. E6 or E7  
CC protein, which give rise to chimeric capsomers, combines prophylactic and  
CC therapeutic functions of a vaccine. Capsomers can promote elimination of  
CC persistently infected cells. Capsomers can also escape neutralization by  
CC pre-existing anti-capsid antibodies and hence possess longer circulating  
CC half-life as compared to chimeric virus-like particles. The fusion  
CC protein, which forms the capsomer, provides increased antigenicity.  
CC (Updated on 27-AUG-2003 to correct OS field.)  
XX  
XX Sequence 98 AA;  
SQ  
Query Match 97.5%; Score 504; DB 2; Length 98;  
Best Local Similarity 95.9%; Pred. No. 2.3e-56;  
Matches 94; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
Qy 1 MHGDTPTLHEXYMDLQPEPTTDLVYXXQLNDSSEDEIDPAGQAEPRAHYNIYTFCK 60  
Db 1 MHGDTPTLHEXYMDLQPEPTTDLVYEQQLNDSSEDEIDPAGQAEPRAHYNIYTFCK 60  
Qy 61 CDSTLRLCVOSTHVDITLEDLMTGLGIYXPICSQKP 98  
Db 61 CDSTLRLCVOSTHVDITLEDLMTGLGIYCPICQKP 98  
RESULT 90  
ADJ32548  
ID ADJ32548 standard; protein; 98 AA.  
XX  
AC ADJ32548;  
XX  
DT 22-APR-2004 (first entry)  
XX  
DE Human papillomavirus (HPV) type 16 E7 protein.  
XX  
KM Integrin; cell proliferation; cancer; melanoma; adenoma; lymphoma;  
KM myeloma; carcinoma; glioma; plasmacytoma; sarcoma; thymoma; leukemia;  
KM brain tumour; cytostatic.  
XX  
OS Human papillomavirus.  
XX  
XX US2003224993-A1.  
XX  
XX 04-DEC-2003.  
XX  
XX 17-MAR-2003; 2003US-00392113.  
XX  
XX 12-OCT-2000; 2000US-0239705P.  
XX  
XX 24-OCT-2000; 2000US-024812P.  
XX  
XX 12-OCT-2001; 2001WO-US032127.  
XX  
XX 15-MAR-2002; 2002US-0365078P.  
XX  
XX (LAND/) LAND H.  
XX  
XX (DELE/) DELEU L.  
XX  
XX Land H., Deleu L;  
XX  
XX WPI; 2004-154528/15.  
XX  
XX N-PSDB; ADJ32547.  
XX  
XX Reducing the proliferation of a cancer cell involves inhibiting ligand  
XX binding to an integrin receptor on the cancer cell, where the integrin  
XX receptor comprises an integrin.  
XX  
XX Disclosure; SEQ ID NO 29; 161pp; English.  
XX

CC The present invention relates to compositions and methods for reducing  
CC the proliferation of cancer cells through interaction with integrins. The  
CC invention is useful for reducing the proliferation of cancer cells e.g.  
CC melanoma, adenoma, lymphoma, myeloma, carcinoma, glioma, plasmacytoma,  
CC sarcoma, thymoma, leukemia, skin cancer, esophageal cancer, stomach cancer,  
CC prostate cancer, colon cancer, brain tumours, lung cancer, cervical  
CC pancreas cancer, breast cancer, gastrointestinal cancer, ovarian cancer, cervical  
CC cancer, hepatic cancer, and head and neck cancer  
CC cells. The invention is also useful for identifying a therapeutic target  
CC which involves assaying potential reagent for activity. The present  
CC sequence is human papillomavirus (HPV) type 16 E7 protein.  
XX  
XX Sequence 98 AA;  
SQ  
Query Match 97.5%; Score 504; DB 8; Length 98;  
Best Local Similarity 95.9%; Pred. No. 2.3e-56;  
Matches 94; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
Qy 1 MHGDTPTLHEXYMDLQPEPTTDLVYXXQLNDSSEDEIDPAGQAEPRAHYNIYTFCK 60  
Db 1 MHGDTPTLHEXYMDLQPEPTTDLVYEQQLNDSSEDEIDPAGQAEPRAHYNIYTFCK 60  
Qy 61 CDSTLRLCVOSTHVDITLEDLMTGLGIYXPICSQKP 98  
Db 61 CDSTLRLCVOSTHVDITLEDLMTGLGIYCPICQKP 98  
RESULT 91  
AAB31607  
ID AAB31607 standard; protein; 98 AA.  
XX  
XX AAB31607;  
XX  
XX 30-APR-2001 (first entry)  
XX  
DE Amino acid sequence of the HPV16 E7 protein.  
XX  
XX Heat shock protein; Hsp; Th1 response; Th1 cell; CD4+ T lymphocyte cell;  
XX lymphocyte; Hsp65; Hsp40; Hsp10; Hsp60; Hsp71; microbial pathogen;  
XX E7 protein.  
XX  
OS Human papillomavirus.  
XX  
XX WO200104344-A2.  
XX  
XX 18-JAN-2001.  
XX  
XX 10-JUL-2000; 2000WO-US018828.  
XX  
XX 08-JUL-1999; 99US-0143757P.  
XX  
XX (STRE-) STRESSGEN BIOTECHNOLOGIES CORP.  
XX  
XX Siegel M, Chu NR, Mizen LA;  
XX  
XX WPI; 2001-138361/14.  
XX  
XX N-PSDB; AAF25005.  
XX  
XX Screening for compounds that stimulate Th1-like responses in CD4+ T  
XX lymphocyte cells.  
XX  
XX Example 3; Fig 2; 88pp; English.  
XX  
XX The present sequence represents the HPV16 E7 protein. HPV16 E7 was fused  
XX to a heat shock protein (hsp), and used used in the method of the  
XX invention. The specification describes a method of determining whether a  
XX compound stimulates a Th1-like response. Th1 cells are a subset of CD4+ T  
XX lymphocyte cells. The method comprises contacting native lymphocytes in  
XX vitro with a fusion protein comprising at least a fragment of Hsp, and  
XX then detecting the Th1-like response exhibited by the cell sample. The  
XX proteins which may be used in the method of the invention are Hsp65,  
XX Hsp40, Hsp10, Hsp60, and Hsp71. The method may be used to identify  
XX compounds that stimulate Th1-like responses in response to microbial

CC	pathogens
XX	
SQ	Sequence 98 AA;
OY	Query Match            97.3%; Score 503; DB 4; Length 98; Best Local Similarity 95.9%; Pred. No. 3.1e-56; Matches     94; Conservative     0; Mismatches     4; Indels     0; Gaps     0.
OY	1 MHGDTPTLHEMYMLDIQPETTDLYXXYLQNDSSSEDEIDPGAGAEPPRAHNYITFCKK 60 Db        1 MDGDTPTLHEMYMLDIQPETTDLYCYEQUNDSSSEDEIDPGAGAEPPRAHNYITFCKK 60
OY	61 CDSLTRLCVOSTHVDIRFTLEDILMGTLGIYVPICSOKP 98 Db        61 CDSLTRLCVOSTHVDIRFTLEDILMGTLGIYVPICSOKP 98
RESULT 92	
ID	ADZ42209 standard; protein; 490 AA.
AC	ADZ42209;
XX	
DT	30-JUN-2005 (first entry)
XX	
DE	N. meningitidis P1.7.16 delta 5 and HPV-16 E7 fusion protein.
XX	
KM	papillomavirus infection; cytostatic; immune stimulation; vaccine;
XX	Cancer.
OS	Neisseria meningitidis.
OS	Human papillomavirus type 16.
XX	Chimeric.
PN	WO2005032585-A1.
PD	14-APR-2005.
PF	04-OCT-2004; 2004WO-CU000010.
PR	09-OCT-2003; 2003CU-00000224.
PA	(INGG-) CENT ING GENETICA & BIOTECNOLOGIA.
PI	Torrens Madrazo IDC, Guillen Nieto GE, Fernandez Molina LE;
DR	Pajon Feyt R, Reyes Acosta O;
DR	N-PSDB; ADZ42208.
XX	WPI; 2005-296057/30.
XX	
PT	Vaccine composition for boosting cellular immune response against human
PT	papilloma virus (HPV) antigens, contains HPV antigens linked via
XX	hydrophobic bonds or mixed with very small size proteoliposomes (VSP's).
PS	Example 1; SEQ ID NO 7; 62pp; Spanish.
XX	
CC	The invention relates to a novel composition comprising human
CC	papillomavirus (HPV) antigens or portions linked via hydrophobic bonds or
CC	mixed with very small size proteoliposomes (VSP's). The invention
CC	further comprises a method for treating a tumor expressing an HPV antigen
CC	by administering an effective amount of this composition. The novel
CC	composition has cytostatic activity. The composition is useful for
CC	boosting the immune response against HPV antigens. The compositions are
CC	suitable for use in the pharmaceutical industry as vaccines in human
CC	therapeutics for cancer treatment. The cellular immune response against
CC	HPV antigens is significantly boosted, especially with respect to cell
CC	cytotoxicity, ensuring that cells which exhibit the HPV antigen are
CC	destroyed more effectively. This sequence represents a Neisseria
CC	meningitidis P1.7.16 delta 5 and HPV-16 E7 fusion protein, used in the
CC	expression of HPV antigens of the invention.
XX	
XQ	Sequence 490 AA;

	Query Match	97.3%;	Score 503;	DB 9;	Length 490;	
	Best Local Similarity	94.9%;	Pred. No. 2.5e-55;			
	Matches	93;	Conservative	2;	Mismatches	3;
Oy	1 MHGDTPTLHEMYMDLOPETTDLXXYYXQUNDSSSEDEIDGPAGCAEPDRAHYNIYVTFCKK	60				
Dd	270 IHGGTPTLHEMYMDLOPETTDLXXCYEQUNDSSEDEIDGPAGCAEPDRAHYNIYVTFCKK	329				
Oy	61 CDSTLRFCVGSTHVDIRTEEDLLMGTLGIYVPCISQKP	98				
Dd	330 CDSTLRFCVGSTHVDIRTEEDLLMGTLGIYVPCISQKR	367				
	RESULT 93					
xx	AABJ1614					
xx	ID AABJ1614 standard; protein; 648 AA.					
xx	AC AABJ1614;					
xx	AT 30-APR-2001 (first entry)					
xx	DE Amino acid sequence of Hsp65-E7 fusion protein.					
xx	KM Heat shock protein; Hsp; Th1 response; Th1 cell; CD4+ T lymphocyte cell;					
xx	KN Lymphocyte; Hsp65; Hsp40; Hsp10; Hsp60; Hsp71; microbial pathogen;					
xx	E7 protein.					
xx	Synthetic.					
OS	Mycobacterium bovis.					
OS	Human papillomavirus.					
xx	MO200104344-A2.					
PN	18-JAN-2001.					
PD	10-JUL-2000; 2000MO-USO18828.					
PE	08-JUL-1999; 99US-0143757P.					
PR	(STRE-) STRESSGEN BIOTECHNOLOGIES CORP.					
xx	PA Siegel M, Chu NR, Mizzen LA;					
PI	WP1; 2001-138361/14.					
DR	N-PSDB; AAF25019.					
xx	Screening for compounds that stimulate Th1-like responses in CD4+ T					
PT	Lymphocyte cells.					
xx	Example 11; Fig 10A-B; 88pp; English.					
PS	The present sequence represents a fusion protein comprising Mycobacterium					
CC	bovis heat shock protein (Hsp) 65 fused at its C terminal to a HPV16 E7					
CC	protein. The fusion protein is used in the method of the invention. The					
CC	specification describes a method of determining whether a compound					
CC	stimulates a Th1-like response. Th1 cells are a subset of CD4+ T					
CC	lymphocyte cells. The method comprises contacting native lymphocytes in					
CC	vitro with a fusion protein comprising at least a fragment of Hsp, and					
CC	then detecting the Th1-like response exhibited by the cell sample. The					
CC	proteins which may be used in the method of the invention are Hsp65,					
CC	Hsp40, Hsp10, Hsp60, and Hsp71. The method may be used to identify					
CC	compounds that stimulate Th1-like responses in response to microbial					
CC	pathogens					
SO	Sequence 648 AA;					
Oy	Query Match	97.3%;	Score 503;	DB 4;	Length 648;	
	Best Local Similarity	95.9%;	Pred. No. 3.5e-55;			
	Matches	94;	Conservative	0;	Mismatches	4;
Oy	1 MHGDTPTLHEMYMDLOPETTDLXXYYXQUNDSSSEDEIDGPAGCAEPDRAHYNIYVTFCKK	60				
Dd	1 MDGGTPTLHEMYMDLOPETTDLXXCYEQUNDSSEDEIDGPAGCAEPDRAHYNIYVTFCKK	60				

OY 61 CDSTLRLCVQSTHVDIRLTEDLLMGTLGIYVPCISQKP 98  
 DB 61 CDSTLRLCVQSTHVDIRLTEDLLMGTLGIYVPCISQKP 98

## RESULT 94

ID AAB31617 standard; protein; 711 AA.

AC AAB31617;

DT 30-APR-2001 (first entry)

DE Amino acid sequence of Hsp71-E7 fusion protein.

XX Heat shock protein; Hsp; Th1 response; Th1 cell; CD4+ T lymphocyte cell;  
 KM lymphocyte; Hsp65; Hsp40; Hsp10; Hsp60; Hsp71; microbial pathogen;  
 KM E7 protein.

OS Synthetic.  
 OS Mycobacterium tuberculosis.

OS Human papillomavirus.

PN WO200104344-A2.

PD 18-JAN-2001.

PF 10-JUL-2000; 2000WO-US018828.

PR 08-JUL-1999; 99US-0143757P.

PA (STRE-) STRESSGEN BIOTECHNOLOGIES CORP.

PI Siegel M, Chu NR, Mizzen LA;

DR WPI; 2001-138361/14.

DR N-PSDB; AAF25028.

PT Screening for compounds that stimulate Th1-like responses in CD4+ T  
 lymphocyte cells.

PS Example 14; Fig 13A-B; 88pp; English.

XX The present sequence represents a fusion protein comprising Mycobacterium  
 CC tuberculosis heat shock protein (Hsp) 71 fused to a HPV16 E7 protein. The  
 CC fusion protein is used in the method of the invention. The specification  
 CC describes a method of determining whether a compound stimulates a Th1-  
 CC like response. Th1 cells are a subset of CD4+ T lymphocyte cells. The  
 CC method comprises contacting naive lymphocytes in vitro with a fusion  
 CC protein comprising at least a fragment of Hsp, and then detecting the Th1  
 CC -like response exhibited by the cell sample. The proteins which may be  
 CC used in the method of the invention are Hsp65, Hsp40, Hsp10, Hsp60, and  
 CC Hsp71. The method may be used to identify compounds that stimulate Th1-  
 CC like responses in response to microbial pathogens

XX Sequence 711 AA;

Query Match 97.3%; Score 503; DB 4; Length 711;

Best Local Similarity 95.9%; Pred. No. 4e-55; Mismatches 4; Indels 0; Gaps 0;

DB 1 MHGDPPTLHEWMLDQPEPTDLYXXXLNDSSSEDEIDGPAQAEPPRAHYNIVTFCK 60  
 1 MDGDPPTLHEWMLDQPEPTDLYXXXLNDSSSEDEIDGPAQAEPPRAHYNIVTFCK 60  
 OY 61 CDSTLRLCVQSTHVDIRLTEDLLMGTLGIYVPCISQKP 98  
 DB 61 CDSTLRLCVQSTHVDIRLTEDLLMGTLGIYVPCISQKP 98

RESULT 95  
 AAB31618

ID AAB31618 standard; protein; 724 AA.

AC AAB31618;

DT 30-APR-2001 (first entry)

DE Amino acid sequence of E7-Hsp71 fusion protein.

XX Heat shock protein; Hsp; Th1 response; Th1 cell; CD4+ T lymphocyte cell;  
 KM lymphocyte; Hsp65; Hsp40; Hsp10; Hsp60; Hsp71; microbial pathogen;  
 KM E7 protein.

OS Synthetic.  
 OS Human papillomavirus.

OS Mycobacterium tuberculosis.

PN WO200104344-A2.

PD 18-JAN-2001.

PF 10-JUL-2000; 2000WO-US018828.

PR 08-JUL-1999; 99US-0143757P.

PA (STRE-) STRESSGEN BIOTECHNOLOGIES CORP.

PI Siegel M, Chu NR, Mizzen LA;

DR WPI; 2001-138361/14.

DR N-PSDB; AAF25031.

PT Screening for compounds that stimulate Th1-like responses in CD4+ T  
 lymphocyte cells.

PS Example 14; Fig 14A-B; 88pp; English.

XX The present sequence represents a fusion protein comprising a HPV16 E7  
 CC protein fused to a Mycobacterium tuberculosis heat shock protein (Hsp)  
 CC 71. The fusion protein is used in the method of the invention. The  
 CC specification describes a method of determining whether a compound  
 CC stimulates a Th1-like response. Th1 cells are a subset of CD4+ T  
 CC lymphocyte cells. The method comprises contacting naive lymphocytes in  
 CC vitro with a fusion protein comprising at least a fragment of Hsp, and  
 CC then detecting the Th1-like response exhibited by the cell sample. The  
 CC proteins which may be used in the method of the invention are Hsp65,  
 CC Hsp40, Hsp10, Hsp60, and Hsp71. The method may be used to identify  
 CC compounds that stimulate Th1-like responses in response to microbial  
 CC pathogens

XX Sequence 724 AA;

Query Match 97.3%; Score 503; DB 4; Length 724;

Best Local Similarity 95.9%; Pred. No. 4.1e-55; Mismatches 4; Indels 0; Gaps 0;

DB 1 MHGDPPTLHEWMLDQPEPTDLYXXXLNDSSSEDEIDGPAQAEPPRAHYNIVTFCK 60  
 1 MDGDPPTLHEWMLDQPEPTDLYXXXLNDSSSEDEIDGPAQAEPPRAHYNIVTFCK 60  
 OY 61 CDSTLRLCVQSTHVDIRLTEDLLMGTLGIYVPCISQKP 98  
 DB 61 CDSTLRLCVQSTHVDIRLTEDLLMGTLGIYVPCISQKP 98

## RESULT 96

ID AAB81111 standard; protein; 99 AA.

AC AAB81111;

DT 05-NOV-2002 (first entry)

DE HPV E7 antigenic protein.

XX Major histocompatibility complex; MHC; antigen presenting cell; APC;  
KM antigen; cytostatic; virucide; gene therapy; CD8; vaccine; therapeutic;  
KM cancer; viral infection; HPV; E7.  
XX  
OS Human papillomavirus.  
XX  
PN WO200261113-A2.  
XX  
PD 08-AUG-2002.  
XX  
PF 01-FEB-2002; 2002WO-US002598.  
XX  
PR 01-FEB-2001; 2001US-0265334P.  
XX  
PA (UYJO ) UNIV JOHNS HOPKINS.  
XX  
PI Wu T, Hung C;  
XX  
DR WPI; 2002-619261/66.  
DR N-PSDB; ABN86677.  
XX  
XX  
XX Nucleic acid molecule encoding a fusion polypeptide that promotes  
PT processing via the Major Histocompatibility Complex class I pathway  
PT and/or promotes activity of an antigen presenting cell, useful as vaccine  
PT for cancer and viral infections.  
PS Disclosure; Page 16; 127pp; English.  
XX  
XX The invention relates to a new nucleic acid molecule (I) encoding a  
CC fusion polypeptide useful as a vaccine composition. (I) comprises a first  
CC nucleic acid sequence encoding a first polypeptide or peptide that  
CC promotes processing via the Major Histocompatibility Complex (MHC) class  
CC I pathway (MHC-I-p) and/or promotes development or activity of an  
CC antigen presenting cell (APC). The second nucleic acid sequence is linked  
CC in frame to the first nucleic acid sequence or to a linker nucleic acid  
CC sequence and encodes an antigenic polypeptide or peptide. The methods and  
CC compositions of the present invention are useful as therapeutic vaccine  
CC for cancer and for major viral infections, such as hepatoma and cervical  
CC cancer, that cause morbidity and mortality. They can also be used in  
CC treating animal diseases, such as equine herpesvirus, bovine viruses,  
CC Marek's disease, retroviral and lentiviral diseases and rabies, in the  
CC veterinary medicine context. The present sequence represents the human  
CC papillomavirus (HPV) E7 antigenic protein  
XX  
SQ Sequence 99 AA;  
Query Match 96.7%; Score 500; DB 5; Length 99;  
Best Local Similarity 96.9%; Pred. No. 7.6e-56;  
Matches 93; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 MHGDTPLHRYMDLQPEETDLYXXQLNDSSEDEIDGPAGQAEPRRAHYNIIVTFCK 60  
Db 1 MHGDTPLHRYMDLQPEETDLYCYEQLNDSSEDEIDGPAGQAEPRRAHYNIIVTFCK 60  
QY 61 CDSTLRLCVOSTHVDIRLTEDLMGTIGIYCPICSQ 96  
Db 61 CDSTLRLCVOSTHVDIRLTEDLMGTIGIYCPICSQ 96  
RESULT 97  
ABB82376  
ID ABB82376 standard; protein; 99 AA.  
XX  
XX ABB82376;  
XX  
XX  
DT 08-JAN-2003 (first entry)  
XX  
XX Modified HPV-E7 amino acid sequence.  
XX  
XX Immunogenicity; cytostatic; virucide; protozoacide; antibacterial; CTL;  
KM hepatotropic; anti-HIV; vaccine. cytotoxic T lymphocyte; tumour; HPV;  
KM E7 protein.

XX  
OS Human papillomavirus.  
XX  
XX  
XX WO200274920-A2.  
XX  
XX 26-SEP-2002.  
XX  
XX 18-MAR-2002; 2002WO-US008033.  
XX  
XX 16-MAR-2001; 2001US-0276854P.  
XX  
XX  
XX (UYJO ) UNIV JOHNS HOPKINS.  
XX  
XX Wu T, Hung C;  
XX  
XX WPI; 2002-740856/80.  
DR N-PSDB; ABV73162.  
XX  
XX  
XX New nucleic acid molecule encoding an antigenic fusion polypeptide useful  
PT as vaccines for enhancing or inducing immune responses, primarily  
PT cytotoxic T lymphocytes (CTL) responses to specific antigens such as  
PT tumour or viral antigens.  
PS Disclosure; Page 20; 93pp; English.  
XX  
XX The invention relates to a nucleic acid molecule that encodes a fusion  
CC polypeptide, comprising a first nucleic acid sequence encoding a  
CC polypeptide that comprises at least one immunogenically-potentiating  
CC polypeptide, optionally, fused in frame with the nucleic acid, a linker  
CC nucleic acid encoding a linker peptide, and a nucleic acid that is linked  
CC in frame to them, and that encodes an antigenic peptide or polypeptide.  
CC The nucleic acid molecule, polypeptides and vectors are useful as  
CC vaccines for enhancing immune responses, primarily cytotoxic T  
CC lymphocytes (CTL) responses to specific antigens such as tumour or viral  
CC antigens, and for inhibiting growth or preventing re-growth of a tumour.  
CC The packaging cell line is useful for generating alphavirus replicon  
CC particles without contamination from replicon-competent virus. The  
CC pathogenic organisms include viruses such as human papilloma virus (HPV),  
CC Epstein Barr virus, hepatitis C virus, human immunodeficiency virus,  
CC Epstein Barr virus and herpes simplex virus, intracellular parasites such  
CC as malaria, and bacteria that grow intracellularly such as mycobacteria  
CC and listeria. The present sequence represents a modified HPV E-7 protein  
XX  
SQ Sequence 99 AA;  
Query Match 96.7%; Score 500; DB 5; Length 99;  
Best Local Similarity 96.9%; Pred. No. 7.6e-56;  
Matches 93; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 MHGDTPLHRYMDLQPEETDLYXXQLNDSSEDEIDGPAGQAEPRRAHYNIIVTFCK 60  
Db 1 MHGDTPLHRYMDLQPEETDLYCYEQLNDSSEDEIDGPAGQAEPRRAHYNIIVTFCK 60  
QY 61 CDSTLRLCVOSTHVDIRLTEDLMGTIGIYCPICSQ 96  
Db 61 CDSTLRLCVOSTHVDIRLTEDLMGTIGIYCPICSQ 96  
RESULT 98  
ADE21865  
ID ADE21865 standard; protein; 99 AA.  
XX  
XX ADE21865;  
XX  
XX  
DT 29-JAN-2004 (first entry)  
XX  
XX HPV-16 E7 protein SEQ ID NO:7.  
XX  
XX chimeric fusion; translocation; antigenic; cytostatic; immunotherapy;  
KM gene therapy; cancer; tumour; HPV-16; E7 protein.  
XX  
XX Human papillomavirus.

PN WO2003085085-A2.  
XX  
PD 16-OCT-2003.  
XX  
XX 04-APR-2003; 2003WO-US010235.  
PF  
XX 04-APR-2002; 2002US-00115440.  
PR  
XX (UJJO ) UNIV JOHNS HOPKINS.  
PA  
XX Wu T, Hung C;  
FI  
XX WPI; 2003-877027/81.  
DR  
XX N-PSDB; ADE21864.  
DR  
XX  
PT New nucleic acid encoding a chimeric fusion or fusion polypeptide  
PT comprising a first domain with a translocation polypeptide, and a second  
PT domain with an antigen having at least one antigenic peptide, useful for  
PT treating cancer.  
PS Disclosure; SEQ ID NO 7; 68bp; English.  
XX  
XX The present invention describes a nucleic acid (I) encoding a chimeric  
CC fusion or fusion polypeptide comprising a first domain with a  
CC translocation polypeptide, and a second domain comprising an antigen  
CC having at least one antigenic peptide. Also described: (1) an expression  
CC vector comprising (I) operatively linked to a promoter and optionally, to  
CC one or more regulatory elements that enhance expression of the nucleic  
CC acid in a cell; (2) a particle comprising (I) or the expression vector;  
CC (3) a cell that has been modified to comprise (I) or the expression  
CC vector; (4) a chimeric polypeptide comprising a first domain with a  
CC translocation polypeptide, and a second domain comprising an antigen  
CC having at least one antigenic peptide; (5) a pharmaceutical composition  
CC capable of inducing or enhancing an antigen specific immune response,  
CC comprising (I), expression vector, particle, cell, cell of the particle,  
CC or the chimeric polypeptide; and a carrier or excipient; (6) inducing or  
CC enhancing an antigen specific immune response by administering the  
CC composition described above; (7) increasing the number of CD8 + CTLs  
CC specific for a selected desired antigen in a subject by administering the  
CC composition described above; and (8) inhibiting the growth of a tumour in  
CC a subject by administering the composition described above. (I) has  
CC cytostatic activity, and can be used in immunotherapy, and gene therapy.  
CC The nucleic acids (I), compositions and methods are useful for treating  
CC cancer. The present sequence represents HPV-16 E7, which is used in the  
CC exemplification of the present invention.  
XX  
SQ Sequence 99 AA;  
Query Match 96.7%; Score 500; DB 7; Length 99;  
Best Local Similarity 96.9%; Pred. No. 7.6e-56;  
Matches 93; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 MHGDTPTLHEYMLDLOPETTDLYXXQLNDSSEDEIDGPAGQAEPPRAHYNIIVTEFCK 60  
DB 1 MHGDTPTLHEYMLDLOPETTDLYCYEQLNDSSEDEIDGPAGQAEPPRAHYNIIVTEFCK 60  
QY 61 CDSTLRLCVOSTHYVDIRTDLELDMGTIGIYXPCISQ 96  
DB 61 CDSTLRLCVOSTHYVDIRTDLELDMGTIGIYVPCISQ 96  
RESULT 99  
AD005276  
ID AD005276 standard; protein; 99 AA.  
XX  
AC AD005276;  
XX  
DT 29-JUL-2004 (first entry)  
XX  
DE Human papillomavirus type 16 E7 protein.  
XX  
KW Translocation domain; bacterial toxin; exotoxin A domain II; E7A;  
KW major histocompatibility complex; MHC class I; vaccine; immune response;  
KW

KW CD8+ cytotoxic T lymphocyte; CTL; tumour; E7 antigen.  
XX  
OS Human papillomavirus type 16.  
XX  
XX US2004086845-A1.  
PN  
XX 06-MAY-2004.  
PD  
XX 04-APR-2002; 2002US-00115440.  
PE  
XX 20-OCT-1999; 99US-00421608.  
PR 09-FEB-2000; 2000US-00501097.  
PR 20-OCT-2000; 2000WO-US041422.  
PR 04-APR-2001; 2001US-0281003P.  
XX  
PA (WTTT/) Wu T.  
PA (HUNG/) HUNG C.  
FI  
XX Wu T, Hung C;  
PI  
XX WPI; 2004-356187/33.  
DR N-PSDB; AD005275.  
DR  
XX Novel chimeric polypeptide e.g., Pseudomonas aeruginosa exotoxin A domain  
PT II/human papilloma virus-16 E7 peptide useful for inducing or enhancing  
PT antigen specific immune response, or for inhibiting growth of tumor in  
PT subject.  
XX  
PS Claim 10; SEQ ID NO 7; 48bp; English.  
XX  
XX The invention relates to nucleic acid encoding a chimeric polypeptide  
CC comprising a translocation domain of a bacterial toxin and at least one  
CC antigenic peptide. The preferred translocation domain is domain II of  
CC Pseudomonas aeruginosa exotoxin A (ETA/dII) and the preferred antigen is  
CC human papilloma virus type 16 (HPV-16) E7 which is a model tumour  
CC antigen. The antigenic peptide comprises an epitope that binds to and is  
CC presented on the cell surface by major histocompatibility complex (MHC)  
CC class I protein. The nucleic acid of the invention is useful as vaccine  
CC composition for enhancing antigen specific immune response, increasing  
CC the number of CD8+ cytotoxic T lymphocytes (CTLs) and for inhibiting the  
CC growth of a tumour. The present sequence is HPV-16 E7 protein.  
XX  
SQ Sequence 99 AA;  
Query Match 96.7%; Score 500; DB 8; Length 99;  
Best Local Similarity 96.9%; Pred. No. 7.6e-56;  
Matches 93; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 MHGDTPTLHEYMLDLOPETTDLYXXQLNDSSEDEIDGPAGQAEPPRAHYNIIVTEFCK 60  
DB 1 MHGDTPTLHEYMLDLOPETTDLYCYEQLNDSSEDEIDGPAGQAEPPRAHYNIIVTEFCK 60  
QY 61 CDSTLRLCVOSTHYVDIRTDLELDMGTIGIYXPCISQ 96  
DB 61 CDSTLRLCVOSTHYVDIRTDLELDMGTIGIYVPCISQ 96  
RESULT 100  
ADU6377  
ID ADU6377 standard; protein; 99 AA.  
XX  
AC ADU6377;  
XX  
DT 10-FEB-2005 (first entry)  
XX  
DE Human papillomavirus type 16 (HPV16) E7 protein - SEQ ID 2.  
XX  
KW vaccine; MHC class I pathway; antigen specific immune response; tumor;  
KW E7 protein; E6 protein.  
XX  
OS Human papillomavirus type 16.  
XX  
PN WO2004098526-A2.

```

XX 18-NOV-2004.
PD
XX
XX 05-MAY-2004; 2004MO-US013756.
PF
XX
XX 05-MAY-2003; 2003US-0467602P.
PR
XX
XX (UYJO ) UNIV JOHNS HOPKINS.
PA
XX
XX Wu T, Hung CF;
PI
XX
XX WPI: 2004-813972/80.
DR N-PSDB; ADU66361.
XX
XX New nucleic acid molecules encoding a fusion polypeptide comprising an
PT antigen, a signal peptide, and a heat shock protein, useful as a vaccine
PT for inducing or enhancing immune response or for inhibiting or preventing
PT tumor growth.
XX
XX Claim 8; SEQ ID NO 2; 67bp; English.
PS
XX
XX The invention comprises a nucleic acid molecule (DNA vaccine) that
CC encodes a fusion polypeptide which is useful as a vaccine composition.
CC The nucleic acid of the invention contains: a first nucleic acid encoding
CC a polypeptide that promotes processing via the MHC class I pathway; a
CC second sequence encoding a signal peptide; and a third sequence encoding
CC an antigenic polypeptide. The DNA vaccine of the invention is useful for
CC inducing or enhancing an antigen specific immune response, or to inhibit
CC growth or prevent re-growth of a tumor expressing Human papillomavirus
CC (HPV) E7 or E6 protein. The present amino acid sequence represents a
CC human papillomavirus type 16 (HPV16) E7 protein of the invention.
XX
XX Sequence 99 AA;
SQ
XX
XX Query Match 96.7%; Score 500; DB 8; Length 99;
XX Best local Similarity 96.9%; Pred. No. 7,6e-56;
XX Matches 93; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
OY 1 MHGDTPTLHEVMDLQEPETDLYXXQLNDSSEDEIDGPAQAEPDRAHNYIVTFCK 60
XX |||||||
DB 1 MHGDTPTLHEVMDLQEPETDLYCYEQLNDSSEDEIDGPAQAEPDRAHNYIVTFCK 60
XX |||||||
OY 61 CDSTRLCVOSTHYDRTLEIDLMGTGIVPCISQ 96
XX |||||||
DB 61 CDSTRLCVOSTHYDRTLEIDLMGTGIVPCISQ 96
XX |||||||

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 Job time : 234.273 secs

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## OM protein - protein search, using sw model

Run on: May 27, 2006, 05:16:46 ; Search time 44.2691 Seconds

(Without alignments)  
298.563 Million cell updates/sec

Title: US-10-530-253-13ED

Perfect score: 830  
Sequence: 1 MFQDPQRPKRLPOLCTELQ.....WTGCMSCRSSRRRETQL 151

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

## Database :

Issued Patents AA:\*

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2: /EMC\_Celerra\_SIDS3/prodata/2/iaa/6 COMB pep:\*

3: /EMC\_Celerra\_SIDS3/prodata/2/iaa/7 COMB pep:\*

4: /EMC\_Celerra\_SIDS3/prodata/2/iaa/H COMB pep:\*

5: /EMC\_Celerra\_SIDS3/prodata/2/iaa/PCUS COMB pep:\*

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7: /EMC\_Celerra\_SIDS3/prodata/2/iaa/backfillseq1 pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	826	99.5	162	1	US-08-316-239B-4
2	823	99.2	158	2	US-09-980-523A-2
3	823	99.2	158	3	US-09-763-616-1
4	823	99.2	162	1	US-08-316-239B-3
5	823	99.2	266	2	US-08-860-165-10
6	823	99.2	266	2	US-09-359-382-10
7	823	99.2	266	2	US-09-367-309A-1
8	823	99.2	273	2	US-09-485-885-4
9	823	99.2	297	2	US-09-485-885-10
10	823	99.2	371	2	US-09-485-885-6
11	823	99.2	390	2	US-09-485-885-14
12	818	98.6	151	2	US-09-701-080C-18
13	779.5	93.9	243	2	US-08-462-993-1
14	519	62.5	172	2	US-08-860-165-12
15	519	62.5	172	2	US-09-359-382-12
16	478	57.6	172	2	US-08-860-165-14
17	478	57.6	172	2	US-09-359-382-14
18	477	57.5	182	1	US-08-117-083-10
19	455.5	54.9	158	1	US-08-247-904B-10
20	455.5	54.9	158	2	US-08-767-942A-19
21	455.5	54.9	271	1	US-08-117-083-14
22	455.5	54.9	278	2	US-09-485-885-21
23	455.5	54.9	383	2	US-09-485-885-23
24	304	36.6	368	2	US-09-000-094-20
25	304	36.6	368	2	US-10-011-749-20
26	304	36.6	375	2	US-09-000-094-22

27	304	36.6	375	2	US-10-011-749-22	Sequence 22, Appl
28	304	36.6	465	2	US-09-000-094-24	Sequence 24, Appl
29	304	36.6	465	2	US-10-011-749-24	Sequence 24, Appl
30	304	36.6	1587	2	US-09-000-094-26	Sequence 46, Appl
31	304	36.6	1587	2	US-10-011-749-46	Sequence 46, Appl
32	163	19.6	30	1	US-08-363-586-4	Sequence 4, Appl
33	163	19.6	30	2	US-09-980-523A-4	Sequence 8, Appl
34	159	16.2	29	2	US-09-980-523A-8	Sequence 17, Appl
35	134.5	16.2	137	2	US-09-913-204-17	Sequence 10, Appl
36	130	15.7	23	2	US-09-980-523A-10	Sequence 276, App
37	128	15.4	22	2	US-09-601-729-276	Sequence 6, Appl
38	124	14.9	22	2	US-09-980-523A-6	Sequence 167, App
39	120	14.5	21	1	US-08-934-915-167	Sequence 3, Appl
40	119	14.3	137	2	US-09-913-204-3	Sequence 7, Appl
41	119	14.3	137	2	US-09-913-204-7	Sequence 13, Appl
42	119	14.3	137	2	US-09-913-204-13	Sequence 16, App
43	115	13.9	21	1	US-08-934-915-166	Sequence 2, Appl
44	115	13.9	32	1	US-08-466-285-2	Sequence 278, App
45	115	13.9	32	2	US-08-164-768-2	Sequence 4, Appl
46	114	13.7	20	2	US-09-601-729-278	Sequence 44, Appl
47	114	13.7	22	2	US-10-612-818-4	Sequence 45, Appl
48	109	13.1	20	1	US-08-934-915-44	Sequence 163, App
49	109	13.1	20	1	US-08-934-915-45	Sequence 164, App
50	109	13.1	20	1	US-08-934-915-163	Sequence 165, App
51	104	12.5	20	1	US-08-934-915-164	Sequence 160, App
52	104	12.5	20	1	US-08-934-915-165	Sequence 161, App
53	98	11.8	20	1	US-08-934-915-159	Sequence 46524, A
54	97	11.7	20	1	US-08-934-915-160	Sequence 4, Appl
55	97	11.7	20	1	US-08-934-915-161	Sequence 16, App
56	94	11.3	15	3	US-09-641-528B-46524	Sequence 4, Appl
57	93	11.2	32	1	US-08-466-285-4	Sequence 46535, A
58	93	11.2	32	2	US-08-164-768-4	Sequence 16, App
59	92	11.1	15	3	US-09-641-528B-46535	Sequence 46527, A
60	92	11.1	20	1	US-08-363-586-3	Sequence 46536, A
61	90	10.8	23	1	US-08-363-586-3	Sequence 51599, A
62	89	10.7	15	3	US-09-641-528B-46517	Sequence 46522, A
63	85	10.2	15	3	US-07-909-122-2	Sequence 46526, A
64	85	10.2	15	3	US-09-641-528B-46523	Sequence 46519, A
65	85	10.2	15	3	US-09-641-528B-46525	Sequence 46534, A
66	85	10.2	15	3	US-09-641-528B-46526	Sequence 46532, A
67	85	10.2	15	3	US-09-641-528B-46520	Sequence 46527, A
68	84	10.1	15	3	US-09-641-528B-46519	Sequence 46526, A
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70	83	10.0	15	3	US-09-641-528B-46532	Sequence 46527, A
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73	83	10.0	15	3	US-08-075-541D-52	Sequence 46522, A
74	82	9.9	15	3	US-08-641-528B-51199	Sequence 46522, A
75	82	9.9	15	3	US-09-641-528B-46532	Sequence 46522, A
76	82	9.9	15	3	US-09-641-528B-46536	Sequence 46522, A
77	82	9.9	15	3	US-09-641-528B-46532	Sequence 46522, A
78	81	9.8	15	3	US-09-641-528B-46518	Sequence 46522, A
79	80	9.6	15	3	US-09-641-528B-46520	Sequence 46522, A
80	80	9.6	15	3	US-09-641-528B-46520	Sequence 46522, A
81	80	9.6	15	3	US-09-641-528B-46520	Sequence 46522, A
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83	79	9.5	15	3	US-09-641-528B-46532	Sequence 46522, A
84	78	9.4	15	3	US-09-641-528B-46536	Sequence 46522, A
85	78	9.4	15	3	US-09-641-528B-46536	Sequence 46522, A
86	77.5	9.3	165	2	US-09-270-767-31740	Sequence 46522, A
87	77.5	9.3	165	2	US-09-270-767-31740	Sequence 46522, A
88	77.5	9.3	165	2	US-09-270-767-31740	Sequence 46522, A
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93	76	9.2	15	3	US-09-641-528B-50557	Sequence 46522, A
94	76	9.2	15	3	US-09-641-528B-50557	Sequence 46522, A
95	75.5	9.1	187	2	US-09-248-766A-16235	Sequence 46522, A
96	75.5	9.1	250	2	US-09-949-016-6090	Sequence 46522, A
97	75	9.0	15	3	US-09-641-528B-46533	Sequence 46522, A
98	74.5	9.0	393	1	US-08-377-309-7	Sequence 7, Appl
99	74.5	9.0	393	2	US-09-186-723-7	Sequence 7, Appl

100 74.5 9.0 393 2 US-08-505-012-10

Sequence 10, Appl

## ALIGNMENTS

## RESULT 1

US-08-316-239B-4

; Sequence 4, Application US/08316239B

; Patent No. 5679509

; GENERAL INFORMATION:

; APPLICANT: Wheeler, Cosette M.

; TITLE OF INVENTION: Method and a Diagnostic Aid for

; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an

; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Jagtiani & Associates

; STREET: 6126 Rocky Way Court

; CITY: Centreville

; STATE: VA

; COUNTRY: USA

; ZIP: 20120-3400

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/316,239B

; FILING DATE: 30-SEP-1994

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Jagtiani, Ajay A.

; REGISTRATION NUMBER: 35,205

; REFERENCE/DOCKET NUMBER: UNNE-0001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 817-9453

; TELEFAX: (703) 803-9387

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 162 amino acids

; TYPE: amino acid

; STRANDEDNESS: not relevant

; TOPOLOGY: not relevant

; MOLECULE TYPE: protein

; HYPOTHEICAL: NO

; US-08-316-239B-4

Query Match 99.5%; Score 826; DB 1; Length 162;

Best Local Similarity 98.7%; Pred. No. 8.2e-86;

Matches 149; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 68 AVCDKCLKFYSKISEYRHYCYGVYGTLLLEQYNNKPLCDLLIRCIINXQKPLCEPEKQRHLD 127  
QY 121 KKQRFNIRGRWTGRCMSCCRSSRTRETOL 151  
DB 128 KKQRFNIRGRWTGRCMSCCRSSRTRETOL 158

RESULT 2  
US-09-980-523A-2  
; Sequence 2, Application US/09980523A  
; Patent No. 6783763  
; GENERAL INFORMATION:

APPLICANT: CHOPPIN, JEANNINE

APPLICANT: BOURGAULT VILLADA, ISABELLE

APPLICANT: GUILLET, JEAN-GERARD

APPLICANT: CONNAM, FRANCINE

APPLICANT: FERRIES, ESTELLE

TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 AND E7

TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE

TITLE OF INVENTION: PARTICULARLY IN VACCINATION

FILE REFERENCE: WO91 AO INS

CURRENT APPLICATION NUMBER: US/09/980,523A

CURRENT FILING DATE: 2002-04-29

PRIOR APPLICATION NUMBER: PCT/FR00/01513

PRIOR FILING DATE: 2000-05-31

PRIOR APPLICATION NUMBER: FR 99/07012

PRIOR FILING DATE: 1999-06-03

NUMBER OF SEQ ID NOS: 24

SOFTWARE: Patent in Ver. 2.1

SEQ ID NO 2

LENGTH: 158

TYPE: PRT

ORGANISM: Human Papillomavirus

US-09-980-523A-2

Query Match 99.2%; Score 823; DB 2; Length 158;

Best Local Similarity 98.0%; Pred. No. 1.7e-85;

Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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DB 8 MFQDPQERPRKLPOLCTELQTTIHDIIECYCKQQLLRREYVDFAFRDLCTVVRDGNPY 67  
QY 61 AVXDKCLKFYSKISEYRHYCYGVYGTLLLEQYNNKPLCDLLIRCIINXQKPLCEPEKQRHLD 120  
DB 68 AVCDKCLKFYSKISEYRHYCYGVYGTLLLEQYNNKPLCDLLIRCIINXQKPLCEPEKQRHLD 127  
QY 121 KKQRFNIRGRWTGRCMSCCRSSRTRETOL 151  
DB 128 KKQRFNIRGRWTGRCMSCCRSSRTRETOL 158

RESULT 3  
US-09-763-616-1  
; Sequence 1, Application US/09763616  
; Patent No. 7019000  
; GENERAL INFORMATION:  
; APPLICANT: BERNARD, HANS-ULRICH  
; APPLICANT: TAN, YEE JOO  
; APPLICANT: BEERHEIDE, WALTER  
; APPLICANT: TING, ANTHONY EUGENE  
; APPLICANT: SIM, MUI MUI  
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS AND METHODS  
; FILE REFERENCE: BERN3001/ADB  
; CURRENT APPLICATION NUMBER: US/09/763,616  
; CURRENT FILING DATE: 2001-05-16  
; PRIOR APPLICATION NUMBER: PCT/AU99/00724  
; PRIOR FILING DATE: 1999-09-03  
; PRIOR APPLICATION NUMBER: AU P01645/99  
; PRIOR FILING DATE: 1998-07-15  
; PRIOR APPLICATION NUMBER: AU P5733/98  
; PRIOR FILING DATE: 1998-09-04  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 158  
; TYPE: PRT  
; ORGANISM: Human papillomavirus type 16  
; US-09-763-616-1

Query Match 99.2%; Score 823; DB 3; Length 158;  
Best Local Similarity 98.0%; Pred. No. 1.7e-85;  
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFQDPQERPRKLPOLCTELQTTIHDIIECYCKQQLLRREYVDFAFRDLCTVVRDGNPY 60

Db 8 MFODPOERPRKLPOLCTELQTTIHDIILECYCKQQLRREYDPAFRLDCTIVRDGNPY 67  
Qy 61 AVXDCKLKFYSKISEYRHVCYSVYGTTLLEQYKNPCLDLIRCNXKQPLCPBEKORHLD 120  
Db 68 AVCDKCLKFYSKISEYRHVCYSVYGTTLLEQYKNPCLDLIRCNXKQPLCPBEKORHLD 127  
Qy 121 KKORFHNIRGRWTCRMCSSCRSRTRETOL 151  
Db 128 KKORFHNIRGRWTCRMCSSCRSRTRETOL 158

## RESULT 4

US-08-316-239B-3  
Sequence 3, Application US/08316239B  
Patent No. 5679509  
GENERAL INFORMATION:  
APPLICANT: Wheeler, Cosette M.  
APPLICANT: Parmenter, Cheryl A.  
TITLE OF INVENTION: Methods and a Diagnostic Aid for  
TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an  
TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and  
TITLE OF INVENTION: Cervical Cancer  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Jagtiani & Associates  
STREET: 6126 Rocky Way Court  
CITY: Centerville  
STATE: VA  
COUNTRY: USA  
ZIP: 20120-3400  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/316,239B  
FILING DATE: 30-SEP-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Jagtiani, Ajay A.  
REGISTRATION NUMBER: 35,205  
REFERENCE/DOCKET NUMBER: UNME-0001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 817-9453  
FAX: (703) 803-9387  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 162 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: not relevant  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
US-08-316-239B-3

Query Match 99.2%; Score 823; DB 1; Length 162;  
Best Local Similarity 98.0%; Pred. No. 1.8e-85;  
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MFODPOERPRKLPOLCTELQTTIHDIILECYCKQQLRREYDPAFRLDCTIVRDGNPY 60  
Db 8 MFODPOERPRKLPOLCTELQTTIHDIILECYCKQQLRREYDPAFRLDCTIVRDGNPY 67  
Qy 61 AVXDCKLKFYSKISEYRHVCYSVYGTTLLEQYKNPCLDLIRCNXKQPLCPBEKORHLD 120  
Db 68 AVCDKCLKFYSKISEYRHVCYSVYGTTLLEQYKNPCLDLIRCNXKQPLCPBEKORHLD 127  
Qy 121 KKORFHNIRGRWTCRMCSSCRSRTRETOL 151  
Db 128 KKORFHNIRGRWTCRMCSSCRSRTRETOL 158

RESULT 5  
US-08-860-165-10  
Sequence 10, Application US/08860165A  
Patent No. 6004557  
GENERAL INFORMATION:  
APPLICANT: EDWARDS, Stirling John  
APPLICANT: COX, John Cooper  
APPLICANT: WEBB, Elizabeth Ann  
APPLICANT: FRAZER, Ian  
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS  
FILE REFERENCE: 17227/130  
CURRENT APPLICATION NUMBER: US/08/860,165A  
CURRENT FILING DATE: 1997-09-22  
EARLIER APPLICATION NUMBER: PCT/AU95/00868  
EARLIER FILING DATE: 1995-12-20  
EARLIER APPLICATION NUMBER: AU PN0157  
EARLIER FILING DATE: 1994-12-20  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 10  
LENGTH: 266  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion  
US-08-860-165-10

Query Match 99.2%; Score 823; DB 2; Length 266;  
Best Local Similarity 98.0%; Pred. No. 3.2e-85;  
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MFODPOERPRKLPOLCTELQTTIHDIILECYCKQQLRREYDPAFRLDCTIVRDGNPY 60  
Db 8 MFODPOERPRKLPOLCTELQTTIHDIILECYCKQQLRREYDPAFRLDCTIVRDGNPY 67  
Qy 61 AVXDCKLKFYSKISEYRHVCYSVYGTTLLEQYKNPCLDLIRCNXKQPLCPBEKORHLD 120  
Db 68 AVCDKCLKFYSKISEYRHVCYSVYGTTLLEQYKNPCLDLIRCNXKQPLCPBEKORHLD 127  
Qy 121 KKORFHNIRGRWTCRMCSSCRSRTRETOL 151  
Db 128 KKORFHNIRGRWTCRMCSSCRSRTRETOL 158

## RESULT 6

US-09-359-382-10  
Sequence 10, Application US/09359382  
Patent No. 6306397  
GENERAL INFORMATION:  
APPLICANT: EDWARDS, Stirling John  
APPLICANT: COX, John Cooper  
APPLICANT: WEBB, Elizabeth Ann  
APPLICANT: FRAZER, Ian  
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS  
FILE REFERENCE: 017227/0148  
CURRENT APPLICATION NUMBER: US/09/359,382  
CURRENT FILING DATE: 1999-07-23  
EARLIER APPLICATION NUMBER: US 08/860,165  
EARLIER FILING DATE: 1997-09-22  
EARLIER APPLICATION NUMBER: PCT/AU95/00868  
EARLIER FILING DATE: 1995-12-20  
EARLIER APPLICATION NUMBER: AU PN0157/94  
EARLIER FILING DATE: 1994-12-20  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 10  
LENGTH: 266  
TYPE: PRT  
ORGANISM: Human papillomavirus type 16  
US-09-359-382-10

Query Match 99.2%; Score 823; DB 2; Length 266;

```
Best Local Similarity 98.0%; Pred. No. 3.2e-85;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MFQDQERPRKLPOLCTELQTTIHDIIECYCKQQLRREYDFAFRDLCIVYRDGPNY 60
Db 8 MFQDQERPRKLPOLCTELQTTIHDIIECYCKQQLRREYDFAFRDLCIVYRDGPNY 67
Qy 61 AVXDCKLFYSKISEYRHVCYSVGTTLBOQYNKPLCDLLIRICINXQKPLCPBEKQRHLD 120
Db 68 AVCDKCLFYSKISEYRHVCYSVGTTLBOQYNKPLCDLLIRICINXQKPLCPBEKQRHLD 127
Qy 121 KKQRFHNIRGRWTGRCMSCCRSSRTRETOL 151
Db 128 KKQRFHNIRGRWTGRCMSCCRSSRTRETOL 158

RESULT 7
US-09-367-309A-1
; Sequence 1, Application US/09367309A
; Patent No. 6428807
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODERICK I.
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367,309A
; PRIOR FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
; TYPE: PRN
; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1

Query Match 99.2%; Score 823; DB 2; Length 266;
Best Local Similarity 98.0%; Pred. No. 3.2e-85;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MFQDQERPRKLPOLCTELQTTIHDIIECYCKQQLRREYDFAFRDLCIVYRDGPNY 60
Db 8 MFQDQERPRKLPOLCTELQTTIHDIIECYCKQQLRREYDFAFRDLCIVYRDGPNY 67
Qy 61 AVXDCKLFYSKISEYRHVCYSVGTTLBOQYNKPLCDLLIRICINXQKPLCPBEKQRHLD 120
Db 68 AVCDKCLFYSKISEYRHVCYSVGTTLBOQYNKPLCDLLIRICINXQKPLCPBEKQRHLD 127
Qy 121 KKQRFHNIRGRWTGRCMSCCRSSRTRETOL 151
Db 128 KKQRFHNIRGRWTGRCMSCCRSSRTRETOL 158

RESULT 8
US-09-485-885-4
; Sequence 4, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 971953.5
```

```
;; PRIOR FILING DATE: 1997-08-22
;; NUMBER OF SEQ ID NOS: 23
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 4
;; LENGTH: 273
;; TYPE: PRN
;; ORGANISM: Homo sapien
US-09-485-885-4

Query Match 99.2%; Score 823; DB 2; Length 273;
Best Local Similarity 98.0%; Pred. No. 3.3e-85;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MFQDQERPRKLPOLCTELQTTIHDIIECYCKQQLRREYDFAFRDLCIVYRDGPNY 60
Db 114 MFQDQERPRKLPOLCTELQTTIHDIIECYCKQQLRREYDFAFRDLCIVYRDGPNY 173
Qy 61 AVXDCKLFYSKISEYRHVCYSVGTTLBOQYNKPLCDLLIRICINXQKPLCPBEKQRHLD 120
Db 174 AVCDKCLFYSKISEYRHVCYSVGTTLBOQYNKPLCDLLIRICINXQKPLCPBEKQRHLD 233
Qy 121 KKQRFHNIRGRWTGRCMSCCRSSRTRETOL 151
Db 234 KKQRFHNIRGRWTGRCMSCCRSSRTRETOL 264

RESULT 9
US-09-485-885-10
; Sequence 10, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 971953.5
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 292
; TYPE: PRN
; ORGANISM: Homo sapien
US-09-485-885-10

Query Match 99.2%; Score 823; DB 2; Length 292;
Best Local Similarity 98.0%; Pred. No. 3.6e-85;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MFQDQERPRKLPOLCTELQTTIHDIIECYCKQQLRREYDFAFRDLCIVYRDGPNY 60
Db 133 MFQDQERPRKLPOLCTELQTTIHDIIECYCKQQLRREYDFAFRDLCIVYRDGPNY 192
Qy 61 AVXDCKLFYSKISEYRHVCYSVGTTLBOQYNKPLCDLLIRICINXQKPLCPBEKQRHLD 120
Db 193 AVCDKCLFYSKISEYRHVCYSVGTTLBOQYNKPLCDLLIRICINXQKPLCPBEKQRHLD 252
Qy 121 KKQRFHNIRGRWTGRCMSCCRSSRTRETOL 151
Db 253 KKQRFHNIRGRWTGRCMSCCRSSRTRETOL 283

RESULT 10
US-09-485-885-6
; Sequence 6, Application US/09485885
; Patent No. 6342224
```

GENERAL INFORMATION:  
APPLICANT: Bruck, Claudine  
APPLICANT: Gabizon Silva, Teresa  
APPLICANT: Delisse, Anne-Marie Eva Fernande  
APPLICANT: Gerard, Catherine Marie Ghislaine  
APPLICANT: Lombardo-Bencheikh, Angela  
FILE REFERENCE: B45107  
CURRENT APPLICATION NUMBER: US/09/485,885  
CURRENT FILING DATE: 2000-02-18  
PRIOR APPLICATION NUMBER: PCT/EP98/05285  
PRIOR FILING DATE: 1998-08-17  
PRIOR APPLICATION NUMBER: GB 9717953.5  
PRIOR FILING DATE: 1997-08-22  
NUMBER OF SEQ ID NOS: 23  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 6  
LENGTH: 371  
TYPE: PRT  
ORGANISM: Homo sapien  
US-09-485-885-6

Query Match 99.2%; Score 823; DB 2; Length 371;  
Best Local Similarity 98.0%; Pred. No. 4,8e-85;  
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFODPQERPRKLPOLCTELQTTIHDIIECYCKQQLLRREYDPAFRDLCTVYRDGPNY 60  
DB 114 MFODPQERPRKLPOLCTELQTTIHDIIECYCKQQLLRREYDPAFRDLCTVYRDGPNY 173  
QY 61 AVXDKCLKFYSKISSEYHYCYSVYGTTLLEQYNNKPLCDLLIRCNXOKPLCPBEKQRHLD 120  
DB 174 AVCDKCLKFYSKISSEYHYCYSLVGTTLLEQYNNKPLCDLLIRCNXOKPLCPBEKQRHLD 233  
QY 121 KKORFHNIRGRWTRCWSGCCSSRTRRETOL 151  
DB 234 KKORFHNIRGRWTRCWSGCCSSRTRRETOL 264

RESULT 11  
US-09-485-885-14  
Sequence 14, Application US/09485885  
Patent No. 6342224  
GENERAL INFORMATION:  
APPLICANT: Bruck, Claudine  
APPLICANT: Gabizon Silva, Teresa  
APPLICANT: Delisse, Anne-Marie Eva Fernande  
APPLICANT: Gerard, Catherine Marie Ghislaine  
APPLICANT: Lombardo-Bencheikh, Angela  
FILE REFERENCE: B45107  
CURRENT APPLICATION NUMBER: US/09/485,885  
CURRENT FILING DATE: 2000-02-18  
PRIOR APPLICATION NUMBER: PCT/EP98/05285  
PRIOR FILING DATE: 1998-08-17  
PRIOR APPLICATION NUMBER: GB 9717953.5  
PRIOR FILING DATE: 1997-08-22  
NUMBER OF SEQ ID NOS: 23  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 14  
LENGTH: 390  
TYPE: PRT  
ORGANISM: Homo sapien  
US-09-485-885-14

Query Match 99.2%; Score 823; DB 2; Length 390;  
Best Local Similarity 98.0%; Pred. No. 5,1e-85;  
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFODPQERPRKLPOLCTELQTTIHDIIECYCKQQLLRREYDPAFRDLCTVYRDGPNY 60  
DB 133 MFODPQERPRKLPOLCTELQTTIHDIIECYCKQQLLRREYDPAFRDLCTVYRDGPNY 192

QY 61 AVXDKCLKFYSKISSEYHYCYSVYGTTLLEQYNNKPLCDLLIRCNXOKPLCPBEKQRHLD 120  
DB 193 AVCDKCLKFYSKISSEYHYCYSLVGTTLLEQYNNKPLCDLLIRCNXOKPLCPBEKQRHLD 252  
QY 121 KKORFHNIRGRWTRCWSGCCSSRTRRETOL 151  
DB 253 KKORFHNIRGRWTRCWSGCCSSRTRRETOL 283

RESULT 12  
US-09-701-080C-18  
Sequence 18, Application US/09701080C  
Patent No. 6864054  
GENERAL INFORMATION:  
APPLICANT: INSTITUTE OF MOLECULAR AND CELL BIOLOGY  
FILE REFERENCE: N73477C GCM  
CURRENT APPLICATION NUMBER: US/09/701,080C  
CURRENT FILING DATE: 2001-02-27  
PRIOR APPLICATION NUMBER: GB 9811303.8  
PRIOR FILING DATE: 1998-05-26  
PRIOR APPLICATION NUMBER: GB 9900157.0  
PRIOR FILING DATE: 1999-01-05  
NUMBER OF SEQ ID NOS: 36  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 18  
LENGTH: 151  
TYPE: PRT  
ORGANISM: Human papillomavirus  
US-09-701-080C-18

Query Match 98.6%; Score 818; DB 2; Length 151;  
Best Local Similarity 97.4%; Pred. No. 6,1e-85;  
Matches 147; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MFODPQERPRKLPOLCTELQTTIHDIIECYCKQQLLRREYDPAFRDLCTVYRDGPNY 60  
DB 1 MFODPQERPRKLPOLCTELQTTIHDIIECYCKQQLLRREYDPAFRDLCTVYRDGPNY 60  
QY 61 AVXDKCLKFYSKISSEYHYCYSVYGTTLLEQYNNKPLCDLLIRCNXOKPLCPBEKQRHLD 120  
DB 61 AVCDKCLKFYSKISSEYHYCYSLVGTTLLEQYNNKPLCDLLIRCNXOKPLCPBEKQRHLD 120  
QY 121 KKORFHNIRGRWTRCWSGCCSSRTRRETOL 151  
DB 121 KKORFHNIRGRWTRCWSGCCSSRTRRETOL 151

RESULT 13  
US-09-462-993-1  
Sequence 1, Application US/09462993  
Patent No. 6884786  
GENERAL INFORMATION:  
APPLICANT: KIENEY, Marie-Paule  
APPLICANT: BILLOUT, Jean-Marc  
APPLICANT: BIZOUARNE, Nadine  
FILE REFERENCE: 017753-122  
CURRENT APPLICATION NUMBER: US/09/462,993  
CURRENT FILING DATE: 2000-04-17  
PRIOR APPLICATION NUMBER: PCT/FR98/01576  
PRIOR FILING DATE: 1998-07-17  
PRIOR APPLICATION NUMBER: FR 97/09152  
PRIOR FILING DATE: 1997-07-18  
NUMBER OF SEQ ID NOS: 23  
SOFTWARE: PatentIn Ver. 2.2  
SEQ ID NO 1  
LENGTH: 243  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Derived from  
OTHER INFORMATION: human papillomavirus, strain HPV-16, E6 protein  
OTHER INFORMATION: fused F protein signals, clone E6\*TMF.  
US-09-462-993-1

Query Match 93.9%; Score 779.5; DB 2; Length 243;  
Best Local Similarity 94.7%; Pred. No. 2.5e-80;  
Matches 143; Conservative 1; Mismatches 2; Indels 5; Gaps 1;

QY 1 MFODPOEPRRLPOLCTELQTTIHIIIECVYCKQQLLRREYDFAFRDLCTIVRDGPNY 60  
DB 36 MFODPOEPRRLPOLCTELQTTIHIIIECVYCKQQLLRREYDFAFRDLCTIVRDGPNY 95  
QY 61 AVXDCKLKFYSKISEYRHVCYSVYGTTLLEQYNNKPLCDLLIRCIHXKPLCPBEKQRLD 120  
DB 96 AVCDKCLKFYSKISEYRHVCYSVYGTTLLEQYNNKPLCDLLIRCIHXKPLCPBEKQRLD 150  
QY 121 KQRFHNRGRWTCGCMSCCRSSRTTRRETOL 151  
DB 151 KQRFHNRGRWTCGCMSCCRSSRTTRRETOL 181

RESULT 14  
US-08-860-165-12  
Sequence 12, Application US/08860165A  
Patent No. 6004557

GENERAL INFORMATION:  
APPLICANT: EDWARDS, Scirling John  
APPLICANT: COX, John Cooper  
APPLICANT: WEBB, Elizabeth Ann  
APPLICANT: FRAZER, Ian  
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS  
FILE REFERENCE: 17227/130  
CURRENT APPLICATION NUMBER: US/08/860,165A  
EARLIER FILING DATE: 1997-09-22  
EARLIER APPLICATION NUMBER: PCT/AU95/00868  
EARLIER FILING DATE: 1995-12-20  
EARLIER APPLICATION NUMBER: AU PN0157  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 12  
LENGTH: 172  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion  
US-08-860-165-12

Query Match 62.5%; Score 519; DB 2; Length 172;  
Best Local Similarity 96.8%; Pred. No. 5.7e-51;  
Matches 92; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 57 GNPYAVXDCKLKFYSKISEYRHVCYSVYGTTLLEQYNNKPLCDLLIRCIHXKPLCPBEKQ 116  
DB 2 GNPYAVXDCKLKFYSKISEYRHVCYSVYGTTLLEQYNNKPLCDLLIRCIHXKPLCPBEKQ 61  
QY 117 RHLDDKKQRFHNRGRWTCGCMSCCRSSRTTRRETOL 151  
DB 62 RHLDDKKQRFHNRGRWTCGCMSCCRSSRTTRRETOL 96

RESULT 15  
US-09-359-382-12  
Sequence 12, Application US/09359382  
Patent No. 6306397

GENERAL INFORMATION:  
APPLICANT: EDWARDS, Scirling John  
APPLICANT: COX, John Cooper  
APPLICANT: WEBB, Elizabeth Ann  
APPLICANT: FRAZER, Ian  
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS  
FILE REFERENCE: 017227/0148

CURRENT APPLICATION NUMBER: US/09/359,382  
CURRENT FILING DATE: 1999-07-23  
EARLIER APPLICATION NUMBER: US 08/860,165  
EARLIER FILING DATE: 1997-09-22  
EARLIER APPLICATION NUMBER: PCT/AU95/00868  
EARLIER FILING DATE: 1995-12-20  
EARLIER APPLICATION NUMBER: AU PN0157/94  
EARLIER FILING DATE: 1994-12-20  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 12  
LENGTH: 172  
TYPE: PRT  
ORGANISM: Human papillomavirus type 16  
US-09-359-382-12

Query Match 62.5%; Score 519; DB 2; Length 172;  
Best Local Similarity 96.8%; Pred. No. 5.7e-51;  
Matches 92; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 57 GNPYAVXDCKLKFYSKISEYRHVCYSVYGTTLLEQYNNKPLCDLLIRCIHXKPLCPBEKQ 116  
DB 2 GNPYAVXDCKLKFYSKISEYRHVCYSVYGTTLLEQYNNKPLCDLLIRCIHXKPLCPBEKQ 61  
QY 117 RHLDDKKQRFHNRGRWTCGCMSCCRSSRTTRRETOL 151  
DB 62 RHLDDKKQRFHNRGRWTCGCMSCCRSSRTTRRETOL 96

RESULT 16  
US-08-860-165-14  
Sequence 14, Application US/08860165A  
Patent No. 6004557

GENERAL INFORMATION:  
APPLICANT: EDWARDS, Scirling John  
APPLICANT: COX, John Cooper  
APPLICANT: WEBB, Elizabeth Ann  
APPLICANT: FRAZER, Ian  
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS  
FILE REFERENCE: 17227/130  
CURRENT APPLICATION NUMBER: US/08/860,165A  
EARLIER FILING DATE: 1997-09-22  
EARLIER APPLICATION NUMBER: PCT/AU95/00868  
EARLIER FILING DATE: 1995-12-20  
EARLIER APPLICATION NUMBER: AU PN0157  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 14  
LENGTH: 172  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion  
US-08-860-165-14

Query Match 57.6%; Score 478; DB 2; Length 172;  
Best Local Similarity 92.5%; Pred. No. 2.6e-46;  
Matches 86; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MFODPOEPRRLPOLCTELQTTIHIIIECVYCKQQLLRREYDFAFRDLCTIVRDGPNY 60  
DB 77 MFODPOEPRRLPOLCTELQTTIHIIIECVYCKQQLLRREYDFAFRDLCTIVRDGPNY 136  
QY 61 AVXDCKLKFYSKISEYRHVCYSVYGTTLLEQYNN 93  
DB 137 AVCDKCLKFYSKISEYRHVCYSVYGTTLRSHH 169

RESULT 17  
US-09-359-382-14  
Sequence 14, Application US/09359382  
Patent No. 6306397

GENERAL INFORMATION:  
APPLICANT: EDWARDS, Stirling John  
APPLICANT: COX, John Cooper  
APPLICANT: WEBB, Elizabeth Ann  
APPLICANT: FRAZER, Ian  
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS  
FILE REFERENCE: 017227/0148  
CURRENT APPLICATION NUMBER: US/09/359,382  
CURRENT FILING DATE: 1999-07-23  
EARLIER APPLICATION NUMBER: US 08/860,165  
EARLIER FILING DATE: 1997-09-22  
EARLIER APPLICATION NUMBER: PCT/AU95/00868  
EARLIER FILING DATE: 1995-12-20  
EARLIER APPLICATION NUMBER: AU PNO157/94  
EARLIER FILING DATE: 1994-12-20  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 14  
LENGTH: 172  
TYPE: PRT  
ORGANISM: Human papillomavirus type 16  
US-09-359-382-14

Query Match 57.6%; Score 478; DB 2; Length 172;  
Best Local Similarity 92.5%; Pred. No. 2,6e-46;  
Matches 86; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MFODPQRPRLPOLCTELQTTTHDIIIECYCKQQLRREVDFAFRDLCIVYRDGPNY 60  
DB 77 MFODPQRPRLPOLCTELQTTTHDIIIECYCKQQLRREVDFAFRDLCIVYRDGPNY 136

QY 61 AYXDKLKFYSKISEYRHYCYSGVGTLEEQYN 93  
DB 137 AVCDKLFYSKISEYRHYCYSLYGTILRSHH 169

RESULT 18  
US-08-117-083-10  
Sequence 10 Application US/08117083  
Patent No. 5719054  
GENERAL INFORMATION:  
APPLICANT: Boursnell, Michael E.  
APPLICANT: Inglis, Stephen C.  
APPLICANT: Munro, Alan J.  
TITLE OF INVENTION: Recombinant Virus Vectors Encoding Human  
NUMBER OF SEQUENCES: 70  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Walter H. Dreger  
STREET: 4 Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/117,083  
FILING DATE: 10-SEP-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Dreger, Walter H.  
REGISTRATION NUMBER: 24,190  
REFERENCE/DOCKET NUMBER: A-58783  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-781-1989  
TELEFAX: 415-398-3249  
TELEX: 910 277299  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:

LENGTH: 182 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..182  
OTHER INFORMATION: /note= "Xaa refers to stop codon in  
OTHER INFORMATION: the open reading frame."  
US-08-117-083-10

Query Match 57.5%; Score 477; DB 1; Length 182;  
Best Local Similarity 62.2%; Pred. No. 3,6e-46;  
Matches 97; Conservative 5; Mismatches 8; Indels 46; Gaps 4;

QY 1 MFODPQRPRLPOLCTELQTTTHDIIIECYCKQQLRREVDFAFRDLCIVYRDGPNY 60  
DB 9 MFODPQRPRLPOLCTELQTTTHDIIIECYCKQQLRREVDFAFRDLCI----- 60

QY 61 AYXDKLKFYSKISEYRHYCYSGVGTLEEQYNKPLCDLLIRCLNKKPLCPSEKORHLD 120  
DB 61 -----ISEYRHYCYSLYGTLEEQY-----BEKORHLD 88

QY 121 KKQRFNIRGRWG-----RCMSCRSSRTRRETOL 151  
DB 89 KKQRFNIRGRWSCMETHLHGMNICTIC-NOROVOL 123

RESULT 19  
US-08-247-904B-10  
Sequence 10 Application US/08247904B  
Patent No. 5981899  
GENERAL INFORMATION:  
APPLICANT: Rolfe, Mark  
APPLICANT: Eckstein, Jens W.  
APPLICANT: Diacteta, Giulio  
TITLE OF INVENTION: Human Ubiquitin Conjugating Enzyme  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley, Hoag & Eliot  
STREET: One Post Office Square  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII(text)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/247,904B  
FILING DATE: 23-MAY-1994  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Vincent, Matthew P.  
REGISTRATION NUMBER: 36,709  
REFERENCE/DOCKET NUMBER: MIV-029.01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 832-1000  
TELEFAX: (617) 832-7000  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 158 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-247-904B-10

Query Match 54.9%; Score 455.5; DB 1; Length 158;  
Best Local Similarity 56.1%; Pred. No. 8,2e-44;  
Matches 87; Conservative 21; Mismatches 42; Indels 5; Gaps 1;



APPLICANT: Cabezon Silva, Teresa  
APPLICANT: Delisse, Anne-Marie Eva Fernande  
APPLICANT: Gerard, Catherine Marie Ghislaine  
APPLICANT: Lombardo-Bencheikh, Angela  
FILE OF INVENTION: Vaccine  
FILE REFERENCE: B45107  
CURRENT APPLICATION NUMBER: US/09/485,885  
CURRENT FILING DATE: 2000-02-18  
PRIOR APPLICATION NUMBER: PCT/EP98/05285  
PRIOR FILING DATE: 1998-08-17  
PRIOR APPLICATION NUMBER: GB 9717953.5  
PRIOR FILING DATE: 1997-08-22  
NUMBER OF SEQ ID NOS: 23  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 21  
LENGTH: 278  
TYPE: PRT  
ORGANISM: Homo sapien  
US-09-485-885-21

Query Match 54.9%; Score 455.5; DB 2; Length 278;  
Best Local Similarity 56.1%; Pred. No. 1.6e-43;  
Matches 87; Conservative 21; Mismatches 42; Indels 5; Gaps 1;

QY 2 FODPERPRKLPOLCTELQTHIHIIIECVYCKQOQLRREYVDFAFRLDLCIVYRGNGPYA 61  
DB 115 FEDPFRPRYKLPDLCTELNTSLQDIEITCYCVKTVLETFVEFAFKLPVYVRDSIPHA 174  
QY 62 VXDCKLKFYSKISEYRHYCYSVYGTTLTQQYNNKPLCDLLIRICINXOKPLCEPEKORHLDK 121  
DB 175 ACHCIDPYSRIRLRIHSDSVYGTTLTQYNNKPLCDLLIRICINXOKPLCEPEKORHLDK 234  
QY 122 KQRFNIRGRTGRCMSCCRSSR-----TRRETQL 151  
DB 235 KRPFNINAGHYRGQCHSCCNRAQERLQRRRETQV 269

RESULT 23  
US-09-485-885-23  
Sequence 23, Application US/09485885  
Patent No. 6342224  
GENERAL INFORMATION:  
APPLICANT: Bruck, Claudine  
APPLICANT: Cabezon Silva, Teresa  
APPLICANT: Delisse, Anne-Marie Eva Fernande  
APPLICANT: Gerard, Catherine Marie Ghislaine  
APPLICANT: Lombardo-Bencheikh, Angela  
FILE OF INVENTION: Vaccine  
FILE REFERENCE: B45107  
CURRENT APPLICATION NUMBER: US/09/485,885  
CURRENT FILING DATE: 2000-02-18  
PRIOR APPLICATION NUMBER: PCT/EP98/05285  
PRIOR FILING DATE: 1998-08-17  
PRIOR APPLICATION NUMBER: GB 9717953.5  
PRIOR FILING DATE: 1997-08-22  
NUMBER OF SEQ ID NOS: 23  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 23  
LENGTH: 383  
TYPE: PRT  
ORGANISM: Homo sapien  
US-09-485-885-23

Query Match 54.9%; Score 455.5; DB 2; Length 383;  
Best Local Similarity 56.1%; Pred. No. 2.4e-43;  
Matches 87; Conservative 21; Mismatches 42; Indels 5; Gaps 1;  
QY 2 FODPERPRKLPOLCTELQTHIHIIIECVYCKQOQLRREYVDFAFRLDLCIVYRGNGPYA 61  
DB 115 FEDPFRPRYKLPDLCTELNTSLQDIEITCYCVKTVLETFVEFAFKLPVYVRDSIPHA 174  
QY 62 VXDCKLKFYSKISEYRHYCYSVYGTTLTQQYNNKPLCDLLIRICINXOKPLCEPEKORHLDK 121

DB 175 ACHCIDPYSRIRLRIHSDSVYGTTLTQYNNKPLCDLLIRICINXOKPLCEPEKORHLDK 234  
QY 122 KQRFNIRGRTGRCMSCCRSSR-----TRRETQL 151  
DB 235 KRPFNINAGHYRGQCHSCCNRAQERLQRRRETQV 269

RESULT 24  
US-09-000-094-20  
Sequence 20, Application US/0900094  
Patent No. 6365160  
GENERAL INFORMATION:  
APPLICANT: WEBB, Elizabeth Ann  
MARGRETS, Mary Brigid  
COX, John Cooper  
FRAZER, Ian  
MCMILLAN, Nigel Alan John  
WILLIAMS, Mark Philip  
MOLONEY, Margaret Bridget  
HOLLAND, Stirling John  
EDWARDS, Stirling John  
TITLE OF INVENTION: PAPILLOMAVIRUS POLYPEPTIDE CONSTRUCTS  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FOLEY & LARDNER  
STREET: 3000 K Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/000,094  
FILING DATE: 21-Apr-1998  
CLASSIFICATION: <unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/AU96/00473  
FILING DATE: 26-JUL-1996  
APPLICATION NUMBER: AU PN 4439/95  
FILING DATE: 27-JUL-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29, 768  
REFERENCE/DOCKET NUMBER: 017227/0137  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 368 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 20:  
US-09-000-094-20

Query Match 36.6%; Score 304; DB 2; Length 368;  
Best Local Similarity 39.8%; Pred. No. 3.4e-26;  
Matches 51; Conservative 29; Mismatches 48; Indels 0; Gaps 0;  
QY 12 LPOLCTELQTHIHIIIECVYCKQOQLRREYVDFAFRLDLCIVYRGNGPYAVXDCKLKFYS 71  
DB 13 IDQCKTFNLSMHLQINCVCNKALTTAETISYAYHGLKVLFRGVPYACACCLERHG 72  
QY 72 KISEYRHYCYSVYGTTLTQQYNNKPLCDLLIRICINXOKPLCEPEKORHLDKQRFNIRGR 131  
DB 73 KINQYRHFYDYGAVATVEETKODILDLVLRVCYCHKPLCEVEKVKHLLTARFPIKUNCT 132  
QY 132 WTGRMSC 139



## RESULT 27

US-10-011-749-22

; Sequence 22, Application US/10011749  
; Patent No. 6726912

; GENERAL INFORMATION:

; APPLICANT: WEBB, Elizabeth Ann

; MARGETTS, Mary Brigid

; COX, John Cooper

; FRAZER, Ian

; MCMILLAN, Nigel Alan John

; WILLIAMS, Mark Philip

; MOLONEY, Margaret Bridget

; Holland

; EDWARDS, Stirling John

; TITLE OF INVENTION: PAPILLOMAVIRUS POLYPROTEIN CONSTRUCTS

; NUMBER OF SEQUENCES: 50

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: FOLEY &amp; LARDNER

; STREET: 3000 K Street, N.W.

; CITY: Washington

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20007-5109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/011,749

; FILING DATE: 11-Dec-2001

; CLASSIFICATION: &lt;Unknown&gt;

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/000,094

; FILING DATE: 21-Apr-1998

; APPLICATION NUMBER: WO PCT/AU96/00473

; FILING DATE: 26-JUL-1996

; APPLICATION NUMBER: AU PN 4439/95

; FILING DATE: 27-JUL-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: BENT, Stephen A.

; REGISTRATION NUMBER: 29,768

; REFERENCE/DOCKET NUMBER: 017227/0137

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 672-5300

; TELEFAX: (202) 672-5399

; INFORMATION FOR SEQ ID NO: 22:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 375 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 22:

; US-10-011-749-22

; Query Match 36.6%; Score 304; DB 2; Length 375;

; Best Local Similarity 39.8%; Pred. No. 3.5e-26;

; Matches 51; Conservative 29; Mismatches 48; Indels 0; Gaps 0;

QY 12 LPQLCTEQTTHIHILIECYVCKQOQLRREYVDFAFRLDCTIVRDGNFYAVYADKCLTKFYS 71

DB 13 IDQLCKTFNLSMHLQINCVCCKNALTTAAETYSYAVYKLVLFKGGYVYAAACACCLFPHG 72

QY 72 KISEYRHVYCVSVGTTLEEQYNNKPLCDLLIRICINXQKPLCPBEKQRLDKQRFNINRGR 131

DB 73 KINQYRHFDVAGVATVVEETKQDILDVILNCYLCRPLCEVEKVKHILTKARFIKLNCT 132

QY 132 WTGRCMSC 139

DB 133 WKGRCLHC 140

QY 133 WKGRCLHC 140

DB 133 WKGRCLHC 140

QY 133 WKGRCLHC 140

DB 133 WKGRCLHC 140

QY 133 WKGRCLHC 140

DB 133 WKGRCLHC 140

QY 133 WKGRCLHC 140

DB 133 WKGRCLHC 140

QY 133 WKGRCLHC 140

DB 133 WKGRCLHC 140

QY 133 WKGRCLHC 140

## US-09-000-094-24

; Sequence 24, Application US/09000094

; Patent No. 6365160

; GENERAL INFORMATION:

; APPLICANT: WEBB, Elizabeth Ann

; MARGETTS, Mary Brigid

; COX, John Cooper

; FRAZER, Ian

; MCMILLAN, Nigel Alan John

; WILLIAMS, Mark Philip

; MOLONEY, Margaret Bridget

; Holland

; EDWARDS, Stirling John

; TITLE OF INVENTION: PAPILLOMAVIRUS POLYPROTEIN CONSTRUCTS

; NUMBER OF SEQUENCES: 50

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: FOLEY &amp; LARDNER

; STREET: 3000 K Street, N.W.

; CITY: Washington

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20007-5109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/000,094

; FILING DATE: 21-Apr-1998

; CLASSIFICATION: &lt;Unknown&gt;

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/AU96/00473

; FILING DATE: 26-JUL-1996

; APPLICATION NUMBER: AU PN 4439/95

; FILING DATE: 27-JUL-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: BENT, Stephen A.

; REGISTRATION NUMBER: 29,768

; REFERENCE/DOCKET NUMBER: 017227/0137

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 672-5300

; TELEFAX: (202) 672-5399

; INFORMATION FOR SEQ ID NO: 24:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 465 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 24:

; US-09-000-094-24

; Query Match 36.6%; Score 304; DB 2; Length 465;

; Best Local Similarity 39.8%; Pred. No. 4.5e-26;

; Matches 51; Conservative 29; Mismatches 48; Indels 0; Gaps 0;

QY 12 LPQLCTEQTTHIHILIECYVCKQOQLRREYVDFAFRLDCTIVRDGNFYAVYADKCLTKFYS 71

DB 13 IDQLCKTFNLSMHLQINCVCCKNALTTAAETYSYAVYKLVLFKGGYVYAAACACCLFPHG 72

QY 72 KISEYRHVYCVSVGTTLEEQYNNKPLCDLLIRICINXQKPLCPBEKQRLDKQRFNINRGR 131

DB 73 KINQYRHFDVAGVATVVEETKQDILDVILNCYLCRPLCEVEKVKHILTKARFIKLNCT 132

QY 132 WTGRCMSC 139

DB 133 WKGRCLHC 140

QY 133 WKGRCLHC 140

DB 133 WKGRCLHC 140

QY 133 WKGRCLHC 140

DB 133 WKGRCLHC 140

QY 133 WKGRCLHC 140

DB 133 WKGRCLHC 140

QY 133 WKGRCLHC 140

DB 133 WKGRCLHC 140

QY 133 WKGRCLHC 140

DB 133 WKGRCLHC 140

QY 133 WKGRCLHC 140

DB 133 WKGRCLHC 140

QY 133 WKGRCLHC 140

DB 133 WKGRCLHC 140

## RESULT 28

## RESULT 29

US-10-011-749-24

; Sequence 24, Application US/10011749

; Patent No. 6726912



```

FRAZER, Ian
MCILLAN, Nigel Alan John
WILLIAMS, Mark Philip
MOLONEY, Margaret Bridget
Holland
EDWARDS, Stirling John
TITLE OF INVENTION: PAPILLOMAVIRUS POLYPROTEIN CONSTRUCTS
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/011,749
FILING DATE: 11-Dec-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/000,094
FILING DATE: 21-Apr-1998
APPLICATION NUMBER: WO PCT/AU96/00473
FILING DATE: 26-JUL-1996
APPLICATION NUMBER: AU PN 4439/95
FILING DATE: 27-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 017227/0137
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 1587 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 46:
US-10-011-749-46

Query Match          36.6%; Score 304; DB 2; Length 1587;
Best Local Similarity 39.8%; Pred. No. 2e-25; Indels 0; Gaps 0;
Matches 51; Conservative 29; Mismatches 48;

QY 12 LPOLCTELQTTIHDIIECYCKQQLLRREYVDFAFRDLCTIVYRDGNFYAVYDKCLKPEYS 71
   :|||:  :|||:  :|||:  :|||:  :|||:  :|||:  :|||:  :|||:  :|||:  :|||:
Db 699 IDQCTENLMSHTLQINCVCCKNALTTAETSYAYKHLKVLFRGGYVYAACACCLBPHG 758
   :|||:  :|||:  :|||:  :|||:  :|||:  :|||:  :|||:  :|||:  :|||:  :|||:
QY 72 KISERAHCYGVYGTTLTQQNKPKLDLLIRCLNKKQLCEPEKRRHLDKORFNINIGR 131
   :|||:  :|||:  :|||:  :|||:  :|||:  :|||:  :|||:  :|||:  :|||:  :|||:
Db 759 KINQVRHDDYAGYATVTEETKQDILDLIRCYLCKPLCEVEKYKHILITARFKLNCT 818
   :|||:  :|||:  :|||:  :|||:  :|||:  :|||:  :|||:  :|||:  :|||:  :|||:
QY 132 WTRGCMSC 139
   :|||:  :|||:  :|||:  :|||:  :|||:  :|||:  :|||:  :|||:  :|||:  :|||:
Db 819 WKGRCLHC 826
   :|||:  :|||:  :|||:  :|||:  :|||:  :|||:  :|||:  :|||:  :|||:  :|||:

RESULT 32
US-08-363-586-4
Sequence 4, Application US/08363586
Patent No. 5629161
GENERAL INFORMATION:
APPLICANT: Mueller, Martin
APPLICANT: Gissmann, Lutz
TITLE OF INVENTION: Use of HPV-16 E6 and E7-Gene Derived
TITLE OF INVENTION: Peptides for the Diagnostic Purpose

```

```

NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
Dunneer
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/363,586
FILING DATE: 23-DEC-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/909,296
FILING DATE: 09-JUL-1992
APPLICATION NUMBER: EP 9111720.8
FILING DATE: 13-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Madler, Linda A.
REGISTRATION NUMBER: 33,218
REFERENCE/DOCKET NUMBER: 02481-1195-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4400
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-363-586-4

Query Match          19.6%; Score 163; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.7e-11;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFODQERRRKLPOLCTELQTTIHDIIEC 30
   :|||:  :|||:  :|||:  :|||:  :|||:  :|||:  :|||:  :|||:  :|||:  :|||:
Db 1 MFODQERRRKLPOLCTELQTTIHDIIEC 30
   :|||:  :|||:  :|||:  :|||:  :|||:  :|||:  :|||:  :|||:  :|||:  :|||:

RESULT 33
US-09-980-523A-4
Sequence 4, Application US/09980523A
Patent No. 6783763
GENERAL INFORMATION:
APPLICANT: CHOPPIN, JEANNINE
APPLICANT: BOURGAULT VILLADA, ISABELLE
APPLICANT: GUILLET, JEAN-GERARD
APPLICANT: CONNAN, FRANCINE
APPLICANT: FERRIES, ESTELLE
TITLE OF INVENTION: POLYPEPTIDIC PROTEIN FRAGMENTS OF THE E6 AND E7
TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
TITLE OF INVENTION: PARTICULARLY IN VACCINATION
FILE REFERENCE: WOBI AO INS
CURRENT APPLICATION NUMBER: US/09/980,523A
CURRENT FILING DATE: 2002-04-29
PRIOR APPLICATION NUMBER: PCT/FR00/01513
PRIOR FILING DATE: 2000-05-31
PRIOR APPLICATION NUMBER: FR 99/07012
PRIOR FILING DATE: 1999-06-03
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 30
TYPE: PRT
ORGANISM: Human Papillomavirus

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US-09-980-523A-4

Query Match	19.6%	Score 163	DB 2	Length 30
Best Local Similarity	100.0%	Pred. No. 1.7e-11		
Best Match	30	Conservative	0	Indels 0
				Gaps 0

Oy 8 RPKLPLQCTELQTTHIDILIECVYCKKQL 37  
| | | | |  
Db 1 RPKLPQLCVELQTTIHIDILECVYCKKQL 30

RESULT 34  
US-09-980-523A-8

```

QY      73 ISEYRHYCYSVYGTTLLEQQYNKPKCDLLI 101
        |||||:|||||
Db      1 ISEYRHYCYSLYGTTLEQQYNKPKCDLLI 29

```

RESULT 35  
US-09-913-204-17

Query Match	16.2%	Score 134.5;	DB 2;	Length 137;
Best Local Similarity	32.5%;	Pred. No. 1.8e-07;		
Matches 38;	Conservative 15;	Mismatches 59;	Indels 5;	Gaps 3;

**Oy** 28 LECVCKQQLRLREVVDFAPRDLCIYVRDGNPYAVXDKCLKFYKISEYHYHCYSYVGTT 87  
| | | : : : : | : | : : : |  
**Db** 15 IACWICREPFLTEVDARFCMIKDPIHVYVRDGVKGCACTTLE--NCLDKERLIMKGPVPVTG 72

QY 88 LEQ--YKPECDLLIRCIHQKPLCEBEKORHLDKQRFHINIGR-WTGRCSGCC 141  
| : | | | | : | | | |  
Db 73 EEAQLLHGKSLDRLCIRCCYGGGKLTAKKQKQHVLYNEPFCRTSRNITGRCYDCC 129

RESULT 36  
US-09-980-523A-10

Query Match	15.7%	Score 130;	DB 2;	Length 22;
Best Local Similarity	100.0%;	Pred. No. 6.4e-08;		
Matches 22;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	111	CPEEKQRHLDDKQRFHNIRGRW	132
Db	1	CPEEKQRHLDDKQRFHNIRGRW	22

```

: RESULT 37
: US-09-601-729-276
: Sequence 276, Application US/09601729
: Patent No. 6683052
: GENERAL INFORMATION:
: APPLICANT: THIAM, KADER
: APPLICANT: AURIAULT, CLAUDE
: APPLICANT: GRAS-MASSE, HELENE
: APPLICANT: LOING, ESTELLE
: APPLICANT: VERWAERDE, CLAUDIE
: APPLICANT: GUILLET, JEAN GERARD
: TITLE OF INVENTION: LIPOPEPTIDES CONTAINING AN INTERFERON FRAGMENT AND USES
: TITLE OF INVENTION: THEREOF IN PHARMACEUTICAL COMPOSITIONS
: FILE REFERENCE: USB-97-AU-IN
: CURRENT APPLICATION NUMBER: US/09/601,729
: CURRENT FILING DATE: 2000-11-20
: PRIOR APPLICATION NUMBER: PCT/FR99/00259
: PRIOR FILING DATE: 1999-02-05
: PRIOR APPLICATION NUMBER: 98 01439
: PRIOR FILING DATE: 1998-02-06
: NUMBER OF SEQ ID NOS: 281
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 276

```

LENGTH: 23  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-601-729-276

Query Match 15.4%; Score 128; DB 2; Length 23;  
Best Local Similarity 100.0%; Pred. No. 1.1e-07;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 38 LRREYDFAFRDLCIVYRDGNPY 60  
Db 1 LRREYDFAFRDLCIVYRDGNPY 23

RESULT 38  
US-09-980-523A-6  
Sequence 6, Application US/09980523A  
Patent No. 6783763

GENERAL INFORMATION:  
APPLICANT: CHOPPIN, JEANNINE  
APPLICANT: BOURGAULT VILLADA, ISABELLE  
APPLICANT: GUILLET, JEAN-GERARD  
APPLICANT: CONNAN, FRANCINE  
APPLICANT: FERRIES, ESTELLE  
TITLE OF INVENTION: POLYPEPTIDIC PROTEIN FRAGMENTS OF THE E6 AND E7  
TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE  
TITLE OF INVENTION: PARTICULARLY IN VACCINATION  
FILE REFERENCE: WO/01/00105  
CURRENT APPLICATION NUMBER: US/09/980,523A  
CURRENT FILING DATE: 2002-04-29  
PRIOR APPLICATION NUMBER: PCT/FR00/01513  
PRIOR FILING DATE: 2000-05-31  
PRIOR APPLICATION NUMBER: FR 99/07012  
PRIOR FILING DATE: 1999-06-03  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 6  
LENGTH: 22  
TYPE: PRT  
ORGANISM: Human Papillomavirus  
US-09-980-523A-6

Query Match 14.9%; Score 124; DB 2; Length 22;  
Best Local Similarity 100.0%; Pred. No. 3.1e-07;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 39 RREYDFAFRDLCIVYRDGNPY 60  
Db 1 RREYDFAFRDLCIVYRDGNPY 22

RESULT 39  
US-08-934-915-167  
Sequence 167, Application US/08934915  
Patent No. 5932412

GENERAL INFORMATION:  
APPLICANT: DILLNER, JOAKIM  
APPLICANT: CHENG, HWEI-MING  
TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN  
TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,  
TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,  
TITLE OF INVENTION: USEFUL IN IMMUNOSSAY FOR  
TITLE OF INVENTION: DIAGNOSTIC PURPOSES  
NUMBER OF SEQUENCES: 193  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MASON & ASSOCIATES, P.A.  
STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500  
CITY: CLEARWATER  
STATE: FLORIDA

COUNTRY: U.S.A.  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Windows 3.0  
SOFTWARE: Microsoft Word 6.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/934,915  
FILING DATE: 22-SEP-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/949,836  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: LOUISE A. FOUTCH  
REGISTRATION NUMBER: 37,133  
REFERENCE/DOCKET NUMBER: 1946.6  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 813-538-3800  
TELEFAX: 813-538-3820  
TELEX:  
INFORMATION FOR SEQ ID NO: 167:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-934-915-167

Query Match 14.5%; Score 120; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 8.2e-07;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 131 RWTGRMSCCRSRRTRETOL 151  
Db 1 RWTGRMSCCRSRRTRETOL 21

RESULT 40  
US-09-913-204-3  
Sequence 3, Application US/09913204  
Patent No. 6953579  
GENERAL INFORMATION:  
APPLICANT: GISSMAN, Lutz  
APPLICANT: MULLER, Martin  
APPLICANT: MULLER, Herman  
TITLE OF INVENTION: CHIMERIC VIRUS-LIKE PARTICLES OR  
TITLE OF INVENTION: CHIMERIC CAPSOMERS FROM BPV  
FILE REFERENCE: 035280134PCUS00  
CURRENT APPLICATION NUMBER: US/09/913,204  
CURRENT FILING DATE: 2001-08-10  
PRIOR APPLICATION NUMBER: PCT/DE00/00426  
PRIOR FILING DATE: 2000-02-10  
PRIOR APPLICATION NUMBER: DE 199 05 883.0  
PRIOR FILING DATE: 1999-02-11  
NUMBER OF SEQ ID NOS: 25  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 3  
LENGTH: 137  
TYPE: PRT  
ORGANISM: Bovine papilloma virus  
US-09-913-204-3

Query Match 14.3%; Score 119; DB 2; Length 137;  
Best Local Similarity 28.9%; Pred. No. 1e-05;  
Matches 35; Conservative 16; Mismatches 60; Indels 2; Gaps 2;

Qy 28 LECYCKQQLRREYDFAFRDLCIVYRDGNPYAVXDKCLFYKISYRYHYCVYGT 87  
Db 15 LDCIMCRPLREYDFAFRDLCIVYRDGNPYAVXDKCLFYKISYRYHYCVYGT 74  
Qy 86 LEOYKPKLCLLIRCLINXQKPLCEEKQRHLDDKQRFHNIRGR-WTGRMSCCR-SSRT 145

Db 75 AELLHGKTLDRICRCYCGKLTNKKRHVLFNEPFCKTRANIRGRCTDCCHGSR 134

QY 146 R 146

Db 135 K 135

RESULT 41

US-09-913-204-7

; Sequence 7, Application US/09913204

; Patent No. 6953579

; GENERAL INFORMATION:

; APPLICANT: GISSMAN, Lutz

; APPLICANT: MULLER, Herman

; TITLE OF INVENTION: CHIMERIC VIRUS-LIKE PARTICLES OR

; FILE REFERENCE: 035280134PCUS00

; CURRENT APPLICATION NUMBER: US/09/913,204

; PRIOR FILING DATE: 2001-08-10

; PRIOR APPLICATION NUMBER: PCT/DE00/00426

; PRIOR FILING DATE: 2000-02-10

; PRIOR APPLICATION NUMBER: DE 199 05 883.0

; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 7

; LENGTH: 137

; TYPE: PRT

; ORGANISM: Bovine papilloma virus

US-09-913-204-7

Query Match

Best Local Similarity 14.3%; Score 119; DB 2; Length 137;

Matches 35; Conservative 16; Mismatches 68; Indels 2; Gaps 2;

QY 28 LECVYCKQQLRREYVDFAPRDLCTVYRDGNPYAVXDKLFYSKISEYRHVCYSVYGT 87

Db 15 LDCIWCREFPLEVDFAFCWVDFHVIYREGCGYACTICLENCLATERLMQGVPTGEE 74

QY 88 LEOQYNKPLCDLLIRCTINXQKPLCEBEKQRLDKKORFNINRGR-WTGRCMSCCR-SSRT 145

Db 75 AELLHGKTLDRICRCYCGKLTNKKRHVLFNEPFCKTRANIRGRCTDCCHGSR 134

QY 146 R 146

Db 135 K 135

RESULT 42

US-09-913-204-13

; Sequence 13, Application US/09913204

; Patent No. 6953579

; GENERAL INFORMATION:

; APPLICANT: GISSMAN, Lutz

; APPLICANT: MULLER, Herman

; TITLE OF INVENTION: CHIMERIC VIRUS-LIKE PARTICLES OR

; FILE REFERENCE: 035280134PCUS00

; CURRENT APPLICATION NUMBER: US/09/913,204

; PRIOR FILING DATE: 2001-08-10

; PRIOR APPLICATION NUMBER: PCT/DE00/00426

; PRIOR FILING DATE: 2000-02-10

; PRIOR APPLICATION NUMBER: DE 199 05 883.0

; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 13

; LENGTH: 137

; TYPE: PRT

; ORGANISM: Bovine papilloma virus

US-09-913-204-13

Query Match 14.3%; Score 119; DB 2; Length 137;  
Best Local Similarity 28.9%; Pred. No. 1e-05; Indels 2; Gaps 2;  
Matches 35; Conservative 16; Mismatches 68; Indels 2; Gaps 2;

QY 28 LECVYCKQQLRREYVDFAPRDLCTVYRDGNPYAVXDKLFYSKISEYRHVCYSVYGT 87

Db 15 LDCIWCREFPLEVDFAFCWVDFHVIYREGCGYACTICLENCLATERLMQGVPTGEE 74

QY 88 LEOQYNKPLCDLLIRCTINXQKPLCEBEKQRLDKKORFNINRGR-WTGRCMSCCR-SSRT 145

Db 75 AELLHGKTLDRICRCYCGKLTNKKRHVLFNEPFCKTRANIRGRCTDCCHGSR 134

QY 146 R 146

Db 135 K 135

RESULT 43

US-08-934-915-166

; Sequence 166, Application US/08934915

; Patent No. 5932412

; GENERAL INFORMATION:

; APPLICANT: DILLNER, JOAKIM

; APPLICANT: DILLNER, LENA

; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN

; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,

; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,

; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR

; NUMBER OF SEQUENCES: 193

; CORRESPONDENCE ADDRESS:

STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500

CITY: CLEARWATER

STATE: FLORIDA

COUNTRY: U.S.A.

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

OPERATING SYSTEM: Windows 3.0

SOFTWARE: Microsoft Word 6.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/934,915

FILING DATE: 22-SEP-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/949,836

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: LOUISE A. FOUTCH

REGISTRATION NUMBER: 37,133

REFERENCE/DOCKET NUMBER: 1946.6

TELECOMMUNICATION INFORMATION:

TELEPHONE: 813-538-3800

TELEFAX: 813-538-3820

TELEX:

INFORMATION FOR SEQ ID NO: 166:

SEQUENCE CHARACTERISTICS:

LENGTH: 21 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-934-915-166

Query Match 13.9%; Score 115; DB 1; Length 21;  
Best Local Similarity 95.2%; Pred. No. 3e-06; Indels 0; Gaps 0;  
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 115 KORHLDKKORFNINRGRWGR 135

Db 1 KORHLNKKORFNINRGRWGR 21

RESULT 44  
US-08-466-285-2  
Sequence 2, Application US/08466285  
Patent No. 5753233  
GENERAL INFORMATION:  
APPLICANT: BLEUL, Conrad  
APPLICANT: GISSMANN, Lutz  
APPLICANT: MULLER, Martin  
TITLE OF INVENTION: Seroreactive Epitopes On Proteins Of  
TITLE OF INVENTION: Human Papillomavirus (HPV) 18  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
ADDRESS: Dunner  
STREET: 1300 I Street, N.W., Suite 700  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/466,285  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/164,768  
FILING DATE: 10-DEC-1993  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/947,992  
FILING DATE: 21-SEP-1992  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/696,953  
FILING DATE: 08-MAY-1991  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: P 40 15 044.5  
FILING DATE: 10-MAY-1990  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Manspeizer, David A.  
REGISTRATION NUMBER: 37,540  
REFERENCE/DOCKET NUMBER: 05552.1075-03000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)408-4000  
TELEFAX: (202)408-4400  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 32 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-466-285-2

Query Match 13.9%; Score 115; DB 1; Length 32;  
Best Local Similarity 64.5%; Pred. No. 5e-06;  
Matches 20; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Oy 4 DPOERPKLPOLCTELTOTTTHIDILIECVYCK 34  
Db 1 DPTRRPYKLPDLCTELNTSLDIDIEITCYCK 31

RESULT 45  
US-08-164-768-2

Sequence 2, Application US/08164768  
Patent No. 6322794  
GENERAL INFORMATION:  
APPLICANT: BLEUL, Conrad  
APPLICANT: GISSMANN, Lutz  
APPLICANT: MULLER, Martin  
TITLE OF INVENTION: SEROREACTIVE EPITOPES ON PROTEINS OF  
TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS (HPV) 18  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &  
ADDRESS: DUNNER, L.L.P.  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/164,768  
FILING DATE: 10-DEC-1993  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Forman, David S.  
REGISTRATION NUMBER: 33,694  
REFERENCE/DOCKET NUMBER: 05552.1075-02000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 408-4000  
TELEFAX: (202) 408-4400  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 32 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-164-768-2

Query Match 13.9%; Score 115; DB 2; Length 32;  
Best Local Similarity 64.5%; Pred. No. 5e-06;  
Matches 20; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Oy 4 DPOERPKLPOLCTELTOTTTHIDILIECVYCK 34  
Db 1 DPTRRPYKLPDLCTELNTSLDIDIEITCYCK 31

RESULT 46  
US-09-601-729-278  
Sequence 278, Application US/09601729  
Patent No. 6683052  
GENERAL INFORMATION:  
APPLICANT: THIAM, KADER  
APPLICANT: AURIAULT, CLAUDE  
APPLICANT: GRAS-MASSE, HELENE  
APPLICANT: LOING, ESTELLE  
APPLICANT: VERMAERDE, CLAUDE  
APPLICANT: GUILLET, JEAN GERARD  
TITLE OF INVENTION: LIPOPEPTIDES CONTAINING AN INTERFERON FRAGMENT AND USES  
FILE REFERENCE: USB-97-AU-IN  
CURRENT APPLICATION NUMBER: US/09/601,729  
PRIOR FILING DATE: 2000-11-20  
PRIOR APPLICATION NUMBER: PCT/FR99/00259  
PRIOR FILING DATE: 1999-02-05  
PRIOR APPLICATION NUMBER: 98 01439  
PRIOR FILING DATE: 1998-02-06  
NUMBER OF SEQ ID NOS: 281  
SOFTWARE: Patentin Ver. 2.1

```
; SEQ ID NO 278
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-601-729-278

Query Match      13.7%; Score 114; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.7e-06;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      114 EKORHLDKKORFHNIRGRWT 133
Db      1 EKORHLDKKORFHNIRGRWT 20

RESULT 47
US-10-612-818-4
; Sequence 4, Application US/10612818
; Patent No. 6933123
; GENERAL INFORMATION:
; APPLICANT: Impact Diagnostics
; TITLE OF INVENTION: Peptides from the E2, E6 and E7 Proteins of Human Papillomavirus
; TITLE OF INVENTION: 18 for Detecting and/or Diagnosing Cervical and Other Human Pap
; TITLE OF INVENTION: Associated Cancers
; FILE REFERENCE: 3352-2-2
; CURRENT APPLICATION NUMBER: US/10/612,818
; CURRENT FILING DATE: 2003-07-01
; PRIOR APPLICATION NUMBER: US 60/394,172
; PRIOR FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 09/828,645
; PRIOR FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Derived from the E6 early coding region of HPV 16
US-10-612-818-4

Query Match      13.7%; Score 114; DB 2; Length 22;
Best Local Similarity 95.5%; Pred. No. 4.2e-06;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      55 RDGNPYAVXDKCLKFKYSKISEY 76
Db      1 RDGNPYAVXDKCLKFKYSKISEY 22

RESULT 48
US-08-934-915-44
; Sequence 44, Application US/08934915
; Patent No. 5932412
; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; APPLICANT: DILLNER, LENA
; APPLICANT: CHENG, HWEE-MING
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
; NUMBER OF SEQUENCES: 193
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MASON & ASSOCIATES, P.A.
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
; CITY: CLEARWATER
; STATE: FLORIDA
```

```
; COUNTRY: U.S.A.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 3.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,915
; FILING DATE: 22-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/949,836
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: LOUISE A. FOUTCH
; REGISTRATION NUMBER: 37,133
; REFERENCE/DOCKET NUMBER: 1946.6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 813-538-3800
; TELEFAX: 813-538-3820
; TELEX:
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-934-915-44

Query Match      13.1%; Score 109; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.4e-05;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      70 YKISEYRHYCYSLVGTGLE 89
Db      1 YKISEYRHYCYSLVGTGLE 20

RESULT 49
US-08-934-915-45
; Sequence 45, Application US/08934915
; Patent No. 5932412
; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; APPLICANT: DILLNER, LENA
; APPLICANT: CHENG, HWEE-MING
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
; NUMBER OF SEQUENCES: 193
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MASON & ASSOCIATES, P.A.
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
; CITY: CLEARWATER
; STATE: FLORIDA
; COUNTRY: U.S.A.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 3.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,915
; FILING DATE: 22-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/949,836
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: LOUISE A. FOUTCH
; REGISTRATION NUMBER: 37,133
```

REFERENCE/DOCKET NUMBER: 1946.6  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 813-538-3800  
TELEFAX: 813-538-3820  
TELEX:  
INFORMATION FOR SEQ ID NO: 45:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-934-915-45

Query Match 13.1%; Score 109; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 85 GTTLEQOYNKPLCDLLIRCI 104  
Db 1 GTTLEQOYNKPLCDLLIRCI 20

RESULT 50  
US-08-934-915-163  
Sequence 163, Application US/08934915  
Patent No. 5932412  
GENERAL INFORMATION:  
APPLICANT: DILLNER, JOAKIM  
APPLICANT: DILLNER, LENA  
APPLICANT: CHENG, HWEE-MING  
TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN  
TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,  
TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,  
TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR  
TITLE OF INVENTION: DIAGNOSTIC PURPOSES  
NUMBER OF SEQUENCES: 193  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: MASON & ASSOCIATES, P.A.  
STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500  
CITY: CLEARWATER  
STATE: FLORIDA  
COUNTRY: U.S.A.  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Windows 3.0  
SOFTWARE: Microsoft Word 6.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/934,915  
FILING DATE: 22-SEP-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/949,836  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: LOUISE A. Foutch  
REGISTRATION NUMBER: 37,133  
REFERENCE/DOCKET NUMBER: 1946.6  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 813-538-3800  
TELEFAX: 813-538-3820  
TELEX:  
INFORMATION FOR SEQ ID NO: 163:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-934-915-163

Query Match 13.1%; Score 109; DB 1; Length 20;  
Best Local Similarity 95.0%; Pred. No. 1.4e-05;  
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 70 YKSISEYRHVCYSYVGTITLE 89  
Db 1 YKSISEYRHVCYSYVGTITLE 20

RESULT 51  
US-08-934-915-164  
Sequence 164, Application US/08934915  
Patent No. 5932412  
GENERAL INFORMATION:  
APPLICANT: DILLNER, JOAKIM  
APPLICANT: DILLNER, LENA  
APPLICANT: CHENG, HWEE-MING  
TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN  
TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,  
TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,  
TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR  
TITLE OF INVENTION: DIAGNOSTIC PURPOSES  
NUMBER OF SEQUENCES: 193  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: MASON & ASSOCIATES, P.A.  
STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500  
CITY: CLEARWATER  
STATE: FLORIDA  
COUNTRY: U.S.A.  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Windows 3.0  
SOFTWARE: Microsoft Word 6.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/934,915  
FILING DATE: 22-SEP-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/949,836  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: LOUISE A. Foutch  
REGISTRATION NUMBER: 37,133  
REFERENCE/DOCKET NUMBER: 1946.6  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 813-538-3800  
TELEFAX: 813-538-3820  
TELEX:  
INFORMATION FOR SEQ ID NO: 164:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-934-915-164

Query Match 12.5%; Score 104; DB 1; Length 20;  
Best Local Similarity 95.0%; Pred. No. 5.1e-05;  
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 85 GTTLEQOYNKPLCDLLIRCI 104  
Db 1 GTTLEQOYNKPLCDLLIRCI 20

RESULT 52  
US-08-934-915-165  
Sequence 165, Application US/08934915  
Patent No. 5932412  
GENERAL INFORMATION:  
APPLICANT: DILLNER, JOAKIM  
APPLICANT: DILLNER, LENA  
APPLICANT: CHENG, HWEE-MING  
TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN  
TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,

```

; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
; TITLE OF INVENTION: USEFUL IN IMMUNOSSAY FOR
; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
; NUMBER OF SEQUENCES: 193
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MASON & ASSOCIATES, P.A.
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
; CITY: CLEARWATER
; STATE: FLORIDA
; COUNTRY: U.S.A.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 3.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,915
; FILING DATE: 22-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/949,836
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: LOUISE A. FOUTCH
; REGISTRATION NUMBER: 37,133
; REFERENCE/DOCKET NUMBER: 1946.6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 813-538-3800
; TELEFAX: 813-538-3820
; TELEX:
; INFORMATION FOR SEQ ID NO: 165:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-08-934-915-165
;
Query Match 12.5%; Score 104; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 5.1e-05;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
QY 100 LIRCINXOKPLCPPEKQRHL 119
Db 1 LIRCINXOKPLCPPEKQRHL 20
;
RESULT 53
US-08-934-915-159
; Sequence 159, Application US/08934915
; Patent No. 5932412
; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; APPLICANT: DILLNER, LENA
; APPLICANT: CHENG, HWEI-MING
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
; TITLE OF INVENTION: USEFUL IN IMMUNOSSAY FOR
; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
; NUMBER OF SEQUENCES: 193
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MASON & ASSOCIATES, P.A.
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
; CITY: CLEARWATER
; STATE: FLORIDA
; COUNTRY: U.S.A.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 3.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
;

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; APPLICATION NUMBER: US/08/934,915
; FILING DATE: 22-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/949,836
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: LOUISE A. FOUTCH
; REGISTRATION NUMBER: 37,133
; REFERENCE/DOCKET NUMBER: 1946.6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 813-538-3800
; TELEFAX: 813-538-3820
; TELEX:
; INFORMATION FOR SEQ ID NO: 159:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-08-934-915-159
;
Query Match 11.8%; Score 98; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 0.00024;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
;
QY 10 RRLPOLCTELOTTHDILE 29
Db 1 RRLPOLCTELOTTHDILE 20
;
RESULT 54
US-08-934-915-160
; Sequence 160, Application US/08934915
; Patent No. 5932412
; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; APPLICANT: DILLNER, LENA
; APPLICANT: CHENG, HWEI-MING
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
; TITLE OF INVENTION: USEFUL IN IMMUNOSSAY FOR
; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
; NUMBER OF SEQUENCES: 193
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MASON & ASSOCIATES, P.A.
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
; CITY: CLEARWATER
; STATE: FLORIDA
; COUNTRY: U.S.A.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 3.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,915
; FILING DATE: 22-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/949,836
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: LOUISE A. FOUTCH
; REGISTRATION NUMBER: 37,133
; REFERENCE/DOCKET NUMBER: 1946.6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 813-538-3800
; TELEFAX: 813-538-3820
; TELEX:
; INFORMATION FOR SEQ ID NO: 160:
; SEQUENCE CHARACTERISTICS:
;

```

LENGTH: 20 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-934-915-160

Query Match 11.7%; Score 97; DB 1; Length 20;  
Best Local Similarity 90.0%; Pred. No. 0.00031;  
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 25 DIIECVCKQQLRREYD 44  
:|||||:|||||:|||||:  
Db 1 NIIECVCKQQLRREYV 20

RESULT 55  
US-08-934-915-161  
Sequence 161, Application US/08934915  
Patent No. 5932412

GENERAL INFORMATION:  
APPLICANT: DILLNER, JOAKIM  
APPLICANT: DILLNER, LENA  
TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN  
TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,  
TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,  
TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR  
NUMBER OF SEQUENCES: 193  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: MASON & ASSOCIATES, P.A.  
STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500  
CITY: CLEARWATER  
STATE: FLORIDA  
COUNTRY: U.S.A.

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
OPERATING SYSTEM: Windows 3.0  
SOFTWARE: Microsoft Word 6.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/934,915  
FILING DATE: 22-SEP-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/949,836  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: LOUISE A. FOUTCH  
REGISTRATION NUMBER: 37,133  
REFERENCE/DOCKET NUMBER: 1946.6  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 813-538-3800  
TELEFAX: 813-538-3820  
TELEX:

INFORMATION FOR SEQ ID NO: 161:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-934-915-161

Query Match 11.7%; Score 97; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 0.00031;  
Matches 17; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 40 REVYDFARPDICIVRDGNP 59  
:|||||:|||||:|||||:  
Db 1 REVYNFAFRNLICIVRNANP 20

RESULT 56

US-09-641-5288-46524  
Sequence 46524, Application US/096415288  
Patent No. 7026443

GENERAL INFORMATION:  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Chesnut, Robert  
APPLICANT: Cells, Ectoban

TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS  
TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS  
FILE REFERENCE: 2060.0100001  
CURRENT APPLICATION NUMBER: US/09/641,5288  
CURRENT FILING DATE: 2000-08-15  
PRIOR APPLICATION NUMBER: US 60/172,705  
PRIOR FILING DATE: 1999-12-10  
NUMBER OF SEQ ID NOS: 51505  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 46524  
LENGTH: 15  
TYPE: PPT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Peptide Derived from Human Papillomavirus  
US-09-641-5288-46524

Query Match 11.3%; Score 94; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.00049;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 125 FHNIRGRWTCRCMSC 139  
:|||||:|||||:|||||:  
Db 1 FHNIRGRWTCRCMSC 15

RESULT 57  
US-08-466-285-4  
Sequence 4, Application US/08466285  
Patent No. 5753233

GENERAL INFORMATION:  
APPLICANT: Bleul, Conrad  
APPLICANT: Gissmann, Lutz  
APPLICANT: Muller, Martin  
TITLE OF INVENTION: Seroreactive Epitopes On Proteins Of  
TITLE OF INVENTION: Human Papillomavirus (HPV)18  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
ADDRESS: Dunnet  
STREET: 1300 I Street, N.W., Suite 700  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3315

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/466,285  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/164,768  
FILING DATE: 10-DEC-1993  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/947,992  
FILING DATE: 21-SEP-1992  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:

Query Match 11.3%; Score 94; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.00049;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

APPLICATION NUMBER: US 07/696,953  
FILING DATE: 08-MAY-1991  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: P 40 15 044.5  
FILING DATE: 10-MAY-1990  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Manspeler, David A.  
REGISTRATION NUMBER: 37,540  
REFERENCE/DOCKET NUMBER: 05552.1075-03000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 408-4000  
TELEFAX: (202) 408-4400  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 32 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-466-285-4

Query Match 11.2%; Score 93; DB 1; Length 32;  
Best Local Similarity 60.0%; Pred. No. 0.0016;  
Matches 18; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 61 AVXDCKLFYSKISEYRHVCYVGTLEQ 90  
DB 1 AACHKCIDFYSRIRRLRHYSDSVIGDTLEK 30

RESULT 58  
US-08-164-768-4  
Sequence 4, Application US/08164768  
Patent No. 6322794  
GENERAL INFORMATION:  
APPLICANT: BLEUL, Conrad  
APPLICANT: GISSMANN, Lutz  
APPLICANT: MULLER, Martin  
TITLE OF INVENTION: SEROREACTIVE EPITOPES ON PROTEINS OF  
TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS (HPV) 18  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &  
ADDRESSEE: DUNNER, L.L.P.  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/164,768  
FILING DATE: 10-DEC-1993  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Forman, David S.  
REGISTRATION NUMBER: 33,694  
REFERENCE/DOCKET NUMBER: 05552.1075-02000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 408-4000  
TELEFAX: (202) 408-4400  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 32 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: peptide  
US-08-164-768-4

Query Match 11.2%; Score 93; DB 2; Length 32;  
Best Local Similarity 60.0%; Pred. No. 0.0016;  
Matches 18; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 61 AVXDCKLFYSKISEYRHVCYVGTLEQ 90  
DB 1 AACHKCIDFYSRIRRLRHYSDSVIGDTLEK 30

RESULT 59  
US-09-641-528B-46535  
Sequence 46535, Application US/09641528B  
Patent No. 7026443  
GENERAL INFORMATION:  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Chesnut, Robert  
APPLICANT: Celis, Esceban  
APPLICANT: Grey, Howard  
TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS  
TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS  
FILE REFERENCE: 2060.0100001  
CURRENT APPLICATION NUMBER: US/09/641,528B  
CURRENT FILING DATE: 2000-08-15  
PRIOR APPLICATION NUMBER: US 60/172,705  
PRIOR FILING DATE: 1999-12-10  
NUMBER OF SEQ ID NOS: 51505  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 46535  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Peptide Derived from Human Papillomavirus  
US-09-641-528B-46535

Query Match 11.1%; Score 92; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.00082;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 129 RGRWTRGRCMCCRSS 143  
DB 1 RGRWTRGRCMCCRSS 15

RESULT 60  
US-08-934-915-162  
Sequence 162, Application US/08934915  
Patent No. 5932412  
GENERAL INFORMATION:  
APPLICANT: DILLNER, JOAKIM  
APPLICANT: DILLNER, LENA  
APPLICANT: CHENG, HWEI-MING  
TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN  
TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,  
TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,  
TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR  
TITLE OF INVENTION: DIAGNOSTIC PURPOSES  
NUMBER OF SEQUENCES: 193  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MASON & ASSOCIATES, P.A.  
STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500  
CITY: CLEARWATER  
STATE: FLORIDA  
COUNTRY: U.S.A.  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Windows 3.0

SOFTWARE: Microsoft Word 6.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/934,915  
FILING DATE: 22-SEP-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/949,836  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: LOUISE A. Foutch  
REGISTRATION NUMBER: 37,133  
REFERENCE/DOCKET NUMBER: 1946.6  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 813-538-3800  
TELEFAX: 813-538-3820  
TELEX:  
INFORMATION FOR SEQ ID NO: 162:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-934-915-162

Query Match 11.1%; Score 92; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 0.0012;  
Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 55 RDGNPYAVXDKCLKFYSKIS 74  
|:|||||:|||||  
Db 1 RGNPNYAVCNKCLKFYSKIS 20

RESULT 61  
US-08-363-586-3  
Sequence 3, Application US/08363586  
Patent No. 5629161  
GENERAL INFORMATION:  
APPLICANT: Mueller, Martin  
APPLICANT: Gissmann, Lutz  
TITLE OF INVENTION: Use of HPV-16 E6 and E7-Gene Derived  
TITLE OF INVENTION: Peptides for the diagnostic Purpose  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Flanagan, Henderson, Farabow, Garrett &  
ADDRESS: Dunner  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/363,586  
FILING DATE: 23-DEC-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/909,296  
FILING DATE: 09-JUL-1992  
APPLICATION NUMBER: EP 9111720.8  
FILING DATE: 13-JUL-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Madler, Linda A.  
REGISTRATION NUMBER: 33,218  
REFERENCE/DOCKET NUMBER: 02481-1195-00000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:  
LENGTH: 23 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-363-586-3

Query Match 10.8%; Score 90; DB 1; Length 23;  
Best Local Similarity 100.0%; Pred. No. 0.0023;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFQDPQERPRKLPOLC 16  
|||||  
Db 8 MFQDPQERPRKLPOLC 23

RESULT 62  
US-09-641-528B-46517  
Sequence 46517, Application US/09641528B  
Patent No. 7026443  
GENERAL INFORMATION:  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Chesnut, Robert  
APPLICANT: Celis, Betteban  
TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS  
TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS  
FILE REFERENCE: 2060.0100001  
CURRENT APPLICATION NUMBER: US/09/641,528B  
CURRENT FILING DATE: 2000-08-15  
PRIOR APPLICATION NUMBER: US 60/172,705  
PRIOR FILING DATE: 1999-12-10  
NUMBER OF SEQ ID NOS: 51505  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 46517  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Peptide Derived from Human Papillomavirus  
US-09-641-528B-46517

Query Match 10.7%; Score 89; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.0018;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 66 CLKFYSKISEYRHYC 80  
|||||  
Db 1 CLKFYSKISEYRHYC 15

RESULT 63  
US-07-909-122-2  
Sequence 2, Application US/07909122  
Patent No. 5415995  
GENERAL INFORMATION:  
APPLICANT: SCHOOLNIK, GARY K.  
APPLICANT: PALEFSKY, JOEL M.  
TITLE OF INVENTION: DIAGNOSTIC PEPTIDES OF HUMAN PAPILLOMA  
TITLE OF INVENTION: VIRUS  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible

```

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/909,122
; FILING DATE: 19920706
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: BENZ, WILLIAM H.
; REGISTRATION NUMBER: 25,952
; REFERENCE/DOCKET NUMBER: 28600-20105.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-07-909-122-2

Query Match          10.2%; Score 85; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0051;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 FODPQERPRKLPQLC 16
Db      1 FODPQERPRKLPQLC 15

RESULT 64
US-09-641-528B-46523
; Sequence 46523, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46523
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
;
US-09-641-528B-46523

Query Match          10.2%; Score 85; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0051;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      89 EQQYNKPLCDLLIRC 103
Db      1 EQQYNKPLCDLLIRC 15

RESULT 65
US-09-641-528B-46525
; Sequence 46525, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
```

```

; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46525
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
;
US-09-641-528B-46525

Query Match          10.2%; Score 85; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0051;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      134 GRWMSCCRSSRTRE 148
Db      1 GRWMSCCRSSRTRE 15

RESULT 66
US-09-641-528B-46526
; Sequence 46526, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46526
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
;
US-09-641-528B-46526

Query Match          10.2%; Score 85; DB 3; Length 15;
Best Local Similarity 93.3%; Pred. No. 0.0051;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      78 HVCYSVYGTTLQOY 92
Db      1 HVCYSVYGTTLQOY 15

RESULT 67
US-09-641-528B-51200
; Sequence 51200, Application US/09641528B
; Patent No. 7026443
```

```
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51200
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-51200

Query Match          10.2%; Score 85; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0051;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      107 QKPLCEKQRHLDK 121
Db      1 QKPLCEKQRHLDK 15

RESULT 68
US-09-641-528B-46519
; Sequence 46519, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46519
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-46519

Query Match          10.1%; Score 84; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0067;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      44 DFAFRDLCTVYRDGN 58
Db      1 DFAFRDLCTVYRDGN 15

RESULT 69
US-09-641-528B-46534
; Sequence 46534, Application US/09641528B

; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46534
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-46534

Query Match          10.1%; Score 84; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0067;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      20 OTTHDIILECYCK 34
Db      1 OTTHDIILECYCK 15

RESULT 70
US-09-641-528B-46522
; Sequence 46522, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46522
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-46522

Query Match          10.0%; Score 83; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0086;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      29 ECVYCKQQLLRREV 43
Db      1 ECVYCKQQLLRREV 15

RESULT 71
US-09-641-528B-46527
```

```
Sequence 46527, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46527
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-46527

Query Match          10.0%; Score 83; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0086;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      23 IHDIILECYCKQQL 37
Db      1 IHDIILECYCKQQL 15

RESULT 72
US-09-641-528B-46536
; Sequence 46536, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46536
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-46536

Query Match          10.0%; Score 83; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0086;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      42 VYDFARDCIYVRD 56
Db      1 VYDFARDCIYVRD 15

RESULT 73

Sequence 50556, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50556
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-50556

Query Match          10.0%; Score 83; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0086;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      23 IHDIILECYCKQQL 37
Db      1 IHDIILECYCKQQL 15

RESULT 74
US-08-075-541D-52
; Sequence 52, Application US/08075541D
; Patent No. 6183745
; GENERAL INFORMATION:
; APPLICANT: TINDLE, ROBERT
; APPLICANT: FERNANDO, GERMAIN
; APPLICANT: FRAZER, IAN
; TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
; TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSER: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: 1601 MARKET STREET, 36TH FLOOR
; CITY: PHILADELPHIA
; STATE: PENNSYLVANIA
; COUNTRY: USA
; ZIP: 19103-2398
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/075,541D
; FILING DATE: 10-JUN-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU pk 3876
; FILING DATE: 12-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: pct/au91/00575
; FILING DATE: 12-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: NADEL, ALAN S
; REGISTRATION NUMBER: 27,363
; REFERENCE/DOCKET NUMBER: 8795-4
```

```
TELECOMMUNICATION INFORMATION
TELEPHONE: 215-567-2020
TELEFAX: 215-567-2991
INFORMATION FOR SEQ ID NO: 52:
SOURCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-075-541D-52
```

Query Match	9.9%	Score 82	DB 2	Length 15
Best Local Similarity	93.3%	Pred. No. 0.011		
Matches 14; Conservative	1	Mismatches 0	Indels 0	Gaps 0

```

QY      2 FQDPQERPRKLPQLC 16
Db      1 YQDPQERPRKLPQLC 15

```

RESULT 75  
US-09-641-528B-51199  
Sequence 51199 Application US/09641528B

```

? GENERAL INFORMATION:
? APPLICANT: Sette, Alessandro
? APPLICANT: Sidney, John
? APPLICANT: Southwood, Scott
? APPLICANT: Cheenut, Robert
? APPLICANT: Cells, Esteban
? APPLICANT: Grey, Howard
? TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
? TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
? FILE REFERENCE: 2060.0100001
? CURRENT APPLICATION NUMBER: US/09/641,528B
? CURRENT FILING DATE: 2000-08-15
? PRIOR APPLICATION NUMBER: US 60/172,705
? PRIOR FILING DATE: 1999-12-10
? NUMBER OF SEQ ID NOS: 51505
? SOFTWARE: FASTSEQ for Windows Version 4.0
? SEQ ID NO 51199
? LENGTH: 15
? TYPE: prt
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Peptide Derived from Human Papillomavirus
?S-09-641-528B-51199

```

Query Match	9.9%	Score 82;	DB 3;	Length 15;
Best Local Similarity	100.0%	Pred. No. 0.011,		
Matches 15;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

```
QY      16 CTELQTTIHDIILEC 30
          |||||
Db      1 CTELQTTIHDIILEC 15
```

```

RESULT 76
US-09-641-528B--51250
: Sequence 51250, Application US/09641528B
: Patent No. 7026443
:
: GENERAL INFORMATION:
: APPLICANT: Sette, Alessandro
: APPLICANT: Sidney, John
: APPLICANT: Southwood, Scott
: APPLICANT: Chesnut, Robert
: APPLICANT: Celis, Esteban
: APPLICANT: Grey, Howard
: TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
: TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
: FILE REFERENCE: 2060.0100001
: CURRENT APPLICATION NUMBER: US/09/641,528B

```

```

:
: CURRENT FILING DATE: 2000-08-15
: PRIOR APPLICATION NUMBER: US 60/172,705
: PRIOR FILING DATE: 1999-12-10
: NUMBER OF SEQ ID NOS: 51505
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 51250
: LENGTH: 15
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Peptide Derived from Human Papillomavirus
: US-03-641-528B-51250

```

Query Match	9.9%	Score 82;	DB 3;	Length 15;
Best Local Similarity	93.3%;	Pred. NO. 0.01;		
Matches 14;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;

```
QY      107 QKPLCPPEKQRHLDK 121
         | : ||||| |||||
Db       1 QRP LCPPEKQRHLDK 15
```

RESULT 77  
US-09-270-767-41452  
; Sequence 41452, Application US/09270767

```

: GENERAL INFORMATION:
: APPLICANT: Homburger et al.
: TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
: FILE REFERENCE: File Reference: 7326-094
: CURRENT APPLICATION NUMBER: US/09/270,767
: CURRENT FILING DATE: 1999-03-17
: NUMBER OF SEQ ID NOS: 62517
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 41452
: LENGTH: 654
: TYPE: PRN
: ORGANISM: Drosophila melanogaster
: FEATURE:
: OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-41452

```

Query Match 9.9%; Score 82; DB 2; Length 654;  
Best Local Similarity 19.6%; Pred. No. 1;  
Matches 33; Conservative 15; Mismatches 42; Indels 78; Gaps 6

```

Qy      14 QLTCELTQTTIHDIILECVYCKQQLLRREYVDFAFRDLCTVRRDGNPY----- 60
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      376 QVITALGKTIWHPHEFTCNHNSQELGTRNFE-----RDGFYCEPDYHNLFGPRC 425

```

```

Qy      61  ----AVAXDKCLKPFSKISEYRHY----CYSVYGTT-LEDOQNKPLC----- 97
          | : | | | | | | | | | | | | | | | | | | | | | | | | |
Db      426  AYCNGAILEDKCVTALDKTWHTEHFCAQCCQGFGEFGFHERDGKPRCNDYFEMFADKCN 485

```

```

Qy      98  -----DLIRCIHQ-----KPLCE 113
          : | | |
Db      486 GCNRAIMENTYISALNSQWHDQFVCRDCKAVRGKSFYANEQKPVCPQ 533

```

RESULT 78  
US-09-661-5288--46518  
; Sequence 46518, Application US/09661528B  
; Parent No. 7026443  
; GENERAL INFORMATION:  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Sidney, John  
; APPLICANT: Southwood, Scott  
; APPLICANT: Chesnut, Robert  
; APPLICANT: Celis, Esteban  
; APPLICANT: Grey, Howard  
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS  
; TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS  
; FILE REFERENCE: 2060.0100001

```

; CURRENT APPLICATION NUMBER: US/09/641,528B
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46518
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-46518

Query Match          9.8%; Score 81; DB 3; Length 15;
Best Local Similarity 93.3%; Pred. No. 0.015;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      80 CYSVYGTLEQOYK 94
DB      1 CYSLYGTLEQOYK 15

RESULT 79
US-09-641-528B-46520
; Sequence 46520, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Cheenut, Robert
; APPLICANT: Cells, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46520
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-46520

Query Match          9.6%; Score 80; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      25 DILLECVCCKQQLLR 39
DB      1 DILLECVCCKQQLLR 15

RESULT 80
US-09-641-528B-47291
; Sequence 47291, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Cheenut, Robert
; APPLICANT: Cells, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 47291
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-47291

Query Match          9.6%; Score 80; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12 LPOLCTELQTTIHDI 26
DB      1 LPOLCTELQTTIHDI 15

RESULT 81
US-09-641-528B-50558
; Sequence 50558, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Cheenut, Robert
; APPLICANT: Cells, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50558
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-50558

Query Match          9.6%; Score 80; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      125 FHNIRGRTGRCMSC 139
DB      1 FHNIRGRTGRCIAC 15

RESULT 82
US-09-641-528B-46532
; Sequence 46532, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Cheenut, Robert
; APPLICANT: Cells, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46532
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-46532

Query Match          9.6%; Score 80; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12 LPOLCTELQTTIHDI 26
DB      1 LPOLCTELQTTIHDI 15

RESULT 83
US-09-641-528B-46533
; Sequence 46533, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Cheenut, Robert
; APPLICANT: Cells, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46533
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-46533

Query Match          9.6%; Score 80; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12 LPOLCTELQTTIHDI 26
DB      1 LPOLCTELQTTIHDI 15
```

```

RESULT 86
US-09-270-767-46957
; Sequence 46957, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Hombrugger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0

```

SEQ ID NO 46957  
LENGTH: 165  
TYPE: PRT  
ORGANISM: Drosophila melanogaster  
US-09-270-767-46957

Query Match  
Best Local Similarity 26.0%; Score 77.5; DB 2; Length 165;  
Matches 34; Conservative 14; Mismatches 66; Indels 17; Gaps 5;

QY 29 ECYVCKQQLLRREYVDFARDLCTIYVRD-----NRYAVXDK-LKFSKISERYHY 79  
DB 30 ECTACDIQNTAKASIHFTDCIFMRBAIRSLNVTLSRYFVCNVCLEKFAVTDLQERH 89  
QY 80 CYSV-YGTTLEQYKPL--CDLLRCINXQKPLCEBEKORHLDKORFHNRGRWTR- 135  
DB 90 CTSFHYFPLNLSKGLLPDCDCDVNFPAHDFLAHSEKHLKKRKEKTRNTGAGR 149  
QY 136 ----CMSCRS 142  
DB 150 RQYLDICGKS 160

RESULT 87  
US-09-949-016-6366  
Sequence 6366, Application US/09949016  
Patent No. 6812339

GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949, 016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR FILING DATE: 2000-09-08  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for windows Version 4.0  
SEQ ID NO 6366  
LENGTH: 572  
TYPE: PRT  
ORGANISM: Human  
US-09-949-016-6366

Query Match  
Best Local Similarity 22.4%; Score 77.5; DB 2; Length 572;  
Matches 41; Conservative 21; Mismatches 66; Indels 55; Gaps 11;

QY 1 MROD---PDRPRKLPOLC-----TEIQTTHHLLLECVYKQQLRREYV 43  
DB 366 LMQDMHPORONAVNELGCRCHQPLARQPAVRALGOLFNHLCFTCHCAQQLGQGF 425  
QY 44 DFAFRDLCTIYVRD-----GNPYAVXDK-LKFSKISERYHYGVS-----VYGT 87  
DB 426 SLEGAAYCEGCTYDLTEKCTGCEP--ITDRMLRAHGK--AYHPCTCYVCARPLEGIS 481  
QY 88 -LEQYKPLC-----DLIRCIINXQKPLCEBEKORHLDKORFHNRGRWTRGRC 136  
DB 482 FIVDQANRPHCVVDYHKOYAPRCSVSEPIFMRGDETVRVVALDKNPFH-----KC 534  
QY 137 MSC 139  
DB 535 YKC 537

RESULT 88  
US-09-641-528B-46521  
Sequence 46521, Application US/09641528B  
Patent No. 7026443

GENERAL INFORMATION:  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Chesnut, Robert  
APPLICANT: Celis, Esleben  
APPLICANT: Grey, Howard  
TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS  
TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS  
FILE REFERENCE: 2060.0100001  
CURRENT APPLICATION NUMBER: US/09/641,528B  
CURRENT FILING DATE: 2000-08-15  
PRIOR APPLICATION NUMBER: US 60/172,705  
PRIOR FILING DATE: 1999-12-10  
NUMBER OF SEQ ID NOS: 51505  
SOFTWARE: FastSeq for windows Version 4.0  
SEQ ID NO 46521  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Peptide Derived from Human Papillomavirus  
US-09-641-528B-46521

Query Match  
Best Local Similarity 93.3%; Score 77; DB 3; Length 15;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 98 DLLIRCIINXQKPLCP 112  
DB 1 DLLIRCIINXQKPLCP 15

RESULT 89  
US-09-641-528B-50557  
Sequence 50557, Application US/09641528B  
Patent No. 7026443  
GENERAL INFORMATION:  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Chesnut, Robert  
APPLICANT: Celis, Esleben  
APPLICANT: Grey, Howard  
TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS  
TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS  
FILE REFERENCE: 2060.0100001  
CURRENT APPLICATION NUMBER: US/09/641,528B  
CURRENT FILING DATE: 2000-08-15  
PRIOR APPLICATION NUMBER: US 60/172,705  
PRIOR FILING DATE: 1999-12-10  
NUMBER OF SEQ ID NOS: 51505  
SOFTWARE: FastSeq for windows Version 4.0  
SEQ ID NO 50557  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Peptide Derived from Human Papillomavirus  
US-09-641-528B-50557

Query Match  
Best Local Similarity 93.3%; Score 77; DB 3; Length 15;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 50 LCIIVRDGNPYAVXD 64  
DB 1 LCIIVRDGNPYAVCD 15

RESULT 90  
US-09-641-528B-50559  
Sequence 50559, Application US/09641528B

```
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
; FILE REFERENCE: 2060.010001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50559
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-50559

Query Match          9.3%; Score 77; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      35 QQLRREYVDFAFRD 49
DB      1 QQLRREYVDFAFRD 15

RESULT 91
US-09-939-853A-15
; Sequence 15, Application US/09939853A
; Patent No. 6989232
; GENERAL INFORMATION:
; APPLICANT: Burgess et al.
; TITLE OF INVENTION: No. 6989232el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-099
; CURRENT APPLICATION NUMBER: US/09/939,853A
; PRIOR FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: 60/228,191
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: 60/267,300
; PRIOR FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: 60/269,961
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/277,337
; PRIOR FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 159
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 785
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-939-853A-15

Query Match          9.2%; Score 76.5; DB 2; Length 785;
Best Local Similarity 24.0%; Pred. No. 5.3;
Matches 31; Conservative 12; Mismatches 33; Indels 53; Gaps 7;

QY      16 CTELD-TTIDHILICVCCKQLLRREYVDFAFRDLCIVRDGNFYAVYDKLK-FYSKI 73
DB      321 CTEAGRTMHMGHFGCECHLGGR-----YIMRGKXY-----CLACFDTFW 365

QY      74 SEYRYHCYSVYGTIEEQVKNKPLCDLLRCINXKQPLCPREEQRHLDDKQRHNRGRW- 132
DB      366 AECYCYCEVIG-----VDGQNSHDGQ-FHW 391

QY      133 -TGRGMSCC 140
```

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DB      392 ATDQCFSCC 400

RESULT 92
US-07-909-122-4
; Sequence 4, Application US/07909122
; Patent No. 5415995
; GENERAL INFORMATION:
; APPLICANT: SCHOOLNIK, GARY K.
; APPLICANT: PALEFSKY, JOEL M.
; TITLE OF INVENTION: DIAGNOSTIC PEPTIDES OF HUMAN PAPILLOMA
; TITLE OF INVENTION: VIRUS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/909,122
; FILING DATE: 19920706
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: BENZ, WILLIAM H.
; REGISTRATION NUMBER: 25,952
; REFERENCE/DOCKET NUMBER: 28600-20105-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
US-07-909-122-4

Query Match          9.2%; Score 76; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      38 LRREYVDFAFRDLC 51
DB      1 LRREYVDFAFRDLC 14

RESULT 93
US-09-641-528B-46529
; Sequence 46529, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
; FILE REFERENCE: 2060.010001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
```

```

; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46529
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-46529

Query Match
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 KOQLRREYDPAFR 48
DB 1 KOQLRREYDPAFR 15

RESULT 94
US-09-641-528B-46531
; Sequence 46531, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46531
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-46531

Query Match
Best Local Similarity 9.2%; Score 76; DB 3; Length 15;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 93 NKPLCDLIRICINXQ 107
DB 1 NKPLCDLIRICINQ 15

RESULT 95
US-09-248-796A-16235
; Sequence 16235, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 16235
```

```

; LENGTH: 187
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-16235

Query Match
Best Local Similarity 9.1%; Score 75.5; DB 2; Length 187;
Matches 33; Conservative 18; Mismatches 54; Indels 39; Gaps 8;

QY 14 QLCTBLQF-----TIHIIIEC-----YCK-----OQLRREYDPAFRDLCTIV 54
DB 24 RLCHNRDYYNNHPPYCHHIFCLICGHYCPNDHVPACHHICHCYHGTGRRPCICH 83
QY 55 RDGNFYAVXDKCLKRYS-KISEYRH---YCYSVYGTLEQOYNKPLCDLIRICINXQKP 109
DB 84 --GTYVPYTHRSYLSCLRCLCVCHHTCPICHPHYRDSYLCYIRPCHLSYCHNHQ-- 139
QY 110 LCPREKQRH-----LDKQRFPHNI 128
DB 140 -----QKHVVVYIWSKDRFHNI 157

RESULT 96
US-09-949-016-8090
; Sequence 8090, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYOMPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8090
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8090

Query Match
Best Local Similarity 9.1%; Score 75.5; DB 2; Length 250;
Matches 33; Conservative 14; Mismatches 36; Indels 37; Gaps 7;

QY 40 REVDPAPRDLCIVYRDGNPYAVXD-----KCLKRYSKISEYRHCYSVYGTLEQOYNK 94
DB 26 RCIDESTRCLCDLYM--HPYCCDLHPYPYL-----KRSNSC 65
QY 95 PLCDLIRICINXQKPLCEPKQRHL-----DKQRFHNI RGRWTCRW--SCCRSS 143
DB 66 GLCDLYPCCLQYKYLICARPSLRSLERKAIKRAIIEDEKELAKLR-RTTIRLIASSCCSSN 124

RESULT 97
US-09-641-528B-46533
; Sequence 46533, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 107196.132
```

```
FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 46533
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-46533

Query Match
; Score 9.0%; DB 3; Length 15;
; Best Local Similarity 93.3%; Pred. No. 0.07;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 59 PVAVDKCLKFKYSKI 73
DB 1 PVAVDKCLKFKYSKI 15

RESULT 98
US-08-377-309-7
; Sequence 7, Application US/08377309A
; Patent No. 5965528
; GENERAL INFORMATION:
; APPLICANT: Murgita, Robert A.
; TITLE OF INVENTION: RECOMBINANT HUMAN ALPHA-FETOPROTEIN AS
; FILE REFERENCE: 06727/005001
; CURRENT APPLICATION NUMBER: US/08/377,309A
; CURRENT FILING DATE: 1995-01-24
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 7
; LENGTH: 393
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-377-309-7

Query Match
; Score 9.0%; DB 1; Length 393;
; Best Local Similarity 23.4%; Pred. No. 3.9;
Matches 34; Conservative 26; Mismatches 44; Indels 41; Gaps 8;

QY 6 GERPKLPQLCTELQTTIHDIIECVYCKQQLRREVYDFAFRDLCTIV----- 54
DB 63 QDEKIMSYICSQ-QDTLSNKTIEC--CKLTLE-----RGCTIIHAENDEKREGLS 111
QY 55 -----RDGNPVAVDKCLKFKYSKISEY--RHVCYSVYGTLEEQYNKPLCDLLIR 103
DB 112 PVLNRFGLDRDPNQGSSGEKNIPLASFVHEYSRRHPQLAV---SVILRVAKGYQELLKRC 168
QY 104 INXQKPL-C---PEKQRLDKQ 123
DB 169 FQTENPLECQDGEBELQKYIOESQ 193

RESULT 99
US-09-186-723-7
; Sequence 7, Application US/09186723
; Patent No. 6288034
; GENERAL INFORMATION:
; APPLICANT: Murgita, Robert A.
; TITLE OF INVENTION: RECOMBINANT HUMAN ALPHA-FETOPROTEIN AS
; FILE REFERENCE: 06727/005002
; CURRENT APPLICATION NUMBER: US/09/186,723
; CURRENT FILING DATE: 1998-11-05
; EARLIER APPLICATION NUMBER: 08/377,309
; EARLIER FILING DATE: 1995-01-24
```

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NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 7
; LENGTH: 393
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-186-723-7

Query Match
; Score 9.0%; DB 2; Length 393;
; Best Local Similarity 23.4%; Pred. No. 3.9;
Matches 34; Conservative 26; Mismatches 44; Indels 41; Gaps 8;

QY 6 GERPKLPQLCTELQTTIHDIIECVYCKQQLRREVYDFAFRDLCTIV----- 54
DB 63 QDEKIMSYICSQ-QDTLSNKTIEC--CKLTLE-----RGCTIIHAENDEKREGLS 111
QY 55 -----RDGNPVAVDKCLKFKYSKISEY--RHVCYSVYGTLEEQYNKPLCDLLIR 103
DB 112 PVLNRFGLDRDPNQGSSGEKNIPLASFVHEYSRRHPQLAV---SVILRVAKGYQELLKRC 168
QY 104 INXQKPL-C---PEKQRLDKQ 123
DB 169 FQTENPLECQDGEBELQKYIOESQ 193

RESULT 100
US-08-505-012-10
; Sequence 10, Application US/08505012
; Patent No. 631611
; GENERAL INFORMATION:
; APPLICANT: Murgita, Robert A.
; TITLE OF INVENTION: EXPRESSION AND PURIFICATION OF CLONED
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street, Suite 3100
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/505,012
; FILING DATE: 21-JUL-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/377,317
; FILING DATE: 24-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 06727/007001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 393 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-505-012-10

Query Match
; Score 9.0%; DB 2; Length 393;
; Best Local Similarity 23.4%; Pred. No. 3.9;
Matches 34; Conservative 26; Mismatches 44; Indels 41; Gaps 8;
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```
QY      6 QERPRKLPOLCTELQTTTHDIIIECYCKQQLRREVDPFAPRDLCTIVY----- 54
      | : : : : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db      63 ODGEKIMSYICSO-ODTISNKITEC--CKLTTLE-----RGOCIIHAENDEKPEGIS 111
      | : : : : : | : : | : : | : : | : : | : : | : : | : : | : : |
QY      55 -----RDGNPYAVXDKCLKFYSKIsey--RHycsvyGTTLEQYnKPLCDLLIRc 103
      | : : : : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db      112 PVLNRPFLGDRDPNqSSGSKIIFLASFVHFYSRRHPQLAV---SVILRYAKGYQELLEKc 168
      | : : : : : | : : | : : | : : | : : | : : | : : | : : | : : |
QY      104 INXQKPL-C----PEEKQRHLDPKQ 123
      | : : : : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db      169 FQTENPBLECQDKGEELQKYIQESQ 193
      | : : : : : | : : | : : | : : | : : | : : | : : | : : | : : |
```

Search completed: May 27, 2006, 05:18:32  
Job time : 46.2691 secs

GenCore version 5.1.8  
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OM protein - protein search, using bw model

Run on: May 27, 2006, 04:59:57 ; Search time 351.727 Seconds  
(without alignments)  
196.288 Million cell updates/sec

Title: US-10-530-253-13ED

Perfect score: 830

Sequence: 1 MFQDQERRKUPQLCTELQ.....WTGRCMSCRSRTRRETOL 151

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : A\_Geneseq.8:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*  
9: geneseqp2005s:\*  
10: geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	828	99.8	248	8	Ado44062 Amino aci
2	828	99.8	248	8	Ado44064 Amino aci
3	826	99.5	151	6	Aao22640 HPV-16 pr
4	826	99.5	151	6	Aao22636 HPV (onco
5	826	99.5	151	8	Ado44072 Amino aci
6	826	99.5	151	8	Ado44060 Amino aci
7	826	99.5	151	8	Ado44072 Amino aci
8	823	99.2	158	3	AAY82462 Human pap
9	823	99.2	158	3	AAY82462 Human pap
10	823	99.2	158	3	AAY82462 Human pap
11	823	99.2	158	3	AAY82462 Human pap
12	823	99.2	158	3	AAY82462 Human pap
13	823	99.2	158	3	AAY82462 Human pap
14	823	99.2	158	3	AAY82462 Human pap
15	823	99.2	158	3	AAY82462 Human pap
16	823	99.2	158	3	AAY82462 Human pap
17	823	99.2	158	3	AAY82462 Human pap
18	823	99.2	158	3	AAY82462 Human pap
19	823	99.2	158	3	AAY82462 Human pap
20	823	99.2	158	3	AAY82462 Human pap
21	823	99.2	158	3	AAY82462 Human pap
22	823	99.2	158	3	AAY82462 Human pap
23	823	99.2	158	3	AAY82462 Human pap

24	823	99.2	248	8	Ado44070 Amino aci
25	823	99.2	256	8	AdR47005 Human pap
26	823	99.2	256	10	AdR47005 Human pap
27	823	99.2	263	2	AAR27725 HPV 16 E6
28	823	99.2	266	2	AAR97561 Human pap
29	823	99.2	273	2	AAY25376 HPV fusio
30	823	99.2	273	2	AAY02632 Prot.D1/3
31	823	99.2	273	2	AED52634 Fusion pr
32	823	99.2	292	2	AAY25379 HPV fusio
33	823	99.2	292	2	AAY02635 Fusion pr
34	823	99.2	292	2	AED52642 Fusion pr
35	823	99.2	371	2	AAY25377 HPV fusio
36	823	99.2	371	2	AAY02633 Prot.D1/3
37	823	99.2	371	2	AED52638 Fusion pr
38	823	99.2	390	2	AAY25381 HPV fusio
39	823	99.2	390	2	AAY02637 Fusion pr
40	823	99.2	390	2	AED52646 Fusion pr
41	821	98.9	248	8	Ado44066 Amino aci
42	818	98.6	151	3	AAY57808 HPV-16 E6
43	815	98.2	158	8	AdL90078 Human pap
44	779.5	93.9	243	2	AAW99369 Papilloma
45	580	69.9	149	8	AdR40919 HPV E6 re
46	578	69.6	149	8	Ado44077 Amino aci
47	578	69.6	149	8	Ado44077 Amino aci
48	572	68.9	180	7	AdF31985 Human pap
49	523	63.0	149	4	AdB98434 Human pap
50	523	63.0	149	8	Ado44075 Amino aci
51	523	63.0	149	8	Ado44075 Amino aci
52	523	63.0	149	8	Ado44075 Amino aci
53	523	63.0	149	8	Ado44075 Amino aci
54	520	62.7	149	4	AdB98447 Human pap
55	520	62.7	149	4	Ado44076 Amino aci
56	520	62.7	149	9	AdB98535 HPV (onco
57	520	62.7	149	9	AdB98535 HPV (onco
58	520	62.7	149	9	AdB98535 HPV (onco
59	520	62.7	149	9	AdB98535 HPV (onco
60	496	60.0	149	9	AdB98879 HPV (onco
61	496	59.8	149	8	Ado44083 Amino aci
62	496	59.8	149	9	AdB98534 HPV (onco
63	496	59.8	149	9	AdB98870 HPV-58 En
64	487	58.7	148	8	Ado44081 Amino aci
65	487	58.7	148	9	AdB98536 HPV (onco
66	487	58.7	148	9	AdB98868 HPV-52 En
67	487	58.7	148	9	AdB98868 HPV-52 En
68	484	58.3	148	9	AdB98878 HPV (onco
69	483	58.2	148	9	AdB98878 HPV (onco
70	478	57.6	172	2	AAW97563 Human pap
71	468.5	56.4	158	8	Ado44085 Amino aci
72	468.5	56.4	158	9	AdB98880 HPV (onco
73	468	56.4	172	2	AAW97562 Human pap
74	460	55.4	151	8	Ado44080 Amino aci
75	460	55.4	151	8	Ado44080 Amino aci
76	459.5	55.4	158	8	Ado44079 Amino aci
77	459.5	55.4	158	9	AdB98548 HPV (onco
78	459.5	55.4	158	9	AdB98548 HPV (onco
79	455.5	54.9	158	2	AAW97566 HPV-18 E6
80	455.5	54.9	158	2	AAW97566 HPV-18 E6
81	455.5	54.9	158	2	AAW97566 HPV-18 E6
82	455.5	54.9	158	2	AAW97566 HPV-18 E6
83	455.5	54.9	158	2	AAW97566 HPV-18 E6
84	455.5	54.9	158	2	AAW97566 HPV-18 E6
85	455.5	54.9	158	2	AAW97566 HPV-18 E6
86	455.5	54.9	158	2	AAW97566 HPV-18 E6
87	455.5	54.9	158	2	AAW97566 HPV-18 E6
88	455.5	54.9	158	2	AAW97566 HPV-18 E6
89	455.5	54.9	158	2	AAW97566 HPV-18 E6
90	455.5	54.9	158	2	AAW97566 HPV-18 E6
91	455.5	54.9	158	2	AAW97566 HPV-18 E6
92	455.5	54.9	158	2	AAW97566 HPV-18 E6
93	455.5	54.9	158	2	AAW97566 HPV-18 E6
94	455.5	54.9	158	2	AAW97566 HPV-18 E6
95	455.5	54.9	158	2	AAW97566 HPV-18 E6
96	455.5	54.9	158	2	AAW97566 HPV-18 E6



Matches 149; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFODPQERPRKLPOLCTELQTTIHDIILCEVCYKQQLRREVYDFAFRDLCTIYRDGNPY 60  
 DB 1 MFODPQERPRKLPOLCTELQTTIHDIILCEVCYKQQLRREVYDFAFRDLCTIYRDGNPY 60

QY 61 AYXDKCLKFYFSKISEYRHVCYSYVGTTLLEQYNNKPCDLLIRICINOKPLCPBEKORHLD 120  
 DB 61 AYXDKCLKFYFSKISEYRHVCYSYVGTTLLEQYNNKPCDLLIRICINOKPLCPBEKORHLD 120

QY 121 KKQRFNINRGWTRGCMSCCRSSRTTRRETOL 151  
 DB 121 KKQRFNINRGWTRGCMSCCRSSRTTRRETOL 151

RESULT 3  
 AAO22640  
 ID AAO22640 standard; protein; 151 AA.  
 AC AAO22640;  
 XX  
 DT 15-MAY-2003 (first entry)  
 XX  
 DE HPV-16 protein sequence, SEQ ID No 27.  
 XX  
 KM Cytostatic; peptide therapy; immunotherapy; pre-; cancerous growth;  
 KM cancer; human papilloma virus; cervix; cell-mediated immune response;  
 KM HPV; HPV-16.  
 XX  
 OS Human papilloma virus.  
 XX  
 PN WO2003008649-A1.  
 XX  
 PD 30-JAN-2003.  
 XX  
 PF 19-JUL-2002; 2002MO-US023198.  
 XX  
 PR 20-JUL-2001; 2001US-0306809P.  
 XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 PI Sastry KJ, Tortolero-Luna G, Follen M;  
 XX WPI; 2003-239363/23.  
 XX  
 PT Determining a possible recurrence of a (pre-)cancerous growth in a  
 PT patient infected with human papilloma virus (HPV), comprises incubating  
 PT the sample with an HPV E6 or E7 peptide and detecting a cell-mediated  
 PT immune response.  
 XX  
 PS Disclosure; Page 129-130; 132pp; English.  
 XX  
 CC The invention relates to a novel method for determining the possibility  
 CC of recurrence of a (pre-)cancerous growth in a patient infected with  
 CC human papilloma virus (HPV) or suspected of being infected with HPV, and  
 CC has or had a (pre-)cancerous growth on or around the cervix. The novel  
 CC method comprises incubating an E6 or E7 peptide of HPV with a sample from  
 CC the patient, and assaying the sample for a cell-mediated immune response  
 CC against the peptide. The method is useful for determining the possibility  
 CC and preventing the recurrence of a (pre-)cancerous growth in a patient  
 CC infected with HPV or suspected of being infected with HPV. The HPV E6 or  
 CC E7 peptides are useful in immunotherapy for the preventing or reducing  
 CC the risk of development of (pre-)cancerous growths. This sequence  
 CC represents an HPV-16 protein of the invention  
 XX  
 SQ Sequence 151 AA;

Query Match 99.5%; Score 826; DB 6; Length 151;  
 Best Local Similarity 98.7%; Pred. No. 4.2e-84;  
 Matches 149; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFODPQERPRKLPOLCTELQTTIHDIILCEVCYKQQLRREVYDFAFRDLCTIYRDGNPY 60  
 DB 1 MFODPQERPRKLPOLCTELQTTIHDIILCEVCYKQQLRREVYDFAFRDLCTIYRDGNPY 60

DB 1 MFODPQERPRKLPOLCTELQTTIHDIILCEVCYKQQLRREVYDFAFRDLCTIYRDGNPY 60  
 QY 61 AYXDKCLKFYFSKISEYRHVCYSYVGTTLLEQYNNKPCDLLIRICINOKPLCPBEKORHLD 120  
 DB 61 AYXDKCLKFYFSKISEYRHVCYSYVGTTLLEQYNNKPCDLLIRICINOKPLCPBEKORHLD 120

QY 121 KKQRFNINRGWTRGCMSCCRSSRTTRRETOL 151  
 DB 121 KKQRFNINRGWTRGCMSCCRSSRTTRRETOL 151

RESULT 4  
 AAO22636  
 ID AAO22636 standard; protein; 151 AA.  
 AC AAO22636;  
 XX  
 DT 15-MAY-2003 (first entry)  
 XX  
 DE HPV protein sequence, SEQ ID No 20.  
 XX  
 KM Cytostatic; peptide therapy; immunotherapy; pre-; cancerous growth;  
 KM cancer; human papilloma virus; cervix; cell-mediated immune response;  
 KM HPV; HPV-16.  
 XX  
 OS Human papilloma virus.  
 XX  
 PN WO2003008649-A1.  
 XX  
 PD 30-JAN-2003.  
 XX  
 PF 19-JUL-2002; 2002MO-US023198.  
 XX  
 PR 20-JUL-2001; 2001US-0306809P.  
 XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 PI Sastry KJ, Tortolero-Luna G, Follen M;  
 XX WPI; 2003-239363/23.  
 XX  
 PT Determining a possible recurrence of a (pre-)cancerous growth in a  
 PT patient infected with human papilloma virus (HPV), comprises incubating  
 PT the sample with an HPV E6 or E7 peptide and detecting a cell-mediated  
 PT immune response.  
 XX  
 PS Disclosure; Page 125-126; 132pp; English.  
 XX  
 CC The invention relates to a novel method for determining the possibility  
 CC of recurrence of a (pre-)cancerous growth in a patient infected with  
 CC human papilloma virus (HPV) or suspected of being infected with HPV, and  
 CC has or had a (pre-)cancerous growth on or around the cervix. The novel  
 CC method comprises incubating an E6 or E7 peptide of HPV with a sample from  
 CC the patient, and assaying the sample for a cell-mediated immune response  
 CC against the peptide. The method is useful for determining the possibility  
 CC and preventing the recurrence of a (pre-)cancerous growth in a patient  
 CC infected with HPV or suspected of being infected with HPV. The HPV E6 or  
 CC E7 peptides are useful in immunotherapy for the preventing or reducing  
 CC the risk of development of (pre-)cancerous growths. This sequence  
 CC represents an HPV protein of the invention  
 XX  
 SQ Sequence 151 AA;

Query Match 99.5%; Score 826; DB 6; Length 151;  
 Best Local Similarity 98.7%; Pred. No. 4.2e-84;  
 Matches 149; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFODPQERPRKLPOLCTELQTTIHDIILCEVCYKQQLRREVYDFAFRDLCTIYRDGNPY 60  
 DB 1 MFODPQERPRKLPOLCTELQTTIHDIILCEVCYKQQLRREVYDFAFRDLCTIYRDGNPY 60

QY 61 AYXDKCLKFYFSKISEYRHVCYSYVGTTLLEQYNNKPCDLLIRICINOKPLCPBEKORHLD 120  
 DB 61 AYXDKCLKFYFSKISEYRHVCYSYVGTTLLEQYNNKPCDLLIRICINOKPLCPBEKORHLD 120

```

Db      61  AVCDCKLKFYSKISEYRHYCYVYGTTLGQYNKPLCDLLIRCIHQCKPLCEPEKQRLD 120
Qy      121  KKQRFHNIRGWTGRCMSCCRSSRTRETOL 151
Db      121  KKQRFHNIRGWTGRCMSCCRSSRTRETOL 151

RESULT 5
ADO44072
ID      ADO44072 standard; protein, 151 AA.
XX
AC      ADO44072;
XX
DT      15-JUL-2004 (first entry)
XX
DE      Amino acid sequence of a wild type HPV16 E6 protein.
XX
KW      E6 protein; E7 protein; fusion protein; HPV16; HPV-associated cancer;
KM      cervical cancer; immune response; lower gastrointestinal tract cancer;
KM      anal cancer; reproductive system cancer; penile cancer; vulvar cancer.
XX
OS      Human papillomavirus type 16.
OS      Synthetic.
XX
PN      WO2004030636-A2.
XX
PD      15-APR-2004.
XX
PF      02-OCT-2003; 2003WO-US0311726.
XX
PR      03-OCT-2002; 2002US-0415929P.
XX
PA      (AMHP ) WYETH HOLDINGS CORP.
XX
PI      Smith L, Cassecci MC;
XX
DR      WPI; 2004-316328/29.
XX
PT      New polypeptide comprising human papillomavirus E6 and E7 polypeptides,
PT      useful for creating or preventing human papillomavirus (HPV)-associated
PT      cancers, e.g. cervical cancer.
XX
PS      Claim 1; Page 76-77; 101pp; English.
XX
CC      The present sequence represents a wild type E6 protein from human
CC      papillomavirus type 16 (HPV16), which is used to produce fusion proteins
CC      of the invention. The specification describes human papillomavirus E6 and
CC      E7 polypeptides, where the E7 polypeptide has mutations at any one or
CC      more of the amino acids corresponding to amino acids 24, 26 or 91 of the
CC      sequence given in ADO44072 and the E6 polypeptide has no mutations or has
CC      mutations at any one or more of the amino acids corresponding to amino
CC      acids 63 or 106 of the sequence given in ADO44072. The polypeptides of
CC      the invention are useful for treating or preventing human papillomavirus
CC      (HPV)-associated cancers, such as cervical cancer. The fusion proteins
CC      and nucleic acids encoding the fusion proteins are useful for generating
CC      immune responses against HPV. They are also useful for treating lower
CC      gastrointestinal tract cancers, e.g. anal cancer, and other cancers of
CC      the reproductive system, including penile and vulvar cancer.
XX
SQ      Sequence 151 AA;

Query Match      99.5%; Score 826; DB 8; Length 151;
Best Local Similarity 98.7%; Pred. No. 4,2e-84;
Matches 149; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy      121  KKQRFHNIRGWTGRCMSCCRSSRTRETOL 151
Db      121  KKQRFHNIRGWTGRCMSCCRSSRTRETOL 151

RESULT 6
AAW35742
ID      AAW35742 standard; protein, 162 AA.
XX
AC      AAW35742;
XX
DT      25-MAR-2003 (revised)
DT      16-FEB-1998 (first entry)
XX
DE      Human papillomavirus type 16 E6 protein variant.
XX
KW      Complete genome; circular; human papillomavirus type 16; HPV16 E6;
KM      cervical dysplasia; cervical cancer; cervical smear.
XX
OS      Human papillomavirus type 16.
XX
FH      Key
FH      Misc-difference 90 Location/Qualifiers
FT      /note= "Mutated from Leu in the reference sequence
FT      (AAW35741)"
FT      Misc-difference 159
FT      /note= "End of protein sequence even though 3 amino acid
FT      residues are given following on"
XX
PN      US5679509-A.
XX
PD      21-OCT-1997.
XX
PF      30-SEP-1994; 94US-00316239.
XX
PR      28-SEP-1993; 93US-00127906.
XX
PA      (UYNE-) UNIV NEW MEXICO STATE.
XX
PI      Wheeler CM, Parmenter CA;
XX
DR      WPI; 1997-525714/48.
DR      N-PSDB; AAT94742.
XX
PT      Evaluating risk of cervical dysplasia or cervical cancer - by detecting
PT      variant form of human papilloma virus 16.
XX
PS      Claim 7; Col 23-26; 33pp; English.
XX
CC      Methods have been developed for distinguishing a subset of human
CC      papilloma virus (HPV) that is associated with an increased risk of
CC      developing cervical dysplasia or cervical cancer. The methods involve:
CC      (1) preparing a cervical sample to expose any HPV-16 E6 gene in the
CC      sample and determining if the base at position 350 of the E6 gene (see
CC      AAT94723 and AAT94724 for comparison) is T or G, where the presence of G
CC      at position 350 is associated with an increased risk of developing
CC      cervical dysplasia or cervical cancer; and (2) preparing a cervical
CC      sample to expose any HPV-16 E6 protein in the sample and determining if
CC      the amino acid at position 83 of the protein (see position 90 in AAW35741
CC      and AAW35742 for comparison) is Val or Leu, where the presence of Val at
CC      position 83 that is associated with an increased risk of developing
CC      cervical dysplasia or cervical cancer. The present sequence represents
CC      the variant protein sequence for HPV-16 E6. The 350G variant correlates
CC      well with Pap scores: 350T:350G ratios among 45 HPV16 samples were 10:4
CC      for negative Pap scores; 4:2 for CIN I, 1:6 for CIN II; 2:9 for CIN III;
CC      0:3 for cancer. (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ      Sequence 162 AA;

Query Match      99.5%; Score 826; DB 2; Length 162;
Best Local Similarity 98.7%; Pred. No. 4,6e-84;
Matches 149; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

QY 1 MFQDPOBRPKLPOLCTELQTTTHDIIIECVYCKQQLRREYVDFAFRDLCIYVRDGNPY 60  
 DB 8 MFQDPOBRPKLPOLCTELQTTTHDIIIECVYCKQQLRREYVDFAFRDLCIYVRDGNPY 67  
 QY 61 AVXDKCLKFKYSKISEYRHYCYSVYGTTLLEQYNNKPLCDLLIRINCINXQKPLCPBEKORHLD 120  
 DB 68 AVCDKCLKFKYSKISEYRHYCYSVYGTTLLEQYNNKPLCDLLIRINCINXQKPLCPBEKORHLD 127  
 QY 121 KKQRFNINRGWTRGCMSCCRSSRTRETOL 151  
 DB 128 KKQRFNINRGWTRGCMSCCRSSRTRETOL 158

RESULT 7  
 ID ADO44060 standard; protein; 248 AA.  
 XX ADO44060;  
 AC  
 XX  
 DT 15-JUL-2004 (first entry)  
 XX  
 DE Amino acid sequence of an E6E7 fusion protein.  
 XX  
 KM B6 protein; E7 protein; fusion protein; HPV16; HPV-associated cancer;  
 KM cervical cancer; immune response; lower gastrointestinal tract cancer;  
 KM anal cancer; reproductive system cancer; penile cancer; vulvar cancer.  
 XX  
 OS Human papillomavirus type 16.  
 OS Synthetic.  
 OS  
 XX  
 PN MO2004030636-A2.  
 XX  
 PD 15-APR-2004.  
 XX  
 PF 02-OCT-2003; 2003MO-US031726.  
 XX  
 PR 03-OCT-2002; 2002US-0415929P.  
 XX  
 PA (AMHP ) WYETH HOLDINGS CORP.  
 XX  
 PI Smith L, Caserici MC;  
 XX  
 DR WPI; 2004-316328/29.  
 DR N-PSDB; ADO44061.  
 XX  
 XX

PT New polypeptide comprising human papillomavirus E6 and E7 polypeptides,  
 PT useful for treating or preventing human papillomavirus (HPV)-associated  
 PT cancers, e.g. cervical cancer.  
 PT  
 PS Example 1; Page 67-68; 101pp; English.  
 XX

XX The present sequence represents an E6E7 fusion protein, comprising wild  
 CC type E6 and E7 polypeptides from human papillomavirus type 16 (HPV16).  
 CC The specification describes human papillomavirus E6 and E7 polypeptides,  
 CC where the E7 polypeptide has mutations at any one or more of the amino  
 CC acids corresponding to amino acids 24, 26 or 91 of the sequence given in  
 CC ADO44073 and the E6 polypeptide has no mutations or has mutations at any  
 CC one or more of the amino acids corresponding to amino acids 63 or 106 of  
 CC the sequence given in ADO44072. The polypeptides of the invention are  
 CC useful for treating or preventing human papillomavirus (HPV)-associated  
 CC cancers, such as cervical cancer. The fusion proteins and nucleic acids  
 CC encoding the fusion proteins are useful for generating immune responses  
 CC against HPV. They are also useful for treating lower gastrointestinal  
 CC tract cancers, e.g. anal cancer, and other cancers of the reproductive  
 CC system, including penile and vulvar cancer.  
 CC  
 XX

SO Sequence 248 AA;

Query Match 99.5%; Score 826; DB 8; Length 248;  
 Best Local Similarity 98.7%; Pred. No. 7.7e-84;  
 Matches 149; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFQDPOBRPKLPOLCTELQTTTHDIIIECVYCKQQLRREYVDFAFRDLCIYVRDGNPY 60

DB 1 MFQDPOBRPKLPOLCTELQTTTHDIIIECVYCKQQLRREYVDFAFRDLCIYVRDGNPY 60  
 QY 61 AVXDKCLKFKYSKISEYRHYCYSVYGTTLLEQYNNKPLCDLLIRINCINXQKPLCPBEKORHLD 120  
 DB 61 AVCDKCLKFKYSKISEYRHYCYSVYGTTLLEQYNNKPLCDLLIRINCINXQKPLCPBEKORHLD 120  
 QY 121 KKQRFNINRGWTRGCMSCCRSSRTRETOL 151  
 DB 121 KKQRFNINRGWTRGCMSCCRSSRTRETOL 151

RESULT 8  
 ID ADU66364 standard; protein; 151 AA.  
 XX ADU66364;  
 AC  
 XX  
 DT 10-FEB-2005 (first entry)  
 XX  
 DE Human papillomavirus type 16 (HPV16) E6 protein - SEQ ID 5.  
 XX  
 KM vaccine; MHC class I pathway; antigen specific immune response; tumor;  
 KM E7 protein; E6 protein.  
 XX  
 OS Human papillomavirus type 16.  
 OS  
 XX  
 PN MO2004098526-A2.  
 XX  
 PD 18-NOV-2004.  
 XX  
 PF 05-MAY-2004; 2004MO-US013756.  
 XX  
 PR 05-MAY-2003; 2003US-0467602P.  
 XX  
 PA (UYJO ) UNIV JOHNS HOPKINS.  
 XX  
 PI Wu T, Hung CF;  
 XX  
 DR WPI; 2004-813972/80.  
 XX  
 XX

PT New nucleic acid molecules encoding a fusion polypeptide comprising an  
 PT antigen, a signal peptide, and a heat shock protein, useful as a vaccine  
 PT for inducing or enhancing immune response or for inhibiting or preventing  
 PT tumor growth.  
 PT  
 PS Disclosure; SEQ ID NO 5; 67pp; English.  
 XX

CC The invention comprises a nucleic acid molecule (DNA vaccine) that  
 CC encodes a fusion polypeptide which is useful as a vaccine composition.  
 CC The nucleic acid of the invention contains: a first nucleic acid encoding  
 CC a polypeptide that promotes processing via the MHC class I pathway; a  
 CC second sequence encoding a signal peptide; and a third sequence encoding  
 CC an antigenic polypeptide. The DNA vaccine of the invention is useful for  
 CC inducing or enhancing an antigen specific immune response, or to inhibit  
 CC growth or prevent re-growth of a tumor expressing Human papillomavirus  
 CC (HPV) E7 or E6 protein. The present amino acid sequence represents a  
 CC human papillomavirus type 16 (HPV16) E6 protein of the invention.  
 CC  
 XX

SO Sequence 151 AA;

Query Match 99.2%; Score 823; DB 8; Length 151;  
 Best Local Similarity 98.0%; Pred. No. 9.2e-84;  
 Matches 149; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFQDPOBRPKLPOLCTELQTTTHDIIIECVYCKQQLRREYVDFAFRDLCIYVRDGNPY 60  
 DB 1 MFQDPOBRPKLPOLCTELQTTTHDIIIECVYCKQQLRREYVDFAFRDLCIYVRDGNPY 60

QY 61 AVXDKCLKFKYSKISEYRHYCYSVYGTTLLEQYNNKPLCDLLIRINCINXQKPLCPBEKORHLD 120  
 DB 61 AVCDKCLKFKYSKISEYRHYCYSVYGTTLLEQYNNKPLCDLLIRINCINXQKPLCPBEKORHLD 120

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QY      121 KKORFHNIRGRWTCMSCCRSSRTRETOL 151
      |||
      121 KKORFHNIRGRWTCMSCCRSSRTRETOL 151

Db      121 KKORFHNIRGRWTCMSCCRSSRTRETOL 151

RESULT 9
ID AAR22766 standard; peptide; 158 AA.
AAR22766
XX
AC AAR22766;
XX
DT 25-MAR-2003 (revised)
DT 21-SEP-1992 (first entry)
XX
DE HPV E6 peptide.
XX
KM Human; papillomavirus; immunogenic; cervical; warts; carcinoma; cancer.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN MO9205248-A.
XX
PD 02-APR-1992.
XX
PF 26-SEP-1991; 91WO-US007081.
XX
PR 26-SEP-1990; 90US-00588384.
XX
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
PI Thomas EK, Chen L, Blake J, Hellstrom K, Hellstrom I, Hu SL;
DR WPI; 1992-132119/16.
XX
PT Immunogenic peptide(s) derived from E6 or E7 region of HPV16 - and
PT recombinant cells encoding them, useful in treatment and prophylaxis of
PT cervical warts or cancer resulting from HPV infection.
XX
PS Disclosure; Fig 7; 81pp; English.
XX
CC The peptide is the sequence of the human papillomavirus HPV 16 E6
CC nucleoprotein. Peptides corresponding to regions (pref. epitopic regions)
CC of HPV 16 E6 were synthesised by standard Merrifield synthesis. Examples
CC of such peptides are E6 1-20, 8-20, 119-134 or 148-158. Compositions
CC contg. these peptides, antibodies against the peptides, or recombinant
CC cells contg. the gene encoding the immuno- genic peptides may be utilised
CC in methods for inhibiting and treating HPV infection and tumour
CC initiation and progression e.g. in the prevention or retardation of
CC cervical warts and cervical carcinoma resulting from HPV infection. See
CC also AAR22767. (Updated on 25-MAR-2003 to correct PA field.) (Updated on
CC 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 158 AA;

Query Match      99.2%; Score 823; DB 2; Length 158;
Best Local Similarity 98.0%; Pred. No. 9.7e-84;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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AA82462
ID AA82462 standard; protein; 158 AA.
XX
AC AA82462;
XX
DT 30-JUN-2000 (first entry)
XX
DE Human papillomavirus E6 protein containing two zinc finger motifs.
XX
KM Chelated zinc finger; therapeutic; treatment; prophylaxis; HPV;
KM mammalian papillomavirus; antiviral; cytostatic; cervical cancer; lesion;
KM wart.
XX
OS Human papillomavirus.
XX
FH Key Location/Qualifiers
FT Misc-difference 37..73 /note= "forms a zinc finger motif"
FT Misc-difference 110..146 /note= "forms a zinc finger motif"
XX
PN MO200014063-A1.
XX
PD 16-MAR-2000.
XX
PF 03-SEP-1999; 99WO-AU000724.
XX
PR 04-SEP-1998; 98AU-00005733.
PR 15-JUL-1999; 99AU-00001645.
XX
PA (MOLE-) INST MOLECULAR & CELL BIOLOGY.
XX
PI (HUGH/) HUGHES E J L.
XX
PI Bernard H, Tan YJ, Beerheide W, Ting AE, Sim MM;
DR WPI; 2000-256917/22.
XX
PT Polyulfide and dithionosulfide agents, useful for the treatment or
PT prophylaxis of diseases caused by mammalian papillomavirus, are
PT disruptors of a chelated metal cation domain in an MPV gene encoded
PT protein.
XX
PS Disclosure; Fig 1; 78pp; English.
XX
CC The present invention describes an agent used in the treatment or
CC prophylaxis of a disease caused or exacerbated by MPV (mammalian
CC papillomavirus) comprising a compound capable of reducing, inhibiting or
CC otherwise decreasing the activity of a protein encoded by an MPV gene by
CC facilitating disruption of a chelated metal cation domain present in the
CC protein. An agent of the present invention can be used to treat cervical
CC cancer or its HPV associated precursor lesions or other HPV associated
CC cancers and/or warts. The present sequence represents a human
CC papillomavirus E6 protein containing two zinc finger motifs, as given in
CC the exemplification of the present invention
XX
SQ Sequence 158 AA;

Query Match      99.2%; Score 823; DB 3; Length 158;
Best Local Similarity 98.0%; Pred. No. 9.7e-84;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

RESULT 11  
ID AAB98420 standard; protein; 158 AA.  
XX  
AC AAB98420;  
XX  
DT 22-AUG-2001 (first entry)  
XX  
DE Human papillomavirus protein HPV16 E6.  
XX  
KM Human papillomavirus; human leukocyte antigen; HLA; immune response; HPV;  
KM epitope; T cell; identification; vaccine; infection; genital wart;  
KM neoplastic growth; antiviral.  
XX  
OS Human papillomavirus.  
XX  
PN WO20014179-A1.  
XX  
PD 14-JUN-2001.  
XX  
PE 11-DEC-2000; 2000WO-US033549.  
XX  
PR 10-DEC-1999; 99US-0172705P.  
PR 15-AUG-2000; 2000US-00641528.  
XX  
XX (EPIM-) EPIMMUNE INC.  
XX  
PI Sette A, Sidney J, Southwood S, Cheenut R, Celis E, Grey HM;  
XX WPI; 2001-381497/40.  
XX  
PT An isolated human papilloma virus (HPV) epitope, useful in vaccines for  
PT treating HPV infections.  
XX  
XX Disclosure; Page 20-21; 756pp; English.  
XX  
XX The present invention describes an isolated prepared human papillomavirus  
CC (HPV) epitope (I). (I) has antiviral activity, and can be used in vaccine  
CC production. Peptides and corresponding nucleic acid compositions from the  
CC present invention are useful for stimulating an immune response to HPV by  
CC stimulating the production of CTL or HTL responses, specifically in the  
CC treatment or prophylaxis of HPV infection, in persons who have not  
CC manifested symptoms e.g. genital warts or neoplastic growth. The peptides  
CC can also be used in a tetramer staining assay to assess peripheral blood  
CC mononuclear cells for the presence of antigen-specific CTLs following  
CC exposure to a pathogen or immunogen, and as reagents to evaluate immune  
CC recall responses or evaluate the efficacy of a vaccine. The vaccine  
CC compositions are useful for removing warts or treating HPV infections.  
CC The epitopes for inclusion in an epitope-base vaccine may be selected  
CC from conserved regions of viral or tumour-associated antigens, which  
CC reduces the likelihood of escape mutants, also immunosuppressive epitopes  
CC that may be present in whole antigens can be avoided with the use of  
CC epitope-base vaccines. An additional advantage is the ability to combine  
CC selected epitopes (CTL and HTL) and to modify the composition of the  
CC epitopes achieving enhanced immunogenicity, the major benefit of the  
CC vaccine is that is safe and efficacious. AAB98477 represent  
CC polypeptide sequences used in the exemplification of the present  
CC invention  
XX  
SQ Sequence 158 AA;

Query Match 99.2%; Score 823; DB 4; Length 158;  
Best Local Similarity 98.0%; Pred. No. 9.7e-84;  
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFQDPQRRPKLPOLCTELQTTIHDIILCEVCYKQQLLRREVDFAFRDLCIYRRGNPY 60  
DB 8 MFQDPQRRPKLPOLCTELQTTIHDIILCEVCYKQQLLRREVDFAFRDLCIYRRGNPY 67  
QY 61 AYVDCCKLFYSKISEYRHVCYSYVGTTLLEQYNNKPLCDLLIRICINOKPLCPBEKORHLD 120  
DB 68 AVCDCKLFYSKISEYRHVCYSYVGTTLLEQYNNKPLCDLLIRICINOKPLCPBEKORHLD 127

QY 121 KKQRFNIRGRWTRGCMSCCRSSRTRETL 151  
DB 128 KKQRFNIRGRWTRGCMSCCRSSRTRETL 158

RESULT 12  
ID ADF09515 standard; protein; 158 AA.  
XX  
AC ADF09515;  
XX  
DT 12-FEB-2004 (first entry)  
XX  
DE Human papillomavirus 16 B6 SEQ ID NO:16.  
XX  
KM human; protein-protein interaction; virucide; cytostatic; vaccine;  
KM human papilloma virus; HPV; cancer.  
XX  
OS Human papillomavirus.  
XX  
PN WO2003068940-A2.  
XX  
PD 21-AUG-2003.  
XX  
PE 14-FEB-2003; 2003WO-US004594.  
XX  
PR 14-FEB-2002; 2002US-0356911P.  
XX  
XX (CURA-) CURAGEN CORP.  
XX (HOFF) HOFFMANN LA ROCHE INC.  
XX  
PI Jackson A, Ooi CE, Lewin DA, Cuthill S;  
XX WPI; 2003-689668/65.  
XX  
DR N-PSDB; ADF09607.  
XX  
PT New purified complex comprising a first polypeptide and a second  
PT polypeptide, useful for identifying agents for treating/preventing a  
PT condition involving altered level of the complex e.g. human papilloma  
PT virus infection, or cancer.  
XX  
PS Example 3; SEQ ID NO 16; 156pp; English.  
XX  
XX The invention relates to a novel purified complex comprising a first  
CC polypeptide and a second polypeptide, where the polypeptides comprise  
CC defined amino acid sequences listed in the specification, and where the  
CC first polypeptide binds to the second polypeptide. A complex of the  
CC invention has virucide and cytostatic activity, and may have a use as a  
CC vaccine. The complex is useful for identifying agents for treating or  
CC preventing a conditions involving altered level of the complex, e.g.  
CC human papilloma virus (HPV) infection, or cancer. The compositions,  
CC antibodies, vectors and methods are useful for treating such diseases.  
CC The sequences shown in ADF09500-ADF09583 represent proteins of the  
CC invention.  
XX  
SQ Sequence 158 AA;

Query Match 99.2%; Score 823; DB 7; Length 158;  
Best Local Similarity 98.0%; Pred. No. 9.7e-84;  
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFQDPQRRPKLPOLCTELQTTIHDIILCEVCYKQQLLRREVDFAFRDLCIYRRGNPY 60  
DB 8 MFQDPQRRPKLPOLCTELQTTIHDIILCEVCYKQQLLRREVDFAFRDLCIYRRGNPY 67  
QY 61 AYVDCCKLFYSKISEYRHVCYSYVGTTLLEQYNNKPLCDLLIRICINOKPLCPBEKORHLD 120  
DB 68 AVCDCKLFYSKISEYRHVCYSYVGTTLLEQYNNKPLCDLLIRICINOKPLCPBEKORHLD 127  
QY 121 KKQRFNIRGRWTRGCMSCCRSSRTRETL 151  
DB 128 KKQRFNIRGRWTRGCMSCCRSSRTRETL 158

RESULT 13  
ADU66363 standard; protein, 158 AA.  
XX  
AC ADU66363;  
XX  
DT 10-FEB-2005 (first entry)  
XX  
DE Human papillomavirus type 16 (HPV16) E6 protein - SEQ ID 4.  
XX  
KM vaccine; MHC class I pathway; antigen specific immune response; tumor;  
KM E7 protein; E6 protein.  
XX  
OS Human papillomavirus type 16.  
XX  
PN MO2004098526-A2.  
XX  
PD 18-NOV-2004.  
XX  
PF 05-MAY-2004; 2004MO-US013756.  
XX  
PR 05-MAY-2003; 2003US-0467602P.  
XX  
PA (UYJO ) UNIV JOHNS HOPKINS.  
XX  
PI Wu T, Hung CF;  
XX  
DR WPI; 2004-813972/80.  
XX  
PT New nucleic acid molecules encoding a fusion polypeptide comprising an  
PT antigen, a signal peptide, and a heat shock protein, useful as a vaccine  
PT for inducing or enhancing immune response or for inhibiting or preventing  
PT tumor growth.  
XX  
PS Claim 11; SEQ ID NO 4; 67pp; English.  
XX  
CC The invention comprises a nucleic acid molecule (DNA vaccine) that  
CC encodes a fusion polypeptide which is useful as a vaccine composition.  
CC The nucleic acid of the invention contains: a first nucleic acid encoding  
CC a polypeptide that promotes processing via the MHC class I pathway; a  
CC second sequence encoding a signal peptide; and a third sequence encoding  
CC an antigenic polypeptide. The DNA vaccine of the invention is useful for  
CC inducing or enhancing an antigen specific immune response, or to inhibit  
CC growth or prevent re-growth of a tumor expressing Human papillomavirus  
CC (HPV) E7 or E6 protein. The present amino acid sequence represents a  
CC human papillomavirus type 16 (HPV16) E6 protein of the invention.  
XX  
SQ Sequence 158 AA;  
Query Match 99.2%; Score 823; DB 8; Length 158;  
Best Local Similarity 98.0%; Pred. No. 9.7e-84;  
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 MFODPOBRPRKLPOLCTELQTTIHDIILECVYCKQQLLRREYVDFAFRDLCTIYRDGNPY 60  
DB 8 MFODPOBRPRKLPOLCTELQTTIHDIILECVYCKQQLLRREYVDFAFRDLCTIYRDGNPY 67  
QY 61 AVXDCKLKFYSKISEYRHYCYSVYGTTLBEQYNNKPLCDLLIRICINXOKPLCPBEKQRHLD 120  
DB 68 AVCDCKLKFYSKISEYRHYCYSLYGTTLBEQYNNKPLCDLLIRICINXOKPLCPBEKQRHLD 127  
QY 121 KKOBFNIRGRWTRGCMSCCRSSRTRETOL 151  
DB 128 KKOBFNIRGRWTRGCMSCCRSSRTRETOL 158  
RESULT 14  
AEA40817 standard; protein, 158 AA.  
XX  
AC AEA40817;

XX  
DT 28-JUL-2005 (first entry)  
XX  
DE Anti-apoptotic vector HPV E6 antigenic protein, SEQ ID 7.  
XX  
KM immunogenicity; immunogenicity-potentiating polypeptide; IPP; T-cell;  
KM vaccine; immune stimulation; tumor; cytostatic.  
XX  
OS Human papillomavirus - 16.  
XX  
PN MO2005047501-A1.  
XX  
PD 26-MAY-2005.  
XX  
PF 24-FEB-2004; 2004MO-US005292.  
XX  
PR 24-FEB-2003; 2003US-0449429P.  
PR 18-JUL-2003; 2003US-0488527P.  
PR 31-DEC-2003; 2003US-0533792P.  
XX  
PA (UYJO ) UNIV JOHNS HOPKINS.  
XX  
PI Wu T, Hung CF, Kim T;  
XX  
DR WPI; 2005-367009/37.  
DR GENBANK; NC\_001526.  
XX  
PT New nucleic acid composition comprising a first nucleic acid vector  
PT encoding an anti-apoptotic polypeptide, useful as an immunogen for  
PT inhibiting the growth of a tumor.  
XX  
PS Disclosure; SEQ ID NO 7; 158pp; English.  
XX  
CC The invention relates to a novel nucleic acid composition useful as an  
CC immunogen. The composition comprises a combination of: a first nucleic  
CC acid vector comprising a first sequence encoding an antigenic polypeptide  
CC or peptide, and optionally, a second sequence linked to the first  
CC sequence and encoding an immunogenicity-potentiating polypeptide (IPP);  
CC and a second nucleic acid vector encoding an anti-apoptotic polypeptide.  
CC When the second vector is administered with the first vector to a  
CC subject, a T cell mediated immune response to the antigenic polypeptide  
CC or peptide is induced that is greater in magnitude and/or duration than  
CC an immune response induced by administration of the first vector alone.  
CC The invention further includes: a particle comprising a material that is  
CC suitable for introduction into a cell or an animal by particle  
CC bombardment, bound to which is the first and second vectors or  
CC composition; a pharmaceutical composition capable of inducing or  
CC enhancing an antigen specific immune response, comprising the particle  
CC and a carrier or an excipient; inducing or enhancing an antigen specific  
CC immune response in a subject; increasing the numbers of CD8+ CTLs  
CC specific for a selected desired antigen in a subject; and inhibiting the  
CC growth of a tumor in a subject. The nucleic acid composition is useful as  
CC an immunogen for inhibiting the growth of a tumor, hence it has  
CC cytostatic activity. This sequence represents an anti-apoptotic vector HPV  
CC E6 antigenic protein of the invention.  
XX  
SQ Sequence 158 AA;  
Query Match 99.2%; Score 823; DB 9; Length 158;  
Best Local Similarity 98.0%; Pred. No. 9.7e-84;  
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 MFODPOBRPRKLPOLCTELQTTIHDIILECVYCKQQLLRREYVDFAFRDLCTIYRDGNPY 60  
DB 8 MFODPOBRPRKLPOLCTELQTTIHDIILECVYCKQQLLRREYVDFAFRDLCTIYRDGNPY 67  
QY 61 AVXDCKLKFYSKISEYRHYCYSVYGTTLBEQYNNKPLCDLLIRICINXOKPLCPBEKQRHLD 120  
DB 68 AVCDCKLKFYSKISEYRHYCYSLYGTTLBEQYNNKPLCDLLIRICINXOKPLCPBEKQRHLD 127  
QY 121 KKOBFNIRGRWTRGCMSCCRSSRTRETOL 151

Db 128 KKORFNHNRGRMTGRCMSCCRSRTRETL 158

RESULT 15  
AEA98532 standard; protein; 158 AA.  
ID AEA98532  
XX  
AC AEA98532;  
XX  
DT 08-SEP-2005 (first entry)  
XX  
DE HPV (oncogenic strain) E6 amino acid sequence SEQ ID 13.  
XX  
KM Papillomavirus infection; virucide; E6 protein; diagnosis; antibody;  
KW cancer; cervix tumor; cytostatic.  
XX  
OS Human papillomavirus type 16.  
XX  
PN US2005142541-A1.  
XX  
PD 30-JUN-2005.  
XX  
PF 23-DEC-2004; 2004US-00021949.  
XX  
PR 23-DEC-2003; 2003US-0532373P.  
XX  
PA (ARBO-) ARBOR VITA CORP.  
XX  
PI Lu PS, Garman JD, Belmares MP, Somoza DC, Schweizer J;  
XX  
DR WPI; 2005-45781/46.  
XX  
PT New antibody composition comprising a mixture of monoclonal antibodies  
PT for oncogenic strains of human papilloma virus, useful for diagnosing  
PT cancer.  
XX  
PS Disclosure; SEQ ID NO 13; 161pp; English.

CC The invention relates to an antibody composition comprising a mixture of  
CC monoclonal antibodies that specifically bind to E6 proteins of human  
CC papilloma virus (HPV) strains 16, 18, 31, 33 and 45, where at least one  
CC of the monoclonal antibodies specifically binds to E6 proteins of at  
CC least three different oncogenic HPV strains. Also included are a  
CC diagnostic kit (for detecting an HPV E6 polypeptide in a sample,  
CC comprising the antibody composition above), a method of detecting an HPV  
CC E6 protein in a sample, a method of detecting the presence of an  
CC oncogenic HPV E6 protein in a sample and a system for detecting the  
CC presence of an oncogenic HPV E6 polypeptide in a sample (comprising a  
CC first and a second binding partner for an oncogenic HPV E6 polypeptide,  
CC where the first binding partner is a pDZ domain protein and the second  
CC binding partner is an antibody that specifically binds to the E6 proteins  
CC of at least three different oncogenic HPV strains). The antibody  
CC composition, kit, methods, and system are useful for diagnosing cancer,  
CC particularly cervical cancer. The present sequence is an HPV E6 protein.  
XX  
SQ Sequence 158 AA;

Query Match 99.2%; Score 823; DB 9; Length 158;  
Best Local Similarity 98.0%; Pred. No. 9,7e-84;  
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFQDDPQRPRLPOLCTELQTTIHDIILCEVCYKQQLLRREYDFAFRDLCIYRGDNPY 60  
Db 8 MFQDDPQRPRLPOLCTELQTTIHDIILCEVCYKQQLLRREYDFAFRDLCIYRGDNPY 67

QY 61 AYVDCIKLKFYSKISEYRHVCYSYGTLLBOQYNKPLCDLIRINCINOKPLCPBEKQRLD 120  
Db 68 AYVDCIKLKFYSKISEYRHVCYSYGTLLBOQYNKPLCDLIRINCINOKPLCPBEKQRLD 127

QY 121 KKORFNHNRGRMTGRCMSCCRSRTRETL 151  
Db 128 KKORFNHNRGRMTGRCMSCCRSRTRETL 158

RESULT 16  
AEB11990 standard; protein; 158 AA.  
ID AEB11990  
XX  
AC AEB11990;  
XX  
DT 08-SEP-2005 (first entry)  
XX  
DE HPV16 E6 protein.  
XX  
KM Tumor-associated antigen; vaccine; papilloma; cytostatic; neoplasm;  
KW cancer; HPV16 E6.  
XX  
OS Human papillomavirus type 16.  
XX  
PN WO2005060993-A1.  
XX  
PD 07-JUL-2005.  
XX  
PF 24-DEC-2003; 2003WO-NL000929.  
XX  
PR 24-DEC-2003; 2003WO-NL000929.  
XX  
PA (UYLE-) UNIV LEIDEN MEDICAL CENT.  
XX  
PI Van Der Burg SH, Drijfhout JW;  
XX  
DR WPI; 2005-497704/50.  
XX  
PT Producing a synthetic protein of a pathogen or tumor comprises chemically  
PT synthesizing two or more fragments of 2-80 contiguous amino acids of  
PT sequence, the sequence of two or more fragments are neighboring and non-  
PT overlapping.  
XX  
PS Claim 11; SEQ ID NO 2; 53pp; English.

CC The invention relates to a method of producing a synthetic protein  
CC comprising an amino acid sequence that is at least 80% identical to a  
CC naturally occurring antigenic protein of a pathogen or tumor comprising  
CC chemically synthesizing two or more fragments, chemically ligating the C-  
CC termini of a fragment to the N-terminus of a neighboring fragment to  
CC produce the synthetic protein or its part and optionally repeating the  
CC second step to sequentially ligate a further neighboring fragment  
CC obtained from the second step. The invention also relates to a  
CC composition comprising the protein and a method for treating or  
CC preventing human papillomavirus (HPV) associated disease by administering  
CC to the subject the protein or composition in a therapeutically effective  
CC amount. In producing a synthetic protein, the neighboring non-overlapping  
CC fragments are selected to comprise N-terminal cysteine or glycine  
CC residues. The naturally occurring protein is an HPV protein, e.g. E2, E6  
CC or E7 protein from HPV16, HPV18, HPV31, HPV33 or HPV45. The composition  
CC further comprises an anti-CD40 antibody. The composition is useful as a  
CC vaccine for preventing or treating HPV associated disease, such as  
CC cancer. This sequence represents an HPV16 E6 protein used in the method  
CC of the invention.  
XX  
SQ Sequence 158 AA;

Query Match 99.2%; Score 823; DB 9; Length 158;  
Best Local Similarity 98.0%; Pred. No. 9,7e-84;  
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFQDDPQRPRLPOLCTELQTTIHDIILCEVCYKQQLLRREYDFAFRDLCIYRGDNPY 60  
Db 8 MFQDDPQRPRLPOLCTELQTTIHDIILCEVCYKQQLLRREYDFAFRDLCIYRGDNPY 67

QY 61 AYVDCIKLKFYSKISEYRHVCYSYGTLLBOQYNKPLCDLIRINCINOKPLCPBEKQRLD 120  
Db 68 AYVDCIKLKFYSKISEYRHVCYSYGTLLBOQYNKPLCDLIRINCINOKPLCPBEKQRLD 127

QY 121 KKORFNHNRGRMTGRCMSCCRSRTRETL 151  
Db 128 KKORFNHNRGRMTGRCMSCCRSRTRETL 158

Db 128 KKORFHNIRGRWTCRMCSSRSRTRETQL 158

RESULT 17  
AEC98863  
ID AEC98863 standard; protein; 158 AA.  
AC AEC98863;  
XX  
DT 01-DEC-2005 (first entry)  
XX  
DE HPV\_16 Envelope protein E6.  
XX  
KW Human papilloma virus infection; virucide; cancer; cytostatic; vaccine;  
KW epitope mapping; immune stimulation; cytotoxic T-lymphocyte.  
XX  
OS Human papillomavirus type 16.  
PN WO2005089164-A2.  
PD 29-SEP-2005.  
PF 03-JAN-2005; 2005WO-US000077.  
XX  
PR 31-DEC-2003; 2003US-0533211P.  
PR 02-JUL-2004; 2004US-0584652P.  
XX  
PA (EPIM-) EPIMMUNE INC.  
PA (INNO-) INNOGENETICS NV.  
PA (CHES/) CHESNUT R.  
PA (NEMM/) NEWMAN M J.  
PA (MOTH/) MOTHE B.  
PA (BAKE/) BAKER D.  
PA (SOUT/) SOUTHWOOD S.  
PA (BABE/) BABE L M.  
PA (CHEN/) CHEN Y.  
PA (DEYO/) DEYOUNG L M.  
PA (HUAN/) HUANG M T F.  
PA (POME/) POWER S D.  
XX  
PI Chesnut R, Newman MJ, Mothe B, Baker D, Southwood S, Babe LM;  
PI Chen Y, Deyoung LM, Huang MTF, Power SD;  
DR WPI: 2005-658982/67.  
XX  
PT New polynucleotide comprises a multi-epitope construct comprising nucleic  
PT acids encoding the human papillomavirus (HPV) cytotoxic T lymphocyte  
PT (CTL) epitopes, useful in preparing a vaccine against HPV.  
XX  
XX Example 10; Page 349; 518pp; English.  
PS  
CC The invention relates to a new polynucleotide comprising a multi-epitope  
CC construct comprising nucleic acids encoding the human papillomavirus  
CC (HPV) cytotoxic T lymphocyte (CTL) epitopes e.g., HPV16.E1.214, and that  
CC are directly or indirectly joined to one another in the same reading  
CC frame, a vaccine minigene. Also included are a vector comprising the  
CC multi-epitope construct, a polypeptide comprising an amino acid sequence  
CC encoded by the polynucleotide, a composition (comprising the  
CC polynucleotide, vector and/or polypeptide and a carrier), a cell  
CC (comprising the polynucleotide, vector or polypeptide), inducing an  
CC immune response against human papillomavirus virus (HPV) and making the  
CC polynucleotide, vector or polypeptide. The epitopes are derived from  
CC different strains of HPV and are from the E1, E2, E6 and E7 proteins. The  
CC epitopes may be linked via a GP-anchor/spacer peptide. The order of the  
CC epitopes in the vaccine protein are disclosed in the tables referred to  
CC in the claims of the specification. The polynucleotide, vector or  
CC polypeptide is useful in preparing a composition for inducing an immune  
CC response against human papillomavirus virus (HPV) and thus providing a  
CC defense against HPV infection and HPV-related cancers. The present  
CC sequence is an HPV protein used to derive epitopes for the vaccine of the  
CC invention.  
XX  
SQ Sequence 158 AA;

Query Match 99.2%; Score 823; DB 9; Length 158;  
Best Local Similarity 98.0%; Pred. No. 9,7e-84;  
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MFODPQRPRLPOLCTELQTTIHDIILECVCKQQLREVVDFAFRDLCTIVRDGPNY 60  
Db 8 MFODPQRPRLPOLCTELQTTIHDIILECVCKQQLREVVDFAFRDLCTIVRDGPNY 67  
Qy 61 AYADKCLKFYSKISEYHYCYSVYGTLLBOQYKPLCDLLIRCNXKPLCPBEKQRLD 120  
Db 68 AVCDCCLKFYSKISEYHYCYSLYGTLLBOQYKPLCDLLIRCNXKPLCPBEKQRLD 127  
Qy 121 KKORFHNIRGRWTCRMCSSRSRTRETQL 151  
Db 128 KKORFHNIRGRWTCRMCSSRSRTRETQL 158

RESULT 18  
AEC96391  
ID AEC96391 standard; protein; 158 AA.  
AC AEC96391;  
XX  
DT 01-DEC-2005 (first entry)  
XX  
DE HPV protein E6 from HPV16.  
XX  
KW Human papilloma virus infection; virucide; cancer; cytostatic; vaccine;  
KW epitope mapping; immune stimulation; cytotoxic T-lymphocyte.  
XX  
OS Human papillomavirus type 16.  
PN WO2005089164-A2.  
PD 29-SEP-2005.  
PF 03-JAN-2005; 2005WO-US000077.  
XX  
PR 31-DEC-2003; 2003US-0533211P.  
PR 02-JUL-2004; 2004US-0584652P.  
XX  
PA (EPIM-) EPIMMUNE INC.  
PA (INNO-) INNOGENETICS NV.  
PA (CHES/) CHESNUT R.  
PA (NEMM/) NEWMAN M J.  
PA (MOTH/) MOTHE B.  
PA (BAKE/) BAKER D.  
PA (SOUT/) SOUTHWOOD S.  
PA (BABE/) BABE L M.  
PA (CHEN/) CHEN Y.  
PA (DEYO/) DEYOUNG L M.  
PA (HUAN/) HUANG M T F.  
PA (POME/) POWER S D.  
XX  
PI Chesnut R, Newman MJ, Mothe B, Baker D, Southwood S, Babe LM;  
PI Chen Y, Deyoung LM, Huang MTF, Power SD;  
DR WPI: 2005-658982/67.  
XX  
PT New polynucleotide comprises a multi-epitope construct comprising nucleic  
PT acids encoding the human papillomavirus (HPV) cytotoxic T lymphocyte  
PT (CTL) epitopes, useful in preparing a vaccine against HPV.  
XX  
XX Disclosure; Page 56; 518pp; English.  
PS  
CC The invention relates to a new polynucleotide comprising a multi-epitope  
CC construct comprising nucleic acids encoding the human papillomavirus  
CC (HPV) cytotoxic T lymphocyte (CTL) epitopes e.g., HPV16.E1.214, and that  
CC are directly or indirectly joined to one another in the same reading  
CC frame, a vaccine minigene. Also included are a vector comprising the  
CC multi-epitope construct, a polypeptide comprising an amino acid sequence  
CC encoded by the polynucleotide, a composition (comprising the

CC polynucleotide, vector and/or polypeptide and a carrier), a cell  
 CC (comprising the polynucleotide, vector or polypeptide), inducing an  
 CC immune response against human papillomavirus virus (HPV) and making the  
 CC polynucleotide, vector or polypeptide. The epitopes are derived from  
 CC different strains of HPV and are from the E1, E2, E6 and E7 proteins. The  
 CC epitopes may be linked via a GP-anchor/spacer peptide. The order of the  
 CC epitopes in the vaccine protein are disclosed in the tables referred to  
 CC in the claims of the specification. The polynucleotide, vector or  
 CC polypeptide is useful in preparing a composition for inducing an immune  
 CC response against human papillomavirus virus (HPV) and thus providing a  
 CC defense against HPV infection and HPV-related cancers. The present  
 CC sequence is an HPV protein used to derive epitopes for the vaccine of the  
 CC invention.

XX SQ Sequence 158 AA;

Query Match 99.2%; Score 823; DB 9; Length 158;  
 Best Local Similarity 98.0%; Pred. No. 9.7e-84;  
 Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFQDDPQPRPKLPTQLCTELQTTTHDIIIECVYCKQQLRREYVDFAFRDLCTIYRDGNPY 60  
 DB 8 MFQDDPQPRPKLPTQLCTELQTTTHDIIIECVYCKQQLRREYVDFAFRDLCTIYRDGNPY 67

QY 61 AAVDKCLKFYSKI SEVRHYCYSVYGTLEQQYNKPLCDLLIRICINXOKPLCPBEKORHLD 120  
 DB 68 AAVDKCLKFYSKI SEVRHYCYSVYGTLEQQYNKPLCDLLIRICINXOKPLCPBEKORHLD 127

QY 121 KKQRFNIRGRMTGRCMSCCRSSRTRETQL 151  
 DB 128 KKQRFNIRGRMTGRCMSCCRSSRTRETQL 158

RESULT 19  
 AEF88520  
 ID AEF88520 standard; protein; 158 AA.  
 XX AEF88520;  
 AC AEF88520;  
 DT 20-APR-2006 (first entry)  
 DE Human papillomavirus type 16 (HPV16) E7 protein.  
 XX  
 XX Vaccine; gene therapy; papillomavirus infection; virucide; infection;  
 KM uterine cervix tumor; cytostatic; gynecology and obstetrics; neoplasm;  
 KM lung tumor; respiratory disease; E7 protein.  
 XX  
 XX Human papillomavirus type 16.  
 OS  
 XX  
 XX US2006039919-A1.  
 PN  
 XX  
 PD 23-FEB-2006.  
 XX  
 PF 18-AUG-2005; 2005US-00206138.  
 XX  
 PR 20-AUG-2004; 2004TW-00125128.  
 XX  
 PA (HEAL-) HEALTHBANKS BIOTECH CO LTD.  
 XX  
 PI Chang H, Liao C, Cheng W;  
 XX  
 DR WPI; 2006-172399/18.  
 XX  
 PT New fusion protein comprising E7 peptide sequence of human papillomavirus  
 PT type 16, useful for inhibiting or preventing cancer, e.g. cervical or  
 PT lung cancer.  
 XX  
 PS Claim 4; SEQ ID NO 3; 19pp; English.  
 XX  
 CC The present invention relates to novel fusion protein for inhibiting or  
 CC preventing cancer induced by human papillomavirus type 16 (HPV16). The  
 CC fusion protein comprises an E7 peptide sequence of human papillomavirus  
 CC type 16, a translocating peptide for translocation and a peptide fragment

CC having a carboxyl terminal section. The fusion protein of the invention  
 CC is useful as vaccines and for inhibiting or preventing human  
 CC papillomavirus infection and cancers such as cervical and lung cancer.  
 CC The invention is useful in gene therapy. The present sequence is the  
 CC human papillomavirus type 16 (HPV16) E7 protein.

XX SQ Sequence 158 AA;

Query Match 99.2%; Score 823; DB 10; Length 158;  
 Best Local Similarity 98.0%; Pred. No. 9.7e-84;  
 Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFQDDPQPRPKLPTQLCTELQTTTHDIIIECVYCKQQLRREYVDFAFRDLCTIYRDGNPY 60  
 DB 8 MFQDDPQPRPKLPTQLCTELQTTTHDIIIECVYCKQQLRREYVDFAFRDLCTIYRDGNPY 67

QY 61 AAVDKCLKFYSKI SEVRHYCYSVYGTLEQQYNKPLCDLLIRICINXOKPLCPBEKORHLD 120  
 DB 68 AAVDKCLKFYSKI SEVRHYCYSVYGTLEQQYNKPLCDLLIRICINXOKPLCPBEKORHLD 127

QY 121 KKQRFNIRGRMTGRCMSCCRSSRTRETQL 151  
 DB 128 KKQRFNIRGRMTGRCMSCCRSSRTRETQL 158

RESULT 20  
 AAM35741  
 ID AAM35741 standard; protein; 162 AA.  
 XX AAM35741;  
 AC AAM35741;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 16-FEB-1998 (first entry)  
 DE Human papillomavirus type 16 B6 protein.  
 XX  
 XX Complete genome; circular; human papillomavirus type 16; HPV16 E6;  
 KM cervical dysplasia; cervical cancer; cervical smear.  
 XX  
 XX Human papillomavirus type 16.  
 OS  
 XX  
 XX Key Location/Qualifiers  
 FH MISC-difference 90  
 FT MISC-difference 158 /note= "Mutated to Val in the variant"  
 FT MISC-difference 158 /note= "End of protein sequence even though 3 amino acid  
 FT residues are given following on"  
 XX  
 XX US5679509-A.  
 PN  
 XX  
 PD 21-OCT-1997.  
 XX  
 PF 30-SEP-1994; 94US-00316239.  
 XX  
 PR 28-SEP-1993; 93US-00127906.  
 XX  
 PA (UNIV-) UNIV NEW MEXICO STATE.  
 XX  
 PI Wheeler CM, Parmenter CA;  
 XX  
 DR WPI; 1997-525714/48.  
 DR N-PSDB; AAT94723.  
 XX  
 PT Evaluating risk of cervical dysplasia or cervical cancer - by detecting  
 PT variant form of human papilloma virus 16.  
 XX  
 PS Claim 7; Col 23-24; 33pp; English.  
 XX  
 CC Methods have been developed for distinguishing a subset of human  
 CC papilloma virus (HPV) that is associated with an increased risk of  
 CC developing cervical dysplasia or cervical cancer. The methods involve:  
 CC (1) preparing a cervical sample to expose any HPV-16 E6 gene in the  
 CC sample and determining if the base at position 350 of the E6 gene (see

CC AAT94723 and AAT94724 for comparison) is T or G, where the presence of G  
 CC at position 350 is associated with an increased risk of developing  
 CC cervical dysplasia or cervical cancer; and (2) preparing a cervical  
 CC sample to expose any HPV-16 E6 protein in the sample and determining if  
 CC the amino acid at position 83 of the protein (see position 90 in AAM35741  
 CC and AAM35742 for comparison) is Val or Leu, where the presence of Val at  
 CC position 83 that is associated with an increased risk of developing  
 CC cervical dysplasia or cervical cancer. The present sequence represents  
 CC the reference protein sequence for HPV-16 E6. The 3506 variant correlates  
 CC well with Pap scores: 3507:3506 ratios among 45 HPV16 samples were 10:4  
 CC for negative Pap scores; 4:2 for CIN I, 1:6 for CIN II; 2:9 for CIN III;  
 CC 0:3 for cancer. (Updated on 25-MAR-2003 to correct PF field.)

XX Sequence 162 AA;

Query Match 99.2%; Score 823; DB 2; Length 162;  
 Best Local Similarity 98.0%; Pred. No. 1e-83;  
 Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFQDPQERPRKLPOLCTELQTTIHDIILECYCKQQLRREYVDFARFDLCIVYRDGNPY 60  
 DB 8 MFQDPQERPRKLPOLCTELQTTIHDIILECYCKQQLRREYVDFARFDLCIVYRDGNPY 67  
 QY 61 AVXDCKLKFYSKISEYRHVCYSVYGTLEQYNNKPLCDLLIRICINXQKPLCPBEKQRLHD 120  
 DB 68 AVCDCKLKFYSKISEYRHVCYSVYGTLEQYNNKPLCDLLIRICINQKPLCPBEKQRLHD 127  
 QY 121 KKQRFHNIRGRWTRGCMSCCRSSRTRETQL 151  
 DB 128 KKQRFHNIRGRWTRGCMSCCRSSRTRETQL 158

RESULT 21

AAO22922 AAO22922 standard; protein; 171 AA.

XX AAO22922;

DT 12-DEC-2002 (first entry)

XX Human papillomavirus-16 (HPV16) E6T-protein sequence.

XX Virucide; cytostatic; E6; E7 fusion protein; HPV; immunogenic; vaccine;  
 KM fusion partner; immunogenicity; HPV infection; neoplasm; HPV16;  
 KM human papillomavirus-16; E6T-sequence.

XX Human papillomavirus.

XX EPI243655-A1.

XX EPI243655-A1.

XX 25-SEP-2002.

XX 23-MAR-2001; 2001EP-00107271.

XX 23-MAR-2001; 2001EP-00107271.

XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

XX Cid-Atregui A, Zur Hausen H;

XX WPI; 2002-724952/79.

XX N-PSDB; AAL53420.

XX A new DNA sequence encoding a fusion protein comprising a mutagenized HPV  
 PT (human papillomavirus) E6 or E7 coding sequence and a sequence encoding a  
 PT highly immunogenic fusion partner is useful to vaccinate against HPV  
 XX infection.

XX Disclosure; Fig 2; 34pp; English.

XX The invention relates to a new DNA sequence encodes an E6 or E7 fusion  
 CC protein of HPV, where at least 20% of the original codons are replaced by  
 CC codons which lead to enhanced translation in a mammalian cell, containing

CC a mutation which results in production of a truncated non-functional  
 CC protein, and encoding a highly immunogenic polypeptide fusion partner  
 CC capable of enhancing immunogenicity of the E6 or E7 protein in the  
 CC mammalian host. The invention is used as a vaccine for the prevention or  
 CC treatment of an HPV infection or a neoplasm associated with HPV  
 CC infection. This sequence represents the human papillomavirus-16 (HPV16)  
 CC E6T-protein sequence of the invention

XX Sequence 171 AA;

Query Match 99.2%; Score 823; DB 5; Length 171;  
 Best Local Similarity 98.0%; Pred. No. 1.1e-83;  
 Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFQDPQERPRKLPOLCTELQTTIHDIILECYCKQQLRREYVDFARFDLCIVYRDGNPY 60  
 DB 13 MFQDPQERPRKLPOLCTELQTTIHDIILECYCKQQLRREYVDFARFDLCIVYRDGNPY 72  
 QY 61 AVXDCKLKFYSKISEYRHVCYSVYGTLEQYNNKPLCDLLIRICINXQKPLCPBEKQRLHD 120  
 DB 73 AVCDCKLKFYSKISEYRHVCYSVYGTLEQYNNKPLCDLLIRICINQKPLCPBEKQRLHD 132  
 QY 121 KKQRFHNIRGRWTRGCMSCCRSSRTRETQL 151  
 DB 133 KKQRFHNIRGRWTRGCMSCCRSSRTRETQL 163

RESULT 22

AAE63865 AAE63865 standard; protein; 188 AA.

XX AAE63865;

XX 16-OCT-2003 (revised)

DT 25-MAR-2003 (revised)

DT 28-JUN-1995 (first entry)

XX HPV16 E6/E7 proteins.

XX HPV; HPV16; E6 protein; E7 protein; diagnosis; cervical dysplasia;  
 KM cervix cancer.

XX Human papillomavirus; strain 16.

XX Key Location/Qualifiers

FT Protein 1..158

FT Protein /label= B6\_protein

FT Protein /label= E7\_protein

XX W09426934-A2.

XX 24-NOV-1994.

XX 06-MAY-1994; 94WO-US005085.

XX 06-MAY-1993; 93US-00058920.

XX (BAKT ) BAXTER DIAGNOSTICS INC.

XX Brown JT;

XX WPI; 1995-006821/01.

XX P-PSDB; AAQ75470.

XX Human papilloma virus detection assay - by amplification using self  
 PT sustained sequence replication and hybridisation with a detector probe.

XX Disclosure; Page 24-26; 79pp; English.

XX The sequences of the E6 and E7 polypeptide-encoding regions of human  
 CC papillomavirus (HPV) 16 and 18 are given in AAQ75470-71 and the encoded  
 CC proteins in AAE63865-66, respectively. Probes and primers based on these

CC sequences were used for HPV infection diagnosis; expression of E6 and E7  
 CC is diagnostic for cervical cancer or pre-malignant states. (Updated on  
 CC 25-MAR-2003 to correct PN field.) (Updated on 16-OCT-2003 to standardise  
 CC OS field)  
 CC  
 XX  
 SQ Sequence 188 AA;

Query Match 99.2%; Score 823; DB 2; Length 188;  
 Best Local Similarity 98.0%; Pred. No. 1,2e-83;  
 Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFQDPOERPRKLPOLCTELQTTIHDIILECYCKQQLLRREVDFAPRDLCTIVRDGNPY 60  
 DB 8 MFQDPOERPRKLPOLCTELQTTIHDIILECYCKQQLLRREVDFAPRDLCTIVRDGNPY 67  
 QY 61 AVXDKCLKFYSKISEYHVCYVGTTLBOQYNKPLCDLLIRGINXOKPLCPBEKORHLD 120  
 DB 68 AVCDKCLKFYSKISEYHVCYVGTTLBOQYNKPLCDLLIRGINXOKPLCPBEKORHLD 127  
 QY 121 KQRFHNIRGRWGRGCMSCCRSSRTRETOL 151  
 DB 128 KQRFHNIRGRWGRGCMSCCRSSRTRETOL 158

RESULT 23  
 ADO44068  
 ID ADO44068 standard; protein; 248 AA.  
 XX  
 AC ADO44068;  
 XX  
 DT 15-JUL-2004 (first entry)  
 XX  
 DE Amino acid sequence of a fusion protein designated E7E6trem.

XX E6 protein; E7 protein; fusion protein; HPV16; HPV-associated cancer;  
 KM cervical cancer; immune response; lower gastrointestinal tract cancer;  
 KM anal cancer; reproductive system cancer; penile cancer; vulvar cancer.  
 XX Human papillomavirus type 16.  
 OS Synthetic.  
 XX  
 PN WO2004030636-A2.  
 XX  
 PD 15-APR-2004.  
 XX  
 PF 02-OCT-2003; 2003WO-US031726.  
 XX  
 PR 03-OCT-2002; 2002US-0415929P.  
 XX  
 PA (AMHP) WYETH HOLDINGS CORP.  
 XX  
 PI Smith L, Casasetti MC;  
 XX  
 DR WPI; 2004-316328/29.  
 DR N-PSDB; ADO44069.

PT New polypeptide comprising human papillomavirus E6 and E7 polypeptides,  
 PT useful for treating or preventing human papillomavirus (HPV)-associated  
 PT cancers, e.g. cervical cancer.  
 XX  
 PS Claim 22; Page 73-74; 101pp; English.

XX The present sequence represents a fusion protein, comprising E7 and E6  
 CC polypeptides from human papillomavirus type 16 (HPV16). The fusion  
 CC protein is designated E7E6trem, and comprises an E7 amino terminus (where  
 CC residues 24 and 26 have been replaced with glycine) and an E6 carboxy  
 CC terminus (where residues 63 and 106 have been replaced with glycine).  
 CC E7E6trem is representative of fusion proteins of the invention. The  
 CC specification describes human papillomavirus E6 and E7 polypeptides,  
 CC where the E7 polypeptide has mutations at any one or more of the amino  
 CC acids corresponding to amino acids 24, 26 or 91 of the sequence given in  
 CC ADO44073 and the E6 polypeptide has no mutations or has mutations at any  
 CC one or more of the amino acids corresponding to amino acids 63 or 106 of

CC there sequence given in ADO44072. The polypeptides of the invention are  
 CC useful for treating or preventing human papillomavirus (HPV)-associated  
 CC cancers, such as cervical cancer. The fusion proteins and nucleic acids  
 CC encoding the fusion proteins are useful for generating immune responses  
 CC against HPV. They are also useful for treating lower gastrointestinal  
 CC tract cancers, e.g. anal cancer, and other cancers of the reproductive  
 CC system, including penile and vulvar cancer.  
 CC  
 XX  
 SQ Sequence 248 AA;

Query Match 99.2%; Score 823; DB 8; Length 248;  
 Best Local Similarity 98.7%; Pred. No. 1,7e-83;  
 Matches 148; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 FQDPOERPRKLPOLCTELQTTIHDIILECYCKQQLLRREVDFAPRDLCTIVRDGNPY 61  
 DB 99 FQDPOERPRKLPOLCTELQTTIHDIILECYCKQQLLRREVDFAPRDLCTIVRDGNPY 158  
 QY 62 VXDCKCLKFYSKISEYHVCYVGTTLBOQYNKPLCDLLIRGINXOKPLCPBEKORHLDK 121  
 DB 159 VGDCKCLKFYSKISEYHVCYVGTTLBOQYNKPLCDLLIRGINXOKPLCPBEKORHLDK 218  
 QY 122 KQRFHNIRGRWGRGCMSCCRSSRTRETOL 151  
 DB 219 KQRFHNIRGRWGRGCMSCCRSSRTRETOL 248

RESULT 24  
 ADO44070  
 ID ADO44070 standard; protein; 248 AA.  
 XX  
 AC ADO44070;  
 XX  
 DT 15-JUL-2004 (first entry)  
 XX  
 DE Amino acid sequence of a fusion protein designated E7E6pentm.

XX E6 protein; E7 protein; fusion protein; HPV16; HPV-associated cancer;  
 KM cervical cancer; immune response; lower gastrointestinal tract cancer;  
 KM anal cancer; reproductive system cancer; penile cancer; vulvar cancer;  
 KM gene; ss.  
 XX  
 PN WO2004030636-A2.  
 XX  
 PD 15-APR-2004.  
 XX  
 PF 02-OCT-2003; 2003WO-US031726.  
 XX  
 PR 03-OCT-2002; 2002US-0415929P.  
 XX  
 PA (AMHP) WYETH HOLDINGS CORP.  
 XX  
 PI Smith L, Casasetti MC;  
 XX  
 DR WPI; 2004-316328/29.  
 DR N-PSDB; ADO44071.

PT New polypeptide comprising human papillomavirus E6 and E7 polypeptides,  
 PT useful for treating or preventing human papillomavirus (HPV)-associated  
 PT cancers, e.g. cervical cancer.  
 XX  
 PS Claim 22; Page 75-76; 101pp; English.

XX The present sequence represents a fusion protein, comprising E7 and E6  
 CC polypeptides from human papillomavirus type 16 (HPV16). The fusion  
 CC protein is designated E7E6pentm, and comprises an E7 amino terminus  
 CC (where residues 24, 26 and 91 have been replaced with glycine) and an E6  
 CC carboxy terminus (where residues 63 and 106 have been replaced with  
 CC glycine). E7E6pentm is representative of fusion proteins of the  
 CC invention. The specification describes human papillomavirus E6 and E7

CC polypeptides, where the E7 polypeptide has mutations at any one or more  
CC of the amino acids corresponding to amino acids 24, 26 or 31 of the  
CC sequence given in ADO44073 and the E6 polypeptide has no mutations or has  
CC mutations at any one or more of the amino acids corresponding to amino  
CC acids 63 or 106 of the sequence given in ADO44072. The polypeptides of  
CC the invention are useful for treating or preventing human papillomavirus  
CC (HPV)-associated cancers, such as cervical cancer. The fusion proteins  
CC and nucleic acids encoding the fusion proteins are useful for generating  
CC immune responses against HPV. They are also useful for treating lower  
CC gastrointestinal tract cancers, e.g. anal cancer, and other cancers of  
CC the reproductive system, including penile and vulvar cancer.

SO Sequence 248 AA:

Query Match 99.2%; Score 823; DB 8; Length 248;  
Best Local Similarity 98.7%; Pred. No. 1.7e-83;  
Matches 148; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 FQDPQERPRKLPOLCTELQTTIHDIIEECVCKQQLREYVDFAFRDLCIYRDGNPY 61  
DB 99 FQDPQERPRKLPOLCTELQTTIHDIIEECVCKQQLREYVDFAFRDLCIYRDGNPY 158  
QY 62 VXDCKLKFYSKISEYRHVCYSVYGTLEQYNNKPLCDLLIRICINXQKPLCPEEKQRLDK 121  
DB 159 VGDCKLKFYSKISEYRHVCYSVYGTLEQYNNKPLCDLLIRICINXQKPLCPEEKQRLDK 218  
QY 122 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151  
DB 219 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 248

RESULT 25

ADRA47005

ID ADRA47005 standard; procein; 256 AA.

AC ADRA47005;

DT 18-NOV-2004 (first entry)

DE Human papillomavirus type 16 E7 protein for Dengue virus vaccine.

KM cytostatic; virucide; dengue virus; recombinant replicon; deletion;  
KM prem protein; C protein; NS1 protein signal; vaccine; cervical cancer;  
KM viral disease; antigen; dendritic cell; immune response;  
KM human papillomavirus.

OS Human papillomavirus type 16.

XX WO2004072274-A1.

PN 26-AUG-2004.

PF 30-JAN-2004; 2004WO-CN000088.

PR 30-JAN-2003; 2003CN-00115272.

PR 30-JAN-2003; 2003CN-00115273.

XX (SHAN-) SHANGHAI TENGGEN BIOMEDICAL CO LTD.

PA (TENG-) TENGGEN BIOMEDICAL CO.

PA (BEIJ-) BEIJING ORIENTAL TENGGEN TECHNOLOGY DEV C.

PI Pang X;

XX WPI: 2004-625870/60.

DR N-PSDB; ADRA47004.

XX virus-like particle vaccines containing dengue virus recombinant replicon

PT as core for carrier, applicable in preventives or/and remedies for tumors

PS like cervical cancer and viral diseases.

XX Example 2; SEQ ID NO 2; 38pp; Chinese.

XX A dengue virus recombinant replicon has a deletion of the complete coding

CC sequence for prem protein of dengue virus and also includes elements of  
CC e.g. the non-coding region in the whole of the 5'-end, the coding region  
CC of the front 20 amino acids in the C protein, and the coding region of  
CC NS1 protein signal; coding regions of all non-structural proteins. The  
CC obtained vaccines are useful in producing preventives or/and remedies for  
CC cancer like cervical cancer and viral diseases. Such vaccines can  
CC efficiently express antigen in infected cells, which is because dengue  
CC virus can infect dendritic cells, and can effectively present antigen to  
CC provide immunity effect. Different types of dengue virus can be used to  
CC repeatedly produce efficient immune response thereby strengthening the  
CC body's immune system against the pathogen that contains such antigen.  
CC Human papillomavirus (HPV) vaccines were prepared by using a gene-  
CC expressing system using of the full-length dengue virus cDNA clone  
CC (pBS/FLN2). The recombinant virus vectors were transfected into baby  
CC hamster kidney (BHK) cells to enable the screening of BHK-21 Tec-off cell  
CC lines. This sequence corresponds to the HPV type 16 E7 protein whose  
CC encoding gene is used as the gene of interest in the recombinant replicon  
CC of the invention.

SO Sequence 256 AA:

Query Match 99.2%; Score 823; DB 8; Length 256;  
Best Local Similarity 98.0%; Pred. No. 1.7e-83;  
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFQDPQERPRKLPOLCTELQTTIHDIIEECVCKQQLREYVDFAFRDLCIYRDGNPY 60  
DB 106 MFQDPQERPRKLPOLCTELQTTIHDIIEECVCKQQLREYVDFAFRDLCIYRDGNPY 165  
QY 61 AYXDCKLKFYSKISEYRHVCYSVYGTLEQYNNKPLCDLLIRICINXQKPLCPEEKQRLDK 120  
DB 166 AYXDCKLKFYSKISEYRHVCYSVYGTLEQYNNKPLCDLLIRICINXQKPLCPEEKQRLDK 225  
QY 121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151  
DB 226 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 256

RESULT 26

AEFA0157

ID AEFA0157 standard; protein; 256 AA.

AC AEFA0157;

DT 23-MAR-2006 (first entry)

DE Human papillomavirus 16 (HPV-16) E7-E6 oncoprotein.

KM Vaccine; virus-like particle; replicon; therapeutic; cancer; cytostatic;  
KM neoplasm; viral infection; virucide; infection; oncoprotein.

OS Human papillomavirus type 16.

XX US2006018928-A1.

PN 26-JAN-2006.

PF 29-JUL-2005; 2005US-00192923.

PR 30-JAN-2003; 2003CN-00115272.

PR 30-JAN-2003; 2003CN-00115273.

PR 30-JAN-2004; 2004WO-00072274.

XX (PANG/) PANG X.

XX WPI: 2006-109169/11.

DR N-PSDB; AEFA0156.

XX New recombinant DEN replicons with a deletion of prem, useful for

PT producing a drug for the prophylaxis and treatment of cancer or viral

XX Example 2; SEQ ID NO 2; 24bp; English.  
 PS  
 CC The present invention provides a virus-like particle (VLP) vaccine which  
 CC contains dengue virus (DENV) recombinant replicon as its core. The DENV  
 CC replicon contains exogenous nucleotide sequences such as human  
 CC papillomavirus (HPV) antigen proteins, immune regulators or combination  
 CC of HPV antigen and immune regulators. The invention is useful for  
 CC producing a drug for the prophylaxis and treatment of cancer or viral  
 CC infection. The present sequence is a human papillomavirus oncoprotein.  
 CC  
 XX Sequence 256 AA;  
 SQ  
 Query Match 99.2%; Score 823; DB 10; Length 256;  
 Best Local Similarity 98.0%; Pred. No. 1.7e-83;  
 Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 MFQDDPQBRPKLPQLCTELQTTIHDIILCEVCYCKQQLAREVYDFAFRDLCTIVYRDGNPY 60  
 DB 106 MFQDDPQBRPKLPQLCTELQTTIHDIILCEVCYCKQQLAREVYDFAFRDLCTIVYRDGNPY 165  
 QY 61 AVADKCLKFKYSKISEYRHYCYSVYGTTLBQYNNKPLCDLLIRICINXQKPLCPBEKQRHLD 120  
 DB 166 AVCDKCLKFKYSKISEYRHYCYSLYGTTLBQYNNKPLCDLLIRICINXQKPLCPBEKQRHLD 225  
 QY 121 KKQRFNIRGRWGTGRCMSCCRSSRTRETOL 151  
 DB 226 KKQRFNIRGRWGTGRCMSCCRSSRTRETOL 256  
 Db  
 RESULT 27  
 AAR27725  
 ID AAR27725 standard; protein; 263 AA.  
 XX  
 AC AAR27725;  
 XX  
 DT 24-OCT-2003 (revised)  
 DT 25-MAR-2003 (revised)  
 DT 09-MAR-1993 (first entry)  
 XX  
 DE HPV 16 E6 protein fragment.  
 XX  
 KM Virus vector; vaccinia virus; papillomavirus; HPV; human; amplification;  
 KM immunotherapeutic.  
 XX  
 OS Human papillomavirus type 16.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..159 "HPV-16 E6 protein"  
 FT /note="HPV-16 E6 protein"  
 XX  
 PN W09216636-A1.  
 PN  
 PD 01-OCT-1992.  
 PD  
 PF 10-MAR-1992; 92MO-GB000424.  
 PF  
 PR 14-MAR-1991; 91GB-00005383.  
 PR  
 PA (IMMU ) IMMUNOLOGY LTD.  
 PA  
 PI Bourenell MEG, Inglis SC, Munro AJ;  
 PI  
 DR WPI; 1992-349219/42.  
 DR N-PSDB; AAQ29389.  
 DR  
 XX Recombinant virus vectors encoding human papillomavirus proteins - for  
 PT treating and vaccinating against HPV infections and conditions caused by  
 PT them, such as cervical cancer.  
 XX  
 PS Disclosure; Fig 1a; 83bp; English.  
 PS  
 CC The fragment of DNA contg. the HPV-16 E6/E7 coding region was prepd. by

CC PCR from plasmid pBR322/HPV16 (Durst et al., PNAS, 80: 3812 (1983)) using  
 CC oligonucleotides S05 and S06. The prod. of the third reading frame is the  
 CC HPV-16 E6 protein whereas the second reading frame encodes HPV-16 E7. The  
 CC E6 and E7 ORFs are fused together to form a single continuous ORF via  
 CC site directed mutagenesis and the immortalising potential of E7 is  
 CC removed by altering two key codons of the HPV E7 sequence. The single ORF  
 CC of HPV-16 E6/E7 may be inserted into vaccinia virus DNA at neutral sites  
 CC (pref. by inserting two sets of the DNA in opposite orientations to  
 CC overcome the problem of intertypic recombination) to make a recombinant  
 CC virus vector for use immunotherapeutically to activate cells of the  
 CC immune system against HPV. See also AAR27723-43. (Updated on 25-MAR-2003  
 CC to correct PN field.) (Updated on 24-OCT-2003 to standardise OS field)  
 CC  
 XX Sequence 263 AA;  
 SQ  
 Query Match 99.2%; Score 823; DB 2; Length 263;  
 Best Local Similarity 98.0%; Pred. No. 1.8e-83;  
 Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 MFQDDPQBRPKLPQLCTELQTTIHDIILCEVCYCKQQLAREVYDFAFRDLCTIVYRDGNPY 60  
 DB 9 MFQDDPQBRPKLPQLCTELQTTIHDIILCEVCYCKQQLAREVYDFAFRDLCTIVYRDGNPY 68  
 QY 61 AVADKCLKFKYSKISEYRHYCYSVYGTTLBQYNNKPLCDLLIRICINXQKPLCPBEKQRHLD 120  
 DB 69 AVCDKCLKFKYSKISEYRHYCYSLYGTTLBQYNNKPLCDLLIRICINXQKPLCPBEKQRHLD 128  
 QY 121 KKQRFNIRGRWGTGRCMSCCRSSRTRETOL 151  
 DB 129 KKQRFNIRGRWGTGRCMSCCRSSRTRETOL 159  
 Db  
 RESULT 28  
 AAR97561  
 ID AAR97561 standard; protein; 266 AA.  
 XX  
 AC AAR97561;  
 XX  
 DT 27-AUG-2003 (revised)  
 DT 11-JAN-1997 (first entry)  
 XX  
 DE Human papilloma virus E6/E7 protein variant.  
 XX  
 KM Human papilloma virus; E6; E7; deletion mutant; HPV; immune response;  
 KM humoral immune response; cellular immune response; vaccine.  
 XX  
 OS Human papillomavirus.  
 XX  
 PN W09619496-A1.  
 PN  
 PD 27-JUN-1996.  
 PD  
 PF 20-DEC-1995; 95MO-AU000868.  
 PF  
 PR 20-DEC-1994; 94AU-00000157.  
 PR  
 PA (CSLC-) CSL LTD.  
 PA (UYOU ) UNIV QUEENSLAND.  
 PA  
 PI Edwards SJ, Cox J, Webb EA, Frazer I;  
 PI  
 DR WPI; 1996-309518/31.  
 DR N-PSDB; AAT31833.  
 DR  
 XX Vaccine variants of human papilloma virus antigens - contain variants of  
 PT E6 and/or E7 protein, pref. deletion mutants, and are used to treat or  
 PT prevent HPV infection.  
 XX  
 PS Example 1; Page 15-16; 37bp; English.  
 PS  
 CC A variant of the human papilloma virus (HPV) E6 or E7 protein which  
 CC elicits a humoral and/or cellular immune response against HPV can be used  
 CC in vaccines against HPV or to treat HPV infection. The variant is

CC preferably a deletion mutant comprising at least half, and preferably two  
CC thirds of full length E6 or E7 protein starting from the N- or C-  
CC terminal, or is a full length E6 moiety fused to a full length E7 moiety.  
CC The variant optionally has a linkage moiety and a foreign protein or  
CC peptide which facilitates the purification of, and enhances the  
CC immunogenicity of, the fusion protein. This sequence is a full length  
CC E6/E7 fusion protein. (Updated on 27-AUG-2003 to correct OS field.)  
XX

SQ Sequence 266 AA;

Query Match 99.2%; Score 823; DB 2; Length 266;  
Best Local Similarity 98.0%; Pred. No. 1.8e-83;  
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFODPQRRPKLPCLTETLQTTIHDIIECVCKQQLRREVDFAFRDLCTIVRDGPNY 60  
DB 8 MFODPQRRPKLPCLTETLQTTIHDIIECVCKQQLRREVDFAFRDLCTIVRDGPNY 67

QY 61 AVXDCKLFYSKISEYRHVCYVGTTLQOYNKPLCDLLIRCTNXXKPLCPPEKQKHLD 120  
DB 68 AVCDCKLFYSKISEYRHVCYSLVGTTLQOYNKPLCDLLIRCTNXXKPLCPPEKQKHLD 127

QY 121 KKQRFHNIRGRWTCRWCSCCRSSRTRETQL 151  
DB 128 KKQRFHNIRGRWTCRWCSCCRSSRTRETQL 158

RESULT 29  
AAV25376

ID AAV25376 standard; protein; 273 AA.

XX AAV25376;

DT 06-SEP-1999 (first entry)

DE HPV fusion protein D1/3-E6-His/HPV16.

XX Fusion protein; E6 protein; E7 protein; E6/E7; immunomodulator; tumour;  
KM immunological fusion partner; Cpg oligonucleotide; immune response;  
KM HIV antigen; prevention; treatment.

XX Synthetic.

OS Human papillomavirus.

XX WO9933868-A2.

PD 08-JUL-1999.

PF 18-DEC-1998; 98WO-EP008563.

PR 24-DEC-1997; 97GB-00027262.

XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.

PI Dalemans WLJ, Gerard CMG;

DR WPI: 1999-405485/34.

DR N-PSDB; AAX78792.

PT Composition comprising an E6, E7 or E6/E7 fusion protein from HPV to  
PT induce immune response to HPV.

XX Example II; Page 48-49; 62pp; English.

CC AAX78791-X78801 represent nucleic acid sequences which encode novel  
CC constructs comprising an E6 or E7 protein or E6/E7 fusion protein from  
CC HPV (represented in AAV25375-Y25386). These constructs are optionally  
CC linked to an immunological fusion partner and an immunomodulatory Cpg  
CC oligonucleotide. The products of the invention can be used to induce an  
CC immune response in a patient to an HPV antigen. They can also be used for  
CC preventing or treating HPV induced tumours

XX Sequence 273 AA;

Query Match 99.2%; Score 823; DB 2; Length 273;  
Best Local Similarity 98.0%; Pred. No. 1.9e-83;  
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFODPQRRPKLPCLTETLQTTIHDIIECVCKQQLRREVDFAFRDLCTIVRDGPNY 60  
DB 114 MFODPQRRPKLPCLTETLQTTIHDIIECVCKQQLRREVDFAFRDLCTIVRDGPNY 173

QY 61 AVXDCKLFYSKISEYRHVCYVGTTLQOYNKPLCDLLIRCTNXXKPLCPPEKQKHLD 120  
DB 174 AVCDCKLFYSKISEYRHVCYSLVGTTLQOYNKPLCDLLIRCTNXXKPLCPPEKQKHLD 233

QY 121 KKQRFHNIRGRWTCRWCSCCRSSRTRETQL 151  
DB 234 KKQRFHNIRGRWTCRWCSCCRSSRTRETQL 264

RESULT 30

ID AAV02632 standard; protein; 273 AA.

XX AAV02632;

DT 17-OCT-2003 (revised)

DT 22-JUN-1999 (first entry)

DE Prot. D1/3-E6-His/HPV16 protein.

XX Chimeric; E6; E7; fusion protein; protein D; vaccine; immunotherapy;  
KM tumour; lesion; benign; malignant; virus; infection.

XX Human papillomavirus.

OS Haemophilus influenzae.

XX WO9910375-A2.

PD 04-MAR-1999.

PF 17-AUG-1998; 98WO-EP005285.

PR 22-AUG-1997; 97GB-00017953.

XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.

PI Bruck C, Cabezon Silva T, Delisse AEF, Gerard CMG;

PI Lombardo-Bencheikh A;

DR WPI: 1999-190587/16.

DR N-PSDB; AAX29781.

PT Human Papilloma Virus (HPV) fusion proteins - useful in vaccines for  
PT treatment or prophylaxis of HPV induced lesions.

XX Disclosure; Fig 3; 95pp; English.

CC This sequence represents a chimeric E6 or E7 protein or E6/E7 fusion  
CC protein from Human papillomavirus (HPV) linked to an immunological fusion  
CC partner, in this case, a fragment of the Haemophilus influenzae B protein  
CC D. The sequence also contains a histidine tag at the C-terminus of the  
CC encoded protein. The protein can be used in a vaccine, for immuno-  
CC therapeutically treating HPV induced tumour lesions (benign or malignant)  
CC and preventing HPV viral infection. (Updated on 17-OCT-2003 to  
CC standardise OS field)

XX Sequence 273 AA;

Query Match 99.2%; Score 823; DB 2; Length 273;  
Best Local Similarity 98.0%; Pred. No. 1.9e-83;  
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFODPQRRPKLPCLTETLQTTIHDIIECVCKQQLRREVDFAFRDLCTIVRDGPNY 60

```

Db      114 MFQDPQERPRKLPQLCTELQTTIHDIILCEVCYCKQQLRREYVDFAFRDLCTIYRDGNPY 173
Qy      61 AVXDCKLKFYSKISEYRHYCYSYGTTLEQOYNKPLCDLLIRGINXOKPLCPBEKORHLD 120
Db      174 AVCDCKLKFYSKISEYRHYCYSLYGTTLEQOYNKPLCDLLIRGINCOKPLCPBEKORHLD 233
Qy      121 KKQRFNINIRGRWTRGCMSCCRSSRTRETOL 151
Db      234 KKQRFNINIRGRWTRGCMSCCRSSRTRETOL 264

RESULT 31
AEDS2634
ID      AEDS2634 standard; protein; 273 AA.
XX
AC      AEDS2634;
XX
DT      29-DEC-2005 (first entry)
XX
DE      Fusion protein DI/3-E6-His/HPV16.
XX
KM      Fusion protein; vaccine; papilloma; cytostatic; papillomavirus infection;
KM      virucide; uterine cervix tumor; E6; D protein.
XX
OS      Haemophilus influenzae; strain 772.
OS      Synthetic.
OS      Human papillomavirus type 16.
OS      Chimeric.
XX
PN      IN9801903-14.
XX
PD      04-MAR-2005.
XX
PF      24-AUG-1998; 98IN-CH001903.
XX
PR      22-AUG-1997; 97EP-00179535.
XX
PA      (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI      Tyrell AMR;
XX
DR      WPI: 2005-557648/57.
XX
DR      N-PSDB; AEDS2633.
XX
PT      Vaccine.
XX
PS      Example 4; Fig 3; 96pp; English.
XX
CC      The invention relates to human Papilloma virus (HPV) fusion proteins,
CC      linked to an immunological fusion partner that provides T helper epitopes
CC      to the HPV antigen. Vaccine formulations comprising the fusion proteins
CC      are useful in the treatment or prophylaxis of HPV induced lesions
CC      (papillomas, warts and cervical cancer). HPV 16 (and HPV 18) E6 and E7
CC      proteins (singly, as an E6-E7 fusion or mutated) were fused to either
CC      Haemophilus influenzae D protein (20-127), the C-terminus of
CC      Streptococcus pneumoniae Lyta protein (ClyA) or chloroform. The present
CC      sequence represents an HPV-H. influenzae D protein, fusion protein of the
CC      invention.
XX
SQ      Sequence 273 AA;

Query Match      99.2%; Score 823; DB 9; Length 273;
Best Local Similarity 98.0%; Pred. No. 1.9e-83;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Qy      121 KKQRFNINIRGRWTRGCMSCCRSSRTRETOL 151
Db      234 KKQRFNINIRGRWTRGCMSCCRSSRTRETOL 264

RESULT 32
AAV25379
ID      AAV25379 standard; protein; 292 AA.
XX
AC      AAV25379;
XX
DT      06-SEP-1999 (first entry)
XX
DE      HPV fusion protein CLYTA-E6-His/HPV16.
XX
KM      Fusion protein; E6 protein; E7 protein; E6/E7; immunomodulator; tumour;
KM      immunological fusion partner; Cpg oligonucleotide; immune response;
KM      HPV antigen; prevention; treatment.
XX
OS      Synthetic.
OS      Human papillomavirus.
XX
PN      WO933868-A2.
XX
PD      08-JUL-1999.
XX
PF      18-DEC-1998; 98WO-BE008563.
XX
PR      24-DEC-1997; 97GB-00027262.
XX
PA      (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI      Dalemans WLJ, Gerard CMG;
XX
DR      WPI: 1999-405485/34.
XX
DR      N-PSDB; AAX78795.
XX
PT      Composition comprising an E6, E7 or E6/E7 fusion protein from HPV to
PT      induce immune response to HPV.
XX
PS      Example VI; Page 52-53; 62pp; English.
XX
CC      AAX78791-X78801 represent nucleic acid sequences which encode novel
CC      constructs comprising an E6 or E7 protein or E6/E7 fusion protein from
CC      HPV (represented in AAY25375-Y25386). These constructs are optionally
CC      linked to an immunological fusion partner and an immunomodulatory Cpg
CC      oligonucleotide. The products of the invention can be used to induce an
CC      immune response in a patient to an HPV antigen. They can also be used for
CC      preventing or treating HPV induced tumours
XX
SQ      Sequence 292 AA;

Query Match      99.2%; Score 823; DB 2; Length 292;
Best Local Similarity 98.0%; Pred. No. 2e-83;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

```

RESULT 33
AAV02635
ID      AAV02635 standard; protein; 292 AA.

```

```

XX AC AAY02635;
XX DT 17-OCT-2003 (revised)
XX DT 22-JUN-1999 (first entry)
XX DE CLYTA-E6-His protein.
XX KM Chimeric; E6; E7; fusion protein; CLYTA; vaccine; immunotherapy; tumour;
XX KM lesion; benign; malignant; virus; infection.
XX OS Human papillomavirus.
XX OS Streptococcus pneumoniae.
XX OS Chimeric.
XX PN MO9910375-A2.
XX PD 04-MAR-1999.
XX PF 17-AUG-1998; 98MO-EP005285.
XX PR 22-AUG-1997; 97GB-00017953.
XX PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX PI Bruck C, Cabezon Silva T, Deliese AEF, Gerard CMG;
XX PI Lombardo-Bencheikh A;
XX DR WPI; 1999-190587/16.
XX DR N-PSDB; AAX29784.
XX PT Human Papilloma Virus (HPV) fusion proteins - useful in vaccines for
XX PT treatment or prophylaxis of HPV induced lesions.
XX PS Disclosure; Fig 10; 95pp; English.
XX CC This sequence represents a chimeric E6 or E7 protein or E6/E7 fusion
XX CC protein from Human papillomavirus (HPV) linked to an immunological fusion
XX CC partner, in this case, a fragment of the Streptococcus pneumoniae CLYTA
XX CC protein of the encoded protein. The protein can be used in a vaccine, for
XX CC immuno-therapeutically creating HPV induced tumour lesions (benign or
XX CC malignant) and preventing HPV viral infection. (Updated on 17-OCT-2003 to
XX CC standardise OS field)
XX SQ Sequence 292 AA;

Query Match 99.2%; Score 823; DB 2; Length 292;
Best Local Similarity 98.0%; Pred. No. 2e-83; 2; Indels 0; Gaps 0;
Matches 148; Conservative 1; Mismatches 2;

QY 1 MFODPQERPRKLPQLCTELQTTIHDIIECVYCKQQLLRREYVDFAFRDLCIYVRDGNPY 60
DB 133 MFODPQERPRKLPQLCTELQTTIHDIIECVYCKQQLLRREYVDFAFRDLCIYVRDGNPY 192
QY 61 AVXDCKLKFSKISEYRHYCYSYGTTLEQYNNKPLCDLLIRICINXOKPLCPBEKQRHLD 120
DB 193 AVCDCKLKFSKISEYRHYCYSLYGTLEQYNNKPLCDLLIRICINXOKPLCPBEKQRHLD 252
QY 121 KKORFHNIRGRWTCRMCSCCRSSRTRETOL 151
DB 253 KKORFHNIRGRWTCRMCSCCRSSRTRETOL 283

RESULT 34
AEDS2642
ID AEDS2642 standard; protein: 292 AA.
AC AEDS2642;
XX
XX 29-DEC-2005 (first entry)
XX
XX Fusion protein clyta-E6-His/HPV16.
XX

```

```

KM Fusion protein; vaccine; papilloma; cytostatic; papillomavirus infection;
KM virucide; uterine cervix tumor; E7; Lyta.
XX
XX OS Streptococcus pneumoniae.
XX OS Human papillomavirus type 16.
XX OS Synthetic.
XX OS Chimeric.
XX PN IN9801903-14.
XX PD 04-MAR-2005.
XX PF 24-AUG-1998; 98IN-CH001903.
XX PR 22-AUG-1997; 97EP-00179535.
XX PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX PI Tytrell AMR;
XX PI Tytrell AMR;
XX DR WPI; 2005-557648/57.
XX DR N-PSDB; AEDS2641.
XX PT Vaccine.
XX PS Example 10; Fig 10; 96pp; English.
XX CC The invention relates to human Papilloma virus (HPV) fusion proteins,
XX CC linked to an immunological fusion partner that provides T helper epitopes
XX CC to the HPV antigen. Vaccine formulations comprising the fusion proteins
XX CC are useful in the treatment or prophylaxis of HPV induced lesions
XX CC (papillomas, warts and cervical cancer). HPV 16 (and HPV 18) E6 and E7
XX CC proteins (singly, as an E6-E7 fusion or mutated) were fused to either
XX CC Haemophilus influenzae D protein (20-127), the C-terminus of
XX CC Streptococcus pneumoniae Lyta protein (CLYTA) or thiorodoxin. The present
XX CC sequence represents an HPV-Lyta, fusion protein of the invention.
XX SQ Sequence 292 AA;

Query Match 99.2%; Score 823; DB 9; Length 292;
Best Local Similarity 98.0%; Pred. No. 2e-83; 2; Indels 0; Gaps 0;
Matches 148; Conservative 1; Mismatches 2;

QY 1 MFODPQERPRKLPQLCTELQTTIHDIIECVYCKQQLLRREYVDFAFRDLCIYVRDGNPY 60
DB 133 MFODPQERPRKLPQLCTELQTTIHDIIECVYCKQQLLRREYVDFAFRDLCIYVRDGNPY 192
QY 61 AVXDCKLKFSKISEYRHYCYSYGTTLEQYNNKPLCDLLIRICINXOKPLCPBEKQRHLD 120
DB 193 AVCDCKLKFSKISEYRHYCYSLYGTLEQYNNKPLCDLLIRICINXOKPLCPBEKQRHLD 252
QY 121 KKORFHNIRGRWTCRMCSCCRSSRTRETOL 151
DB 253 KKORFHNIRGRWTCRMCSCCRSSRTRETOL 283

RESULT 35
AAY25377
ID AAY25377 standard; protein: 371 AA.
AC AAY25377;
XX
XX 06-SEP-1999 (first entry)
XX
XX HPV fusion protein DL/3-E6E7-His/HPV16.
XX
XX Fusion protein; E6 protein; E7 protein; E6/E7; immunomodulator; tumour;
XX KM immunological fusion partner; CpG oligonucleotide; immune response;
XX KM HPV antigen; prevention; treatment.
XX
XX Synthetic.
XX OS Human papillomavirus.
XX

```

PN W09933868-A2.  
 XX  
 PD 08-JUL-1999.  
 XX  
 PF 18-DEC-1998; 98MO-EP008563.  
 XX  
 PR 24-DEC-1997; 97GB-00027262.  
 XX  
 PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
 PI Dalemans WLJ, Gerard CMG;  
 XX WPI; 1999-405485/34.  
 DR N-PSDB; AAX78793.  
 XX  
 PT Composition comprising an E6, E7 or E6/E7 fusion protein from HPV to  
 XX induce immune response to HPV.  
 PS Example III; Page 50; 62pp; English.  
 CC AAX78791-X78801 represent nucleic acid sequences which encode novel  
 CC constructs comprising an E6 or E7 protein or E6/E7 fusion protein from  
 CC HPV (represented in AAY25375-Y25386). These constructs are optionally  
 CC linked to an immunological fusion partner and an immunomodulatory Cpg  
 CC oligonucleotide. The products of the invention can be used to induce an  
 CC immune response in a patient to an HPV antigen. They can also be used for  
 CC preventing or treating HPV induced tumours  
 XX  
 SQ Sequence 371 AA;  
 XX  
 Query Match 99.2%; Score 823; DB 2; Length 371;  
 Best Local Similarity 98.0%; Pred. No. 2.7e-83;  
 Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 MFQDDPQPRPKLPOLCTELQTTIHDIILECVYCKQQLRREYVDFAFRDLCIYRDGNPY 60  
 DB 114 MFQDDPQPRPKLPOLCTELQTTIHDIILECVYCKQQLRREYVDFAFRDLCIYRDGNPY 173  
 QY 61 AVXDCKLKFYSKISEYRHICYSYGTTLEQYNNKPLCDLLIRICINXKPLCPBEKQRLD 120  
 DB 174 AVCDCKLKFYSKISEYRHICYSLYGTTLEQYNNKPLCDLLIRICINXKPLCPBEKQRLD 233  
 QY 121 KKQRFNIRGRMTGRMCSSCRSSRTRETOL 151  
 DB 234 KKQRFNIRGRMTGRMCSSCRSSRTRETOL 264  
 RESULT 36  
 AAY02633  
 ID AAY02633 standard; protein; 371 AA.  
 XX  
 AC AAY02633;  
 XX  
 DT 17-OCT-2003 (revised)  
 DT 22-JUN-1999 (first entry)  
 XX  
 DE Prot. D1/3-E6-E7-His/HPV16 protein.  
 XX  
 KM Chimeric; E6; E7; fusion protein; protein D; vaccine; immunotherapy;  
 KM tumour; lesion; benign; malignant; virus; infection.  
 XX  
 OS Human papillomavirus.  
 OS Haemophilus influenzae.  
 OS Chimeric.  
 XX  
 PN W09910375-A2.  
 XX  
 PD 04-MAR-1999.  
 XX  
 PF 17-AUG-1998; 98MO-EP005285.  
 XX  
 PR 22-AUG-1997; 97GB-00017953.  
 XX

PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
 XX  
 PI Bruck C, Cabezon Silva T, Delisse AEF, Gerard CMG;  
 PI Lombardo-Bencheikh A;  
 XX  
 DR WPI; 1999-190587/16.  
 DR N-PSDB; AAX29782.  
 XX  
 PT Human Papilloma Virus (HPV) fusion proteins - useful in vaccines for  
 PT treatment or prophylaxis of HPV induced lesions.  
 XX  
 PS Disclosure; Fig 6; 95pp; English.  
 CC This sequence represents a chimeric E6 or E7 protein or E6/E7 fusion  
 CC protein from human papillomavirus (HPV) linked to an immunological fusion  
 CC partner, in this case, a fragment of the Haemophilus influenzae B protein  
 CC D. The sequence also contains a histidine tag at the C-terminus of the  
 CC encoded protein. The protein can be used in a vaccine, for immuno-  
 CC therapeutically treating HPV induced tumour lesions (benign or malignant)  
 CC and preventing HPV viral infection. (Updated on 17-OCT-2003 to  
 CC standardise OS field)  
 XX  
 SQ Sequence 371 AA;  
 XX  
 Query Match 99.2%; Score 823; DB 2; Length 371;  
 Best Local Similarity 98.0%; Pred. No. 2.7e-83;  
 Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 MFQDDPQPRPKLPOLCTELQTTIHDIILECVYCKQQLRREYVDFAFRDLCIYRDGNPY 60  
 DB 114 MFQDDPQPRPKLPOLCTELQTTIHDIILECVYCKQQLRREYVDFAFRDLCIYRDGNPY 173  
 QY 61 AVXDCKLKFYSKISEYRHICYSYGTTLEQYNNKPLCDLLIRICINXKPLCPBEKQRLD 120  
 DB 174 AVCDCKLKFYSKISEYRHICYSLYGTTLEQYNNKPLCDLLIRICINXKPLCPBEKQRLD 233  
 QY 121 KKQRFNIRGRMTGRMCSSCRSSRTRETOL 151  
 DB 234 KKQRFNIRGRMTGRMCSSCRSSRTRETOL 264  
 RESULT 37  
 AED52638  
 ID AED52638 standard; protein; 371 AA.  
 XX  
 AC AED52638;  
 XX  
 DT 29-DEC-2005 (first entry)  
 DT 29-DEC-2005 (first entry)  
 XX  
 DE Fusion protein D1/3-E6-E7-His/HPV16.  
 XX  
 KM Fusion protein; vaccine; papilloma; cytostatic; papillomavirus infection;  
 KM virucide; uterine cervix tumor; E7; D protein.  
 XX  
 OS Haemophilus influenzae; strain 772.  
 OS Synthetic.  
 OS Chimeric.  
 XX  
 PN IN9801903-14.  
 XX  
 PD 04-MAR-2005.  
 XX  
 PF 24-AUG-1998; 98IN-CH001903.  
 XX  
 PR 22-AUG-1997; 97EP-00179535.  
 XX  
 PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
 PI Tytrell AMR;  
 XX  
 DR WPI; 2005-557648/57.  
 DR N-PSDB; AED52637.

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XX XX Vaccine.
XX XX Example 6; Fig 6; 96pp; English.
XX
CC The invention relates to human Papilloma virus (HPV) fusion proteins,
CC linked to an immunological fusion partner that provides T helper epitopes
CC to the HPV antigen. Vaccine formulations comprising the fusion proteins
CC are useful in the treatment or prophylaxis of HPV induced lesions
CC (papillomas, warts and cervical cancer). HPV 16 (and HPV 18) E6 and E7
CC proteins (singly, as an E6-E7 fusion or mutated) were fused to either
CC Haemophilus influenzae D protein (20-127), the C-terminus of
CC Streptococcus pneumoniae Lyta protein (CLYTA) or thiodoxin. The present
CC sequence represents an HPV-H. influenzae D protein, fusion protein of the
CC invention.
XX
SQ Sequence 371 AA:
Query Match 99.2%; Score 823; DB 9; Length 371;
Best Local Similarity 98.0%; Pred. No. 2.7e-83;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 MFQDPQERPRKLPOLCTELQTTIHDIIECVYCKQQLRREYVDFAFRDLCIYRDGNPY 60
DB 114 MFQDPQERPRKLPOLCTELQTTIHDIIECVYCKQQLRREYVDFAFRDLCIYRDGNPY 173
QY 61 AVXDCKLFYSKISEYRHYCYSVYGTTLQOYNKPLCDLLIRCIINXOKPLCPREKORHLD 120
DB 174 AVCDCKLFYSKISEYRHYCYSLVGTTLQOYNKPLCDLLIRCIINXOKPLCPREKORHLD 233
QY 121 KKQRFHNIRGRWTRGCMSCCRSSRTRETQL 151
DB 234 KKQRFHNIRGRWTRGCMSCCRSSRTRETQL 264
RESULT 38
AAV25381
ID AAV25381 standard; protein; 390 AA.
XX
AC AAV25381;
XX
DT 06-SEP-1999 (first entry)
XX
DE HPV fusion protein CLYTA-E6E7-His/HPV16.
XX
KM Fusion protein; E6 protein; E7 protein; E6/E7; immunomodulator; tumour;
KM immunological fusion partner; CpG oligonucleotide; immune response;
KM HPV antigen; prevention; treatment.
XX
OS Synthetic.
OS Human papillomavirus.
XX
PN WO9933866-A2.
XX
PD 08-JUL-1999.
XX
PF 18-DEC-1998; 98WO-EP008563.
XX
PR 24-DEC-1997; 97GB-00027262.
XX
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI Dalemans WLJ, Gerard CMG;
XX
DR WPI: 1999-405485/34.
XX
PT N-PsDB; AAX78797.
XX
CC Composition comprising an E6, E7 or E6/E7 fusion protein from HPV to
XX induce immune response to HPV.
XX
PS Example VIII; Page 55-56; 62pp; English.
XX
CC AAX78791-X78801 represent nucleic acid sequences which encode novel

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CC constructs comprising an E6 or E7 protein or E6/E7 fusion protein from
CC HPV (represented in AAV25375-Y25386). These constructs are optionally
CC linked to an immunological fusion partner and an immunomodulatory CpG
CC oligonucleotide. The products of the invention can be used to induce an
CC immune response in a patient to an HPV antigen. They can also be used for
CC preventing or treating HPV induced tumours
XX
SQ Sequence 390 AA:
Query Match 99.2%; Score 823; DB 2; Length 390;
Best Local Similarity 98.0%; Pred. No. 2.9e-83;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 MFQDPQERPRKLPOLCTELQTTIHDIIECVYCKQQLRREYVDFAFRDLCIYRDGNPY 60
DB 133 MFQDPQERPRKLPOLCTELQTTIHDIIECVYCKQQLRREYVDFAFRDLCIYRDGNPY 192
QY 61 AVXDCKLFYSKISEYRHYCYSVYGTTLQOYNKPLCDLLIRCIINXOKPLCPREKORHLD 120
DB 193 AVCDCKLFYSKISEYRHYCYSLVGTTLQOYNKPLCDLLIRCIINXOKPLCPREKORHLD 252
QY 121 KKQRFHNIRGRWTRGCMSCCRSSRTRETQL 151
DB 253 KKQRFHNIRGRWTRGCMSCCRSSRTRETQL 283
RESULT 39
AAV2637
ID AAV2637 standard; protein; 390 AA.
XX
AC AAV2637;
XX
DT 17-OCT-2003 (revised)
DT 22-JUN-1999 (first entry)
XX
DE CLYTA-E6E7-His protein.
XX
KM Chimeric; E6; E7; fusion protein; CLYTA; vaccine; immunotherapy; tumour;
KM lesion; benign; malignant; virus; infection.
XX
OS Human papillomavirus.
OS Streptococcus pneumoniae.
OS Chimeric.
XX
PN WO9910375-A2.
XX
PD 04-MAR-1999.
XX
PF 17-AUG-1998; 98WO-EP005285.
XX
PR 22-AUG-1997; 97GB-00017953.
XX
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI Bruck C, Caberon Silva T, Delisse AEF, Gerard CMG;
XX
DR Lombardo-Bencheikh A;
XX
DR WPI: 1999-190587/16.
XX
PT N-PsDB; AAX29786.
XX
CC Human Papilloma Virus (HPV) fusion proteins - useful in vaccines for
XX treatment or prophylaxis of HPV induced lesions.
XX
PS Disclosure; Fig 14; 95pp; English.
XX
CC This sequence represents a chimeric E6 or E7 protein or E6/E7 fusion
XX protein from Human papillomavirus (HPV) linked to an immunological fusion
XX partner, in this case, a fragment of the Streptococcus pneumoniae CLYTA
XX protein of the encoded protein. The protein can be used in a vaccine, for
XX immuno-therapeutically treating HPV induced tumour lesions (benign or
XX malignant) and preventing HPV viral infection. (Updated on 17-OCT-2003 to
XX standardise OS field)

```

SO Sequence 390 AA:

Query Match 99.2%; Score 823; DB 2; Length 390;  
 Best Local Similarity 98.0%; Pred. No. 2.9e-83;  
 Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFQDPERPRKLPOLCTELQTTIHDIILECVYCKQQLRREYVDFAFRDLCTIYRGNPY 60  
 |||  
 DB 133 MFQDPERPRKLPOLCTELQTTIHDIILECVYCKQQLRREYVDFAFRDLCTIYRGNPY 192  
 |||  
 QY 61 AVXDKCLKFYSKISEYRHYCYSVYGTLEEQYNNKPLCDLLIRCNXQKPLCPBEKORHLD 120  
 |||  
 DB 193 AVCDKCLKFYSKISEYRHYCYSLYGTLEEQYNNKPLCDLLIRCNCKPLCPBEKORHLD 252  
 |||

QY 121 KKQRFNINRGWTRGCMSCCRSSRTRETQL 151  
 |||  
 DB 253 KKQRFNINRGWTRGCMSCCRSSRTRETQL 283  
 |||

RESULT 40  
 AED52646  
 ID AED52646 standard; protein; 390 AA.  
 XX  
 AC AED52646;  
 XX  
 DT 29-DEC-2005 (first entry)  
 DE Fusion protein cLYCA-E6-E7-His/HPV16.  
 XX  
 KM Fusion protein; vaccine; papilloma; cytostatic; papillomavirus infection;  
 KM virucide; uterine cervix tumor; E7; Lyta.  
 XX  
 OS Streptococcus pneumoniae.  
 OS Human papillomavirus type 16.  
 OS Synthetic.  
 OS Chimeric.  
 XX  
 PN IN9801903-14.  
 XX  
 PD 04-MAR-2005.  
 XX  
 PF 24-AUG-1998; 98IN-CH001903.  
 XX  
 PR 22-AUG-1997; 97EP-00179535.  
 XX  
 PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
 XX  
 PI Tyrrell AMR;  
 XX  
 DR WPI; 2005-557648/57.  
 DR N-PSDB; AED52645.  
 XX  
 PT Vaccine.  
 XX  
 PS Example 12; Fig 14; 96pp; English.  
 CC The invention relates to human Papilloma virus (HPV) fusion proteins,  
 CC linked to an immunological fusion partner that provides T helper epitopes  
 CC to the HPV antigen. Vaccine formulations comprising the fusion proteins  
 CC are useful in the treatment or prophylaxis of HPV induced lesions  
 CC (papillomas, warts and cervical cancer). HPV 16 (and HPV 18) E6 and E7  
 CC proteins (singly, as an E6-E7 fusion or mutated) were fused to either  
 CC Haemophilus influenzae D protein (20-127), the C-terminus of  
 CC Streptococcus pneumoniae Lyta protein (cLYCA) or chloroixin. The present  
 CC sequence represents an HPV-Lyta, fusion protein of the invention.  
 CC  
 SO Sequence 390 AA:

Query Match 99.2%; Score 823; DB 9; Length 390;  
 Best Local Similarity 98.0%; Pred. No. 2.9e-83;  
 Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFQDPERPRKLPOLCTELQTTIHDIILECVYCKQQLRREYVDFAFRDLCTIYRGNPY 60

DB 133 MFQDPERPRKLPOLCTELQTTIHDIILECVYCKQQLRREYVDFAFRDLCTIYRGNPY 192  
 |||  
 QY 61 AVXDKCLKFYSKISEYRHYCYSVYGTLEEQYNNKPLCDLLIRCNXQKPLCPBEKORHLD 120  
 |||  
 DB 193 AVCDKCLKFYSKISEYRHYCYSLYGTLEEQYNNKPLCDLLIRCNCKPLCPBEKORHLD 252  
 |||

QY 121 KKQRFNINRGWTRGCMSCCRSSRTRETQL 151  
 |||  
 DB 253 KKQRFNINRGWTRGCMSCCRSSRTRETQL 283  
 |||

RESULT 41  
 ADO44066  
 ID ADO44066 standard; protein; 248 AA.  
 XX  
 AC ADO44066;  
 XX  
 DT 15-JUL-2004 (first entry)  
 DE Amino acid sequence of an E7E6 fusion protein.  
 XX  
 KM E6 protein; E7 protein; fusion protein; HPV16; HPV-associated cancer;  
 KM cervical cancer; immune response; lower gastrointestinal tract cancer;  
 KM anal cancer; reproductive system cancer; penile cancer; vulvar cancer.  
 XX  
 OS Human papillomavirus type 16.  
 OS Synthetic.  
 XX  
 PN WO2004030636-A2.  
 XX  
 PD 15-APR-2004.  
 XX  
 PF 02-OCT-2003; 2003WO-US031726.  
 XX  
 PR 03-OCT-2002; 2002US-0415929P.  
 XX  
 PA (AMHP ) WYETH HOLDINGS CORP.  
 XX  
 PI Smith L, Cassecci MC;  
 XX  
 DR WPI; 2004-316328/29.  
 DR N-PSDB; ADO44067.  
 XX  
 PT New polypeptide comprising human papillomavirus E6 and E7 polypeptides,  
 PT useful for treating or preventing human papillomavirus (HPV)-associated  
 PT cancers, e.g. cervical cancer.  
 XX  
 PS Example 1; Page 72-73; 101pp; English.  
 CC The present sequence represents an E7E6 fusion protein, comprising wild  
 CC type E7 and E6 polypeptides from human papillomavirus type 16 (HPV16).  
 CC The specification describes human papillomavirus E6 and E7 polypeptides,  
 CC where the E7 polypeptide has mutations at any one or more of the amino  
 CC acids corresponding to amino acids 24, 26 or 91 of the sequence given in  
 CC ADO44073 and the E6 polypeptide has no mutations or has mutations at any  
 CC one or more of the amino acids corresponding to amino acids 63 or 106 of  
 CC the sequence given in ADO44072. The polypeptides of the invention are  
 CC useful for treating or preventing human papillomavirus (HPV)-associated  
 CC cancers, such as cervical cancer. The fusion proteins and nucleic acids  
 CC encoding the fusion proteins are useful for generating immune responses  
 CC against HPV. They are also useful for treating lower gastrointestinal  
 CC tract cancers, e.g. anal cancer, and other cancers of the reproductive  
 CC system, including penile and vulvar cancer.  
 CC  
 SO Sequence 248 AA:

Query Match 98.9%; Score 821; DB 8; Length 248;  
 Best Local Similarity 98.7%; Pred. No. 2.8e-83;  
 Matches 148; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 FQDPERPRKLPOLCTELQTTIHDIILECVYCKQQLRREYVDFAFRDLCTIYRGNPY 61  
 |||

```

Db      99 FQDPQERPRKLPQLCTELQTTIHDIILECVYCKQOQLLREVVYDFAFRDLCTIVYRDSNPYA 158
Qy      62 VXDCKLKFYSKISSEYRHYCYSVYGTTLLEQYNNKPLCDLLIRICINQKPLCPBEKQKRLHD 121
Db      159 VCDCKLKFYSKISSEYRHYCYSVYGTTLLEQYNNKPLCDLLIRICINQKPLCPBEKQKRLHD 218
Qy      122 KORFHNIRGRWTRGRCMCCRSSRTRRETOL 151
Db      219 KORFHNIRGRWTRGRCMCCRSSRTRRETOL 248

RESULT 42
AAV57808
ID AAV57808 standard; peptide; 151 AA.
AC AAV57808;
DT 20-MAR-2000 (first entry)
XX
XX HPV-16 E6 protein amino acid sequence.
DE
XX Transcriptional adaptor motif; TRAM; TRAM interaction motif; TRIM;
KM creb binding protein; transcriptional regulation; cytosolic; antiviral;
KM cell cycle inhibitor; viral transcription inhibitor; cancer; tumour;
KM viral disease; viral infection; cell cycle; apoptosis; growth arrest.
XX
OS Human papillomavirus.
XX
XX W09961608-A2.
XX
XX 02-DEC-1999.
XX
XX 26-MAY-1999; 99WO-GB001668.
XX
XX 26-MAY-1998; 98GB-00011303.
XX
XX 05-JAN-1999; 99GB-00000157.
XX
XX (MOLE-) INST MOLECULAR & CELL BIOLOGY.
XX
XX O'Connor MJ, Zimmermann H;
XX
XX WPI; 2000-072620/06.
XX
XX Novel polypeptides cells useful for treating viral disease and cancer.
XX
XX Example 2; Fig 9; 73pp; English.
XX
XX The present invention describes a polypeptide comprising a
XX transcriptional adaptor motif (TRAM) or a TRAM-interaction motif (TRIM)
XX (I). (I) can be used for identifying compounds (II) comprising a
XX polypeptide capable of disrupting an interaction between a TRAM sequence
XX and/or a TRIM sequence. Polypeptides which bind to a TRAM sequence or a
XX TRIM sequence are identified by incubating the polypeptide with (I) and
XX determining if the polypeptide interacts with (I). Compound (II) is
XX useful for preparing a pharmaceutical composition and for disrupting an
XX interaction between TRAM sequence and TRIM sequence in vitro, thereby
XX inhibiting viral transcription or cell cycle progression in mammalian
XX cells especially cancer cell. Compounds which disrupt interaction between
XX TRIM/TRAM containing polypeptides can be used therapeutically to prevent
XX or treat viral diseases and tumours. The polypeptides reduce
XX susceptibility of cells to viral infection and regulate cell cycle
XX including apoptosis and growth arrest and can be used to produce
XX antibodies against the TRIM or TRAM sequences. HPV types associated with
XX high risk or low risk of cervical cancer can be distinguished based on
XX the ability of E6 polypeptides to bind to creb binding protein (CBP) TRAM
XX sequence. The present sequence represents a HPV-16 E6 protein amino acid
XX sequence from an example from the present invention
XX
XX Sequence 151 AA;
XX
XX Query Match 98.6%; Score 818; DB 3; Length 151;
XX Best Local Similarity 97.4%; Pred. No. 3.3e-83;
XX Matches 147; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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Qy      1 MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQOQLLREVVYDFAFRDLCTIVYRDSNPY 60
Db      1 MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQOQLLREVVYDFAFRDLCTIVYRDSNPY 60
Qy      61 AYVDCKLKFYSKISSEYRHYCYSVYGTTLLEQYNNKPLCDLLIRICINQKPLCPBEKQKRLHD 120
Db      61 AYVDCKLKFYSKISSEYRHYCYSVYGTTLLEQYNNKPLCDLLIRICINQKPLCPBEKQKRLHD 120
Qy      121 KORFHNIRGRWTRGRCMCCRSSRTRRETOL 151
Db      121 KORFHNIRGRWTRGRCMCCRSSRTRRETOL 151

RESULT 43
ADL90078
ID ADL90078 standard; protein; 158 AA.
AC ADL90078;
DT 17-JUN-2004 (first entry)
XX
XX Human papillomavirus 16-E6 protein, SEQ ID 18.
DE
XX Immune response; immunoglobulin; Ig; E6.
XX
XX Human papillomavirus.
XX
XX W02004027049-A2.
XX
XX 01-APR-2004.
XX
XX 18-SEP-2003; 2003WO-US030188.
XX
XX 20-SEP-2002; 2002US-0412219P.
XX
XX 14-MAR-2003; 2003WO-US007995.
XX
XX (ASTR-) ASTRAL INC.
XX
XX Bot A, Wang L, Smith D, Phillips B;
XX
XX WPI; 2004-295415/27.
XX
XX Generating an immune response to an antigen, useful for generating
XX desired T cell responses comprises administering an immunoglobulin having
XX one peptide epitope of the antigen attached to the immunoglobulin.
XX
XX Disclosure; Fig 1G; 154pp; English.
XX
XX The present invention relates to a method for generating an immune
XX response to an antigen in a patient. The method comprises administering
XX to the patient an immunoglobulin (Ig) or its portion where the Ig has at
XX least one peptide epitope of the antigen attached to the Ig or its
XX portion and administering the immunoglobulin or its portion in
XX conjunction with a RNA segment. The present sequence is an antigen
XX sequence, used to illustrate the invention.
XX
XX Sequence 158 AA;
XX
XX Query Match 98.2%; Score 815; DB 8; Length 158;
XX Best Local Similarity 97.4%; Pred. No. 7.6e-83;
XX Matches 147; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
XX
Qy      1 MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQOQLLREVVYDFAFRDLCTIVYRDSNPY 60
Db      8 MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQOQLLREVVYDFAFRDLCTIVYRDSNPY 67
Qy      61 AYVDCKLKFYSKISSEYRHYCYSVYGTTLLEQYNNKPLCDLLIRICINQKPLCPBEKQKRLHD 120
Db      68 AYVDCKLKFYSKISSEYRHYCYSVYGTTLLEQYNNKPLCDLLIRICINQKPLCPBEKQKRLHD 127
Qy      121 KORFHNIRGRWTRGRCMCCRSSRTRRETOL 151

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Db 128 KKORFNIRGRWTCMCCRSSRTRRETOL 158

RESULT 44  
AAW9369

ID AAW9369 standard; peptide; 243 AA.

AC AAW9369;

DT 17-OCT-2003 (revised)

DT 21-MAY-1999 (first entry)

DE Papillomavirus E6/protein F signal peptide fusion protein.

KW Antitumour; immunogen; intracellular localisation; cancer; dysplasia;

KM signal peptide; papillomavirus; infection; cervix uteri.

OS Human papillomavirus.

OS Measles virus.

OS Chimeric.

PN WO903885-A1.

PD 28-JAN-1999.

PF 17-JUL-1998; 98WO-FR001576.

PR 18-JUL-1997; 97FR-00009152.

PA (TRGE ) TRANSGENE SA.

PI Kieny M, Balloul J, Bizouarne N;

DR WPI; 1999-132161/11.

PT Antitumour composition containing immunogenic polypeptide with altered

PT localisation - or vector expressing this polypeptide, particularly for

PT treating or preventing cervical cancer associated with human papilloma

PT virus.

PS Claim 16; Page 54-55; 74pp; French.

CC The invention relates to an antitumour composition containing a

CC therapeutic or prophylactic agent or one or more immunogenic

CC polypeptides, where at least one polypeptide is modified so that its

CC intracellular localisation is different from that of the native

CC polypeptide. This sequence represents an example of a modified

CC immunogenic protein and corresponds to the E6 protein from human

CC papillomavirus fused to the measles virus protein F signal peptide. The

CC compositions, vectors and particles are used to treat or prevent cancers

CC and tumours, specifically those associated with papillomavirus infection

CC (e.g. cancer or low grade dysplasia of the cervix uteri). (Updated on 17-

CC OCT-2003 to standardise OS field)

XX Sequence 243 AA;

QY Query Match 93.9%; Score 779.5; DB 2; Length 243;

Db Best Local Similarity 94.7%; Pred. No. 1.2e-78;

Matches 143; Conservative 1; Mismatches 2; Indels 5; Gaps 1;

RESULT 45  
AAR40919

ID AAR40919 standard; protein; 149 AA.

AC AAR40919;

DT 22-FEB-1994 (first entry)

DE HPV E6 region product.

KW Human papilloma virus; HPV; benign; malignant.

OS Synthetic.

FT Key Location/Qualifiers

FT Disulfide-bond 30..33

FT Disulfide-bond 63..66

PN JP05192200-A.

PD 03-AUG-1993.

PF 19-AUG-1991; 91JP-00230839.

PR 20-AUG-1990; 90JP-00217067.

PA (TAKI ) TAKARA SHUZO CO LTD.

DR WPI; 1993-277497/35.

DR N-PSDB; AAQ48575.

PT Detecting benign and/or malignant human papilloma virus - by detecting

PT DNA sequence of E6 and/or E7 region of human papilloma virus.

CC Probes are designed to detect benign and/or malignant human papilloma

CC virus. The probes bind to the E6 and/or E7 region of human papilloma

CC virus

XX Sequence 149 AA;

QY Query Match 69.9%; Score 580; DB 2; Length 149;

Db Best Local Similarity 71.5%; Pred. No. 1.5e-56;

Matches 108; Conservative 13; Mismatches 28; Indels 2; Gaps 1;

QY 1 MFQDPOERPRKLPOLCTELQTTIHDIILBCVYCKQQLRREYVDFAFRDLCTIYRDGPNY 60

Db 1 MFQDPAERPYKHLNDLCNEVESIHEICLNCVYCKQQLRREYVDFACYDLCIYRREGQPY 60

QY 61 AVXDCKLKFYSKISEYRHYCYVYGTTLBOQYNNKPLCDLLIRCLNXXOKPLCPBEKORHLD 120

Db 61 GVCMKCLKFYSKISEYRHYCYVYGTTLBOQYNNKPLCDLLIRCLNXXOKPLCPBEKORHLD 120

QY 121 KKORFNIRGRWTCMCCRSSRTRRETOL 151

Db 121 EKORFNIRGRWTCMCCRSSRTRRETOL 149

RESULT 46  
ADO44077

ID ADO44077 standard; protein; 149 AA.

AC ADO44077;

DT 15-JUL-2004 (first entry)

DE Amino acid sequence of the E6 polypeptide of HPV35.

XX E6 protein; E7 protein; fusion protein; HPV; HPV-associated cancer;

XX cervical cancer; immune response; lower gastrointestinal tract cancer;

XX anal cancer; reproductive system cancer; penile cancer; vulvar cancer.

XX	Human papillomavirus type 35.
OS	WO2004030636-A2.
FN	
XX	
XX	15-APR-2004.
PD	
XX	
Pf	02-OCT-2003; 2003MO-US031726.
XX	
PR	03-OCT-2002; 2002US-0415929P.
XX	
PA	(AMHP ) WYETH HOLDINGS CORP.
XX	
PI	Smith L, Casasetti MC;
DR	WPI: 2004-316328/29.
XX	N-P8DB; ADO44104.
PT	New polypeptide comprising human papillomavirus E6 and E7 polypeptides,
XX	useful for treating or preventing human papillomavirus (HPV)-associated
XX	cancers, e.g. cervical cancer.
PS	Disclosure; Page 80; 101pp; English.
CC	
XX	ADO44074-ADO44085 represent E6 polypeptides from human papillomaviruses.
CC	ADO44098 is the consensus sequence derived from these polypeptides. The
CC	specification describes human papillomavirus E6 and E7 polypeptides,
CC	where the E7 polypeptide has mutations at any one or more of the amino
CC	acids corresponding to amino acids 24, 26 or 91 of the sequence given in
CC	ADO44073 and the E6 polypeptide has no mutations or has mutations at any
CC	one or more of the amino acids corresponding to amino acids 63 or 106 of
CC	this sequence given in ADO44072. The polypeptides of the invention are
CC	useful for treating or preventing human papillomavirus (HPV)-associated
CC	cancer, such as cervical cancer. The fusion proteins and nucleic acids
CC	encoding the fusion proteins are useful for generating immune responses
CC	against HPV. They are also useful for treating lower gastrointestinal
CC	tract cancers, e.g. anal cancer, and other cancers of the reproductive
CC	system, including penile and vulvar cancer.
SQ	
Sequence 149 AA;	
Query Match	69.6%; Score 578; DB 8; Length 149;
Best Local Similarity	71.5%; Pred. No.2.5e-56;
Matches 108; Conservative 13; Mismatches 28; Indels 2; Gaps 1;	
Oy	1 MFODFOERPRKLPQLCTELQTTHDIIIECYCKQOLLREYYDFAFPLDLCTIVRDGNPY 60
Dd	1 MFODFAEPRPKXLDHCNEVEESIHETCLNCVCYCKOELORSEVYDDACVDLCTIVREGOYP 60
Oy	61 AVXDLCLEFYSKISSEYRHVCYSVGTTTLEQOVNRPGLCDLLIRCIHXOKRLCPKEEKORHLD 120
Dd	61 GCMCMLCFYSKISSTRMRYSVGETTEBKQCNKOLCHLLIRCIQCXPCEVKORHLE 120
Oy	121 KQRFPHNIRGRWTGRCMSGCCSSRTRETQL 151
Dd	121 EKGRPHNIGRWTRGRCMSGWKP--TRRETV 149
RESULT 47	
AEA98533	
ID	AEA98533 standard; protein; 149 AA.
XX	
AC	AEA98533;
XX	
DT	08-SEP-2005 (first entry)
XX	
DE	HPV (oncogenic strain) E6 amino acid sequence SEQ ID 14.
XX	
KW	Papillomavirus infection; virucide; E6 protein; diagnosis; antibody;
XX	cancer; cervix tumor; cytostatic.
OS	Human papillomavirus; strain 35.
XX	
UN	US2005142541-A1.

[illegible]

PF 24-APR-2002; 2002CN-00117143.  
XX  
XX 24-APR-2002; 2002CN-00117143.  
XX  
XX (ONCO-) INST ONCOLOGY TUMOR HOSPITAL CHINESE ACA.  
XX  
XX  
PI Zhao Q;  
XX  
XX WPI; 2003-258260/26.  
XX  
XX N-PSDB; ADF31984.  
XX  
XX Human papillomavirus E6/E7 fusion gene and its efficient expression  
XX carrier and fusion protein vaccine.  
XX  
XX Claim 8; SEQ ID NO 2; 16pp; Chinese.  
XX  
XX The present invention relates to human papillomavirus E6/E7 fusion gene,  
XX its preparing process, the process for configuring the efficient  
XX expression carrier containing the gene and resultant expression carrier,  
XX the fusion protein prepared from the gene, and the application of the  
XX fusion gene and expression protein to medical science and medicine to  
XX treat cervical cancer are disclosed. The present sequence represents the  
XX human papillomavirus fusion gene.  
XX  
XX Sequence 180 AA;  
SQ  
Query Match 68.9%; Score 572; DB 7; Length 180;  
Best Local Similarity 93.8%; Pred. No. 1.5e-55;  
Matches 106; Conservative 1; Mismatches 6; Indels 0; Gaps 0;  
QY 1 MFQDPQRRPRKLPOLCTELQTTTHDILIECYCKQQLRRRVNFAFADLCIVYRDGPNY 60  
DB 8 MFQDPQRRPRKLPOLCTELQTTTHDILIECYCKQQLRRRVNFAFADLCIVYRDGPNY 67  
QY 61 AVXDCKLKFYSKISEYHYCYSVYGTLEQOYNRPCLDLIRCIINXOKPLCE 113  
DB 68 AVCDKCLKFYSKISEYHYRYSLVGTLEQOYNRPCLDLIRCIINXOKPLCE 120  
RESULT 49  
AAB98434  
ID AAB98434 standard; protein; 149 AA.  
XX  
XX AAB98434;  
XX  
XX 22-AUG-2001 (first entry)  
XX  
XX Human papillomavirus protein HPV31 E6.  
XX  
XX Human papillomavirus; human leukocyte antigen; HLA; immune response; HPV;  
XX epitope; T cell; identification; vaccine; infection; genital wart;  
XX neoplastic growth; antiviral.  
XX  
XX Human papillomavirus.  
XX  
XX WO200141799-A1.  
XX  
XX 14-JUN-2001.  
XX  
XX 11-DEC-2000; 2000WO-US03549.  
XX  
XX 10-DEC-1999; 99US-012705P.  
XX  
XX 15-AUG-2000; 2000US-00641528.  
XX  
XX (BPI-M-) EPIMUNE INC.  
XX  
XX Sette A, Sidney J, Southwood S, Cheenut R, Celis B, Grey HM;  
XX  
XX WPI; 2001-381497/40.  
XX  
XX An isolated human papilloma virus (HPV) epitope, useful in vaccines for  
XX treating HPV infections.  
XX

PS Disclosure; Page 23; 756pp; English.  
XX  
XX The present invention describes an isolated prepared human papillomavirus  
XX (HPV) epitope (1). (1) has antiviral activity, and can be used in vaccine  
XX production. Peptides and corresponding nucleic acid compositions from the  
XX present invention are useful for stimulating an immune response to HPV by  
XX stimulating the production of CTL or HTL responses, specifically in the  
XX treatment or prophylaxis of HPV infection, in persons who have not  
XX manifested symptoms e.g. genital warts or neoplastic growth. The peptides  
XX can also be used in a tetramer staining assay to assess peripheral blood  
XX mononuclear cells for the presence of antigen-specific CTLs following  
XX exposure to a pathogen or immunogen, and as reagents to evaluate immune  
XX recall responses or evaluate the efficacy of a vaccine. The vaccine  
XX compositions are useful for removing warts or treating HPV infections.  
XX The epitopes for inclusion in an epitope-base vaccine may be selected  
XX from conserved regions of viral or tumor-associated antigens, which  
XX reduces the likelihood of escape mutants, also immunosuppressive epitopes  
XX that may be present in whole antigens can be avoided with the use of  
XX epitope-base vaccines. An additional advantage is the ability to combine  
XX selected epitopes (CTL and HTL) and to modify the composition of the  
XX epitopes achieving enhanced immunogenicity, the major benefit of the  
XX vaccine is that is safe and efficacious. AAB98391 to AAB98477 represent  
XX polypeptide sequences used in the exemplification of the present  
XX invention.  
XX  
XX Sequence 149 AA;  
SQ  
Query Match 63.0%; Score 523; DB 4; Length 149;  
Best Local Similarity 64.9%; Pred. No. 3.6e-50;  
Matches 98; Conservative 18; Mismatches 33; Indels 2; Gaps 1;  
QY 1 MFQDPQRRPRKLPOLCTELQTTTHDILIECYCKQQLRRRVNFAFADLCIVYRDGPNY 60  
DB 1 MFQDPQRRPRKLPOLCTELQTTTHDILIECYCKQQLRRRVNFAFADLCIVYRDGPNY 60  
QY 61 AVXDCKLKFYSKISEYHYCYSVYGTLEQOYNRPCLDLIRCIINXOKPLCEKORHLD 120  
DB 61 GVCCKLKFYSKISEYHYRYSLVGTLEQOYNRPCLDLIRCIINXOKPLCEKORHLD 120  
QY 121 KQRFHNIRGRWTRGCMSCCRSRTRETQI 151  
DB 121 KKRFRHNIRGRWTRGCIACWR--RPRRETQV 149  
RESULT 50  
ADO44075  
ID ADO44075 standard; protein; 149 AA.  
XX  
XX ADO44075;  
XX  
XX 15-JUN-2004 (first entry)  
XX  
XX Amino acid sequence of the E6 polypeptide of HPV31.  
XX  
XX E6 protein; E7 protein; fusion protein; HPV; HPV-associated cancer;  
XX cervical cancer; immune response; lower gastrointestinal tract cancer;  
XX anal cancer; reproductive system cancer; penile cancer; vulvar cancer.  
XX  
XX Human papillomavirus type 31.  
XX  
XX WO2004030636-A2.  
XX  
XX 15-APR-2004.  
XX  
XX 02-OCT-2003; 2003WO-US031726.  
XX  
XX 03-OCT-2002; 2002US-0415929P.  
XX  
XX (AMHP) WYETH HOLDINGS CORP.  
XX  
XX Smith L, Casasetti MC;  
XX  
XX WPI; 2004-316328/29.  
XX

DR N-PSDB; ADO44102.  
 XX  
 PT New polypeptide comprising human papillomavirus E6 and E7 polypeptides,  
 PT useful for treating or preventing human papillomavirus (HPV)-associated  
 PT cancers, e.g. cervical cancer.  
 XX  
 XX Disclosure; Page 78-79; 101pp; English.  
 XX  
 CC ADO44074-ADO44085 represent E6 polypeptides from human papillomaviruses.  
 CC ADO44098 is the consensus sequence derived from these polypeptides. The  
 CC specification describes human papillomavirus E6 and E7 polypeptides.  
 CC where the E7 polypeptide has mutations at any one or more of the amino  
 CC acids corresponding to amino acids 24, 26 or 91 of the sequence given in  
 CC ADO44073 and the E6 polypeptide has no mutations or has mutations at any  
 CC one or more of the amino acids corresponding to amino acids 63 or 106 of  
 CC the sequence given in ADO44072. The polypeptides of the invention are  
 CC useful for treating or preventing human papillomavirus (HPV)-associated  
 CC cancer, such as cervical cancer. The fusion proteins and nucleic acids  
 CC encoding the fusion proteins are useful for generating immune responses  
 CC against HPV. They are also useful for treating lower gastrointestinal  
 CC tract cancers, e.g. anal cancer, and other cancers of the reproductive  
 CC system, including penile and vulvar cancer.  
 CC  
 XX Sequence 149 AA;  
 SQ  
 Query Match 63.0%; Score 523; DB 8; Length 149;  
 Best Local Similarity 64.9%; Pred. No. 3.6e-50;  
 Matches 98; Conservative 18; Mismatches 33; Indels 2; Gaps 1;  
 QY 1 MFQDPQERRRLPOLCTELQTTIHDIIECYCYCKQQLRREYDPAFRDLCTIVRDGMPY 60  
 DB 1 MFKNPAERPRKLHLSALRIPYDELRLNCVCYCKQLTETVLDPAFTDLTVYRDDTPH 60  
 QY 61 AVXDKCLKFYKISRYRYHCYSVGTTLRQOYNKPLCDLIRCTINXQKPLCPBEKQRHLD 120  
 DB 61 GVCIRKCLRFYKSVSEFRWRYRSVGTTLRKLTKNGICDLIRCTICORPLCPBEKQRHLD 120  
 QY 121 KKQRFHNIRGRWTRGSCSCRSRTRRETQL 151  
 DB 121 KKKRFHNIRGRWTRGRCIACWR--RPRTETQV 149

RESULT 51  
 AEA98537  
 ID AEA98537 standard; protein; 149 AA.  
 AC AEA98537;  
 XX  
 DT 08-SEP-2005 (first entry)  
 XX  
 DE HPV (oncogenic strain) E6 amino acid sequence SEQ ID 18.  
 XX  
 KM Papillomavirus infection; virucide; E6 protein; diagnosis; antibody;  
 KM cancer; cervix tumor; cytostatic.  
 XX  
 OS Human papillomavirus; strain 31.  
 XX  
 PN US2005142541-A1.  
 XX  
 PD 30-JUN-2005.  
 XX  
 PF 23-DEC-2004; 2004US-00021949.  
 XX  
 PR 23-DEC-2003; 2003US-0532373P.  
 XX  
 PA (ARBO-) ARBOR VITA CORP.  
 XX  
 PI Lu PS, Garman JD, Belmares MF, Somoza DC, Schweizer J;  
 XX WPI; 2005-457781/46.  
 XX  
 PT New antibody composition comprising a mixture of monoclonal antibodies  
 PT for oncogenic strains of human papilloma virus, useful for diagnosing

PT cancer.  
 XX  
 PS Disclosure; SEQ ID NO 18; 161pp; English.  
 XX  
 CC The invention relates to an antibody composition comprising a mixture of  
 CC monoclonal antibodies that specifically bind to E6 proteins of human  
 CC papilloma virus (HPV) strains 16, 18, 31, 33 and 45, where at least one  
 CC of the monoclonal antibodies specifically binds to E6 proteins of at  
 CC least three different oncogenic HPV strains. Also included are a  
 CC diagnostic kit (for detecting an HPV E6 polypeptide in a sample,  
 CC comprising the antibody composition above), a method of detecting an HPV  
 CC E6 protein in a sample, a method of detecting the presence of an  
 CC oncogenic HPV E6 protein in a sample and a system for detecting the  
 CC presence of an oncogenic HPV E6 polypeptide in a sample (comprising a  
 CC first and a second binding partner for an oncogenic HPV E6 polypeptide,  
 CC where the first binding partner is a PDZ domain protein and the second  
 CC binding partner is an antibody that specifically binds to the E6 proteins  
 CC of at least three different oncogenic HPV strains). The antibody  
 CC composition, kit, methods, and system are useful for diagnosing cancer,  
 CC particularly cervical cancer. The present sequence is an HPV E6 protein.  
 CC  
 XX Sequence 149 AA;  
 SQ  
 Query Match 63.0%; Score 523; DB 9; Length 149;  
 Best Local Similarity 64.9%; Pred. No. 3.6e-50;  
 Matches 98; Conservative 18; Mismatches 33; Indels 2; Gaps 1;  
 QY 1 MFQDPQERRRLPOLCTELQTTIHDIIECYCYCKQQLRREYDPAFRDLCTIVRDGMPY 60  
 DB 1 MFKNPAERPRKLHLSALRIPYDELRLNCVCYCKQLTETVLDPAFTDLTVYRDDTPH 60  
 QY 61 AVXDKCLKFYKISRYRYHCYSVGTTLRQOYNKPLCDLIRCTINXQKPLCPBEKQRHLD 120  
 DB 61 GVCIRKCLRFYKSVSEFRWRYRSVGTTLRKLTKNGICDLIRCTICORPLCPBEKQRHLD 120  
 QY 121 KKQRFHNIRGRWTRGSCSCRSRTRRETQL 151  
 DB 121 KKKRFHNIRGRWTRGRCIACWR--RPRTETQV 149

RESULT 52  
 AEC98865  
 ID AEC98865 standard; protein; 149 AA.  
 AC AEC98865;  
 XX  
 DT 01-DEC-2005 (first entry)  
 XX  
 DE HPV\_31 Envelope protein E6.  
 XX  
 KM Human papilloma virus infection; virucide; cancer; cytostatic; vaccine;  
 KM epitope mapping; immune stimulation; cytotoxic T-lymphocyte.  
 XX  
 OS Human papillomavirus type 31.  
 XX  
 PN WO2005089164-A2.  
 XX  
 PD 29-SEP-2005.  
 XX  
 PF 03-JAN-2005; 2005WO-US000077.  
 XX  
 PR 31-DEC-2003; 2003US-0533211P.  
 XX  
 PR 02-JUL-2004; 2004US-0584652P.  
 XX  
 PA (EPTM-) EPTMONE INC.  
 PA (INNO-) INNOGENETICS NV.  
 PA (CHES/) CHESNUT R.  
 PA (NEWM/) NEWMAN M J.  
 PA (MOTH/) MOTH B.  
 PA (BAKE/) BAKER D.  
 PA (SOUT/) SOUTHWOOD S.  
 PA (BABE/) BABE L M.  
 PA (CHEN/) CHEN Y.

PA (DEYO/) DEYOUNG L M.  
 PA (HUAN/) HUANG M T F.  
 PA (POME/) POWER S D.  
 PI Chesnut R, Newman MJ, Mothe B, Baker D, Southwood S, Babe LM;  
 PI Chen Y, Deyoung LM, Huang MTF, Power SD;  
 XX WPI; 2005-658982/67.  
 DR  
 XX New polynucleotide comprises a multi-epitope construct comprising nucleic  
 PT acids encoding the human papillomavirus (HPV) cytotoxic T lymphocyte  
 PT (CTL) epitopes, useful in preparing a vaccine against HPV.  
 XX  
 PS Example 10, Page 349; 518pp; English.  
 XX  
 CC The invention relates to a new polynucleotide comprising a multi-epitope  
 CC construct comprising nucleic acids encoding the human papillomavirus  
 CC (HPV) cytotoxic T lymphocyte (CTL) epitopes e.g., HPV16.E1.214, and that  
 CC are directly or indirectly joined to one another in the same reading  
 CC frame, a vaccine minigene. Also included are a vector comprising the  
 CC multi-epitope construct, a polypeptide comprising an amino acid sequence  
 CC encoded by the polynucleotide, a composition (comprising the  
 CC polynucleotide, vector and/or polypeptide and a carrier), a cell  
 CC (comprising the polynucleotide, vector or polypeptide), inducing an  
 CC immune response against human papillomavirus virus (HPV) and making the  
 CC polynucleotide, vector or polypeptide. The epitopes are derived from  
 CC different strains of HPV and are from the E1, E2, E6 and E7 proteins. The  
 CC epitopes may be linked via a GP-anchor/spacer peptide. The order of the  
 CC epitopes in the vaccine protein are disclosed in the tables referred to  
 CC in the claims of the specification. The polynucleotide, vector or  
 CC polypeptide is useful in preparing a composition for inducing an immune  
 CC response against human papillomavirus virus (HPV) and thus providing a  
 CC defense against HPV infection and HPV-related cancers. The present  
 CC invention is an HPV protein used to derive epitopes for the vaccine of the  
 CC invention.  
 XX  
 SQ Sequence 149 AA;  
 Query Match 63.0%; Score 523; DB 9; Length 149;  
 Best Local Similarity 64.9%; Pred. No. 3.6e-50;  
 Matches 98; Conservative 18; Mismatches 33; Indels 2; Gaps 1;  
 QY 1 MFODPOEPRKLPOLCTELQTTIHDIIECYCKQQLRREVDPAFRLDIYVRDGPY 60  
 DB 1 MFKNPAERPRKLEHSSALRIPYDELRLNVCYCKQQLTEVLDFAFDITIVRDDPH 60  
 QY 61 AVXDKCLKFYSKISEYRHVCYSVYGTTLQOYNKPLCDLLRCLNXXQKPLCPPEEKORHLD 120  
 DB 61 GVCTKCLRFYSKVESEFRMYRSYVGTTLKLTNKGICDILLRCLTCQRPCLPPEEKORHLD 120  
 QY 121 KKORFHNIRGWRGRCMSSCRSSRTRETOL 151  
 DB 121 KKKRFHNIGRWTRGRCIACWR--RPRRTETOV 149  
 RESULT 53  
 AEC96405  
 ID AEC96405 standard; protein, 149 AA.  
 AC AEC96405;  
 XX  
 DT 01-DEC-2005 (first entry)  
 XX  
 DE HPV protein E6 from HPV31.  
 XX  
 KM Human papilloma virus infection; virucide; cancer; cytostatic; vaccine;  
 KM epitope mapping; immune stimulation; cytotoxic T-lymphocyte.  
 XX  
 OS Human papillomavirus type 31.  
 XX  
 PN WO2005089164-A2.  
 XX  
 PD 29-SEP-2005.

XX  
 PF 03-JAN-2005; 2005MO-US000077.  
 XX  
 XX 31-DEC-2003; 2003US-0533211P.  
 PR 02-JUL-2004; 2004US-0584652P.  
 XX  
 XX (EPIM-) EPIMUNE INC.  
 PA (INNO-) INNOCENTICS NV.  
 PA (CHES/) CHESNUT R.  
 PA (NEWM/) NEWMAN M J.  
 PA (MOTH/) MOTH B.  
 PA (BAKE/) BAKER D.  
 PA (SOUT/) SOUTWOOD S.  
 PA (BABE/) BABE L M.  
 PA (CHEN/) CHEN Y.  
 PA (DEYO/) DEYOUNG L M.  
 PA (HUAN/) HUANG M T F.  
 PA (POME/) POWER S D.  
 PI Chesnut R, Newman MJ, Mothe B, Baker D, Southwood S, Babe LM;  
 PI Chen Y, Deyoung LM, Huang MTF, Power SD;  
 XX WPI; 2005-658982/67.  
 DR  
 XX New polynucleotide comprises a multi-epitope construct comprising nucleic  
 PT acids encoding the human papillomavirus (HPV) cytotoxic T lymphocyte  
 PT (CTL) epitopes, useful in preparing a vaccine against HPV.  
 XX  
 PS Disclosure; Page 59; 518pp; English.  
 XX  
 CC The invention relates to a new polynucleotide comprising a multi-epitope  
 CC construct comprising nucleic acids encoding the human papillomavirus  
 CC (HPV) cytotoxic T lymphocyte (CTL) epitopes e.g., HPV16.E1.214, and that  
 CC are directly or indirectly joined to one another in the same reading  
 CC frame, a vaccine minigene. Also included are a vector comprising the  
 CC multi-epitope construct, a polypeptide comprising an amino acid sequence  
 CC encoded by the polynucleotide, a composition (comprising the  
 CC polynucleotide, vector and/or polypeptide and a carrier), a cell  
 CC (comprising the polynucleotide, vector or polypeptide), inducing an  
 CC immune response against human papillomavirus virus (HPV) and making the  
 CC polynucleotide, vector or polypeptide. The epitopes are derived from  
 CC different strains of HPV and are from the E1, E2, E6 and E7 proteins. The  
 CC epitopes may be linked via a GP-anchor/spacer peptide. The order of the  
 CC epitopes in the vaccine protein are disclosed in the tables referred to  
 CC in the claims of the specification. The polynucleotide, vector or  
 CC polypeptide is useful in preparing a composition for inducing an immune  
 CC response against human papillomavirus virus (HPV) and thus providing a  
 CC defense against HPV infection and HPV-related cancers. The present  
 CC invention is an HPV protein used to derive epitopes for the vaccine of the  
 CC invention.  
 XX  
 SQ Sequence 149 AA;  
 Query Match 63.0%; Score 523; DB 9; Length 149;  
 Best Local Similarity 64.9%; Pred. No. 3.6e-50;  
 Matches 98; Conservative 18; Mismatches 33; Indels 2; Gaps 1;  
 QY 1 MFODPOEPRKLPOLCTELQTTIHDIIECYCKQQLRREVDPAFRLDIYVRDGPY 60  
 DB 1 MFKNPAERPRKLEHSSALRIPYDELRLNVCYCKQQLTEVLDFAFDITIVRDDPH 60  
 QY 61 AVXDKCLKFYSKISEYRHVCYSVYGTTLQOYNKPLCDLLRCLNXXQKPLCPPEEKORHLD 120  
 DB 61 GVCTKCLRFYSKVESEFRMYRSYVGTTLKLTNKGICDILLRCLTCQRPCLPPEEKORHLD 120  
 QY 121 KKORFHNIRGWRGRCMSSCRSSRTRETOL 151  
 DB 121 KKKRFHNIGRWTRGRCIACWR--RPRRTETOV 149  
 RESULT 54  
 AAB98447  
 ID AAB98447 standard; protein, 149 AA.

XX AAB98447;  
AC  
XX  
XX 22-AUG-2001 (first entry)  
DT  
XX  
DE Human papillomavirus protein HPV33 E6.  
XX  
XX Human papillomavirus; human leukocyte antigen; HLA; immune response; HPV;  
KM epitope; T cell; identification; vaccine; infection; genital wart;  
KM neoplastic growth; antiviral.  
XX  
OS Human papillomavirus.  
XX WO200141799-A1.  
PN  
XX 14-JUN-2001.  
PD  
XX 11-DEC-2000; 2000MO-US033549.  
PE  
XX 10-DEC-1999; 99US-0127205P.  
PR 15-AUG-2000; 2000US-00641528.  
PR  
XX (EPRIM-) EPRIMUNE INC.  
PA  
XX Sette A, Sidney J, Southwood S, Chesnut R, Celis E, Grey HM;  
PI WPI; 2001-381497/40.  
DR  
XX An isolated human papilloma virus (HPV) epitope, useful in vaccines for  
PT treating HPV infections.  
PT  
XX Disclosure; Page 26; 756pp; English.  
PS  
XX  
XX The present invention describes an isolated prepared human papillomavirus  
CC (HPV) epitope (I). (I) has antiviral activity, and can be used in vaccine  
CC production. Peptides and corresponding nucleic acid compositions from the  
CC present invention are useful for stimulating an immune response to HPV by  
CC stimulating the production of CTL or HTL responses, specifically in the  
CC treatment or prophylaxis of HPV infection, in persons who have not  
CC manifested symptoms e.g. genital warts or neoplastic growth. The peptides  
CC can also be used in a tetramer staining assay to assess peripheral blood  
CC mononuclear cells for the presence of antigen-specific CTLs following  
CC exposure to a pathogen or immunogen, and as reagents to evaluate immune  
CC recall responses or evaluate the efficacy of a vaccine. The vaccine  
CC compositions are useful for removing warts or treating HPV infections.  
CC The epitopes for inclusion in an epitope-base vaccine may be selected  
CC from conserved regions of viral or tumour-associated antigens, which  
CC reduces the likelihood of escape mutants, also immunosuppressive epitopes  
CC that may be present in whole antigens can be avoided with the use of  
CC epitope-base vaccines. An additional advantage is the ability to combine  
CC selected epitopes (CTL and HTL) and to modify the composition of the  
CC epitopes achieving enhanced immunogenicity, the major benefit of the  
CC vaccine is that is safe and efficacious. AAB98391 to AAB98477 represent  
CC polypeptide sequences used in the exemplification of the present  
CC invention  
XX  
XX  
SQ Sequence 149 AA;  
Query Match 62.7%; Score 520; DB 4; Length 149;  
Best Local Similarity 63.6%; Pred. No. 7.9e-50;  
Matches 96; Conservative 19; Mismatches 34; Indels 2; Gaps 1;

RESULT 55  
ADO44076  
ID ADO44076 standard; protein; 149 AA.  
XX  
XX ADO44076;  
AC  
XX  
DT 15-JUL-2004 (first entry)  
XX  
DE Amino acid sequence of the E6 polypeptide of HPV33.  
XX  
XX E6 protein; E7 protein; fusion protein; HPV; HPV-associated cancer;  
KM cervical cancer; immune response; lower gastrointestinal tract cancer;  
KM anal cancer; reproductive system cancer; penile cancer; vulvar cancer.  
XX  
OS Human papillomavirus type 33.  
XX WO2004030636-A2.  
PN  
XX 15-APR-2004.  
PD  
XX 02-OCT-2003; 2003WO-US031726.  
PE  
XX 03-OCT-2002; 2002US-0415929P.  
PR  
XX (AMHP ) WYETH HOLDINGS CORP.  
PA  
XX Smith L, Casasetti MC;  
PI WPI; 2004-316328/29.  
DR N-PSDB; ADO44103.  
DR  
XX New polypeptide comprising human papillomavirus E6 and E7 polypeptides,  
PT useful for treating or preventing human papillomavirus (HPV)-associated  
PT cancers, e.g. cervical cancer.  
XX  
XX Disclosure; Page 79-80; 101pp; English.  
PS  
XX ADO44074-ADO44085 represent E6 polypeptides from human papillomaviruses.  
CC ADO44098 is the consensus sequence derived from these polypeptides. The  
CC specification describes human papillomavirus E6 and E7 polypeptides,  
CC where the E7 polypeptide has mutations at any one or more of the amino  
CC acids corresponding to amino acids 24, 26 or 91 of the sequence given in  
CC ADO44073 and the E6 polypeptide has no mutations or has mutations at any  
CC one or more of the amino acids corresponding to amino acids 63 or 106 of  
CC the sequence given in ADO44072. The polypeptides of the invention are  
CC useful for treating or preventing human papillomavirus (HPV)-associated  
CC cancers, such as cervical cancer. The fusion proteins and nucleic acids  
CC encoding the fusion proteins are useful for generating immune responses  
CC against HPV. They are also useful for treating lower gastrointestinal  
CC tract cancers, e.g. anal cancer, and other cancers of the reproductive  
CC system, including penile and vulvar cancer.  
XX  
XX  
SQ Sequence 149 AA;  
Query Match 62.7%; Score 520; DB 8; Length 149;  
Best Local Similarity 63.6%; Pred. No. 7.9e-50;  
Matches 96; Conservative 19; Mismatches 34; Indels 2; Gaps 1;

RESULT 56  
AEA98535  
ID AEA98535 standard; protein, 149 AA.  
XX  
XX AEA98535;  
AC  
XX  
XX 08-SEP-2005 (first entry)  
DT  
DE HPV (oncogenic strain) E6 amino acid sequence SEQ ID 16.  
XX  
XX Papillomavirus infection; virucide; E6 protein; diagnosis; antibody;  
XX  
XX cancer; cervix tumor; cytostatic.  
XX  
XX Human papillomavirus; strain 33.  
OS  
XX US2005142541-A1.  
XX  
XX 30-JUN-2005.  
XX  
XX 23-DEC-2004; 2004US-00021949.  
XX  
XX 23-DEC-2003; 2003US-0532373P.  
XX  
XX (ARBO-) ARBOR VITA CORP.  
XX  
XX Lu PS, Garman JD, Belmares MP, Somoza DC, Schweizer J;  
XX  
XX WPI; 2005-457781/46.  
XX  
XX New antibody composition comprising a mixture of monoclonal antibodies  
XX  
XX for oncogenic strains of human papilloma virus, useful for diagnosing  
XX  
XX cancer.  
XX  
XX Disclosure; SEQ ID NO 16; 161pp; English.  
XX  
XX The invention relates to an antibody composition comprising a mixture of  
XX  
XX monoclonal antibodies that specifically bind to E6 proteins of human  
XX  
XX papilloma virus (HPV) strains 16, 18, 31, 33 and 45, where at least one  
XX  
XX of the monoclonal antibodies specifically binds to E6 proteins of at  
XX  
XX least three different oncogenic HPV strains. Also included are a  
XX  
XX diagnostic kit (for detecting an HPV E6 polypeptide in a sample,  
XX  
XX comprising the antibody composition above), a method of detecting an HPV  
XX  
XX E6 protein in a sample, a method of detecting the presence of an  
XX  
XX oncogenic HPV E6 protein in a sample and a system for detecting the  
XX  
XX presence of an oncogenic HPV E6 polypeptide in a sample (comprising a  
XX  
XX first and a second binding partner for an oncogenic HPV E6 polypeptide,  
XX  
XX where the first binding partner is a PDZ domain protein and the second  
XX  
XX binding partner is an antibody that specifically binds to the E6 proteins  
XX  
XX of at least three different oncogenic HPV strains). The antibody  
XX  
XX composition, kit, methods, and system are useful for diagnosing cancer,  
XX  
XX particularly cervical cancer. The present sequence is an HPV E6 protein.  
XX  
XX  
SQ Sequence 149 AA;  
Query Match 62.7%; Score 520; DB 9; Length 149;  
Best Local Similarity 63.6%; Pred. No. 7.9e-50;  
Matches 96; Conservative 19; Mismatches 34; Indels 2; Gaps 1;  
OY 1 MFQDPEPRPKLPOLCTELQTTIHDIIECVYCKOQLRRREYVDPAPDLCTVYRDNAPY 60  
DB 1 MFQDPEPRPKLPOLCTELQTTIHDIIECVYCKOQLRRREYVDPAPDLCTVYRDNAPY 60  
OY 61 AVXDCKLKYKISIEYRYHYCVSVYGTTLBQYNNKPLCDLLIRICINXQKPLCEEKORHLD 120  
DB 61 GICKCKLFLSKISIEYRYHYCVSVYGTTLBQYNNKPLCDLLIRICINXQKPLCEEKORHLD 120  
OY 121 KQORFHNIRGRWTCGSCSSRRTRRETOL 151  
DB 121 LMKRFHNISGRWAGRCACWRS--RRRETAL 149

ID AEC96412 standard; protein, 149 AA.  
XX  
XX AEC96412;  
AC  
XX  
XX 01-DEC-2005 (first entry)  
DT  
XX  
XX HPV protein E6 from HPV33.  
DE  
XX  
XX Human papilloma virus infection; virucide; cancer; cytostatic; vaccine;  
XX  
XX epitope mapping; immune stimulation; cytotoxic T-lymphocyte.  
XX  
XX Human papillomavirus type 33.  
OS  
XX WO2005089164-A2.  
XX  
XX 29-SEP-2005.  
XX  
XX 03-JAN-2005; 2005WO-US000077.  
XX  
XX 31-DEC-2003; 2003US-0533211P.  
XX  
XX 02-JUL-2004; 2004US-0584652P.  
XX  
XX (EPIM-) EPIMUNE INC.  
XX  
XX (INNO-) INNOGENETICS NV.  
XX  
XX (CHES-) CHESNUT R.  
XX  
XX (NEMM-) NEMMAN M J.  
XX  
XX (MOTH-) MOTH B.  
XX  
XX (BAKE-) BAKER D.  
XX  
XX (SOUT-) SOUTHWOOD S.  
XX  
XX (BABE-) BABE L M.  
XX  
XX (CHEN-) CHEN Y.  
XX  
XX (DEYO-) DEYOONG L M.  
XX  
XX (HUAN-) HUANG M T F.  
XX  
XX (POWE-) POWER S D.  
XX  
XX Chensu R, Newman MJ, Mothe B, Baker D, Southwood S, Babe LM;  
XX  
XX Chen Y, Deyoung LM, Huang MTF, Power SD;  
XX  
XX WPI; 2005-658982/67.  
XX  
XX New polynucleotide comprises a multi-epitope construct comprising nucleic  
XX  
XX acids encoding the human papillomavirus (HPV) cytotoxic T lymphocyte  
XX  
XX (CTL) epitopes, useful in preparing a vaccine against HPV.  
XX  
XX Disclosure; Page 61; 518pp; English.  
XX  
XX The invention relates to a new polynucleotide comprising a multi-epitope  
XX  
XX construct comprising nucleic acids encoding the human papillomavirus  
XX  
XX (HPV) cytotoxic T lymphocyte (CTL) epitopes e.g., HPV16 E1.214, and that  
XX  
XX are directly or indirectly joined to one another in the same reading  
XX  
XX frame, a vaccine minigene. Also included are a vector comprising the  
XX  
XX multi-epitope construct, a polypeptide comprising an amino acid sequence  
XX  
XX encoded by the polynucleotide, a composition (comprising the  
XX  
XX polynucleotide, vector and/or polypeptide and a carrier), a cell  
XX  
XX (comprising the polynucleotide, vector or polypeptide), inducing an  
XX  
XX immune response against human papillomavirus virus (HPV) and making the  
XX  
XX polynucleotide, vector or polypeptide. The epitopes are derived from  
XX  
XX different strains of HPV and are from the E1, E2, E6 and E7 proteins. The  
XX  
XX epitopes may be linked via a GP-anchor/spacer peptide. The order of the  
XX  
XX epitopes in the vaccine protein are disclosed in the tables referred to  
XX  
XX in the claims of the specification. The polynucleotide, vector or  
XX  
XX polypeptide is useful in preparing a composition for inducing an immune  
XX  
XX response against human papillomavirus virus (HPV) and thus providing a  
XX  
XX defense against HPV infection and HPV-related cancers. The present  
XX  
XX sequence is an HPV protein used to derive epitopes for the vaccine of the  
XX  
XX invention.  
XX  
XX  
SQ Sequence 149 AA;  
Query Match 62.7%; Score 520; DB 9; Length 149;  
Best Local Similarity 63.6%; Pred. No. 7.9e-50;  
Matches 96; Conservative 19; Mismatches 34; Indels 2; Gaps 1;



CC first and a second binding partner for an oncogenic HPV E6 polypeptide,  
 CC where the first binding partner is a PDZ domain protein and the second,  
 CC binding partner is an antibody that specifically binds to the E6 proteins  
 CC of at least three different oncogenic HPV strains). The antibody  
 CC composition, kit, methods, and system are useful for diagnosing cancer,  
 CC particularly cervical cancer. The present sequence is an HPV E6 protein.  
 XX

XX Sequence 149 AA;

Query Match 60.0%; Score 496; DB 9; Length 149;

Best Local Similarity 60.1%; Pred. No. 2.3e-47;  
 Matches 89; Conservative 22; Mismatches 37; Indels 0; Gaps 0;

QY 1 MFQDQEPKRLPOLCTELQTTIHDIIECVYCKQQLRRRYDPAFRLCIVRDGMPY 60  
 DB 1 MFQDDEKPRNLHDCQALFETVHEISLPVQCKTLRNEVYDFLFDLKLIVYRGMPY 60  
 QY 61 AVXDKLKFYSKISEYRHYSVYGTTLGQYNKPLCDLLIRCIINXQKPLCEPKQRHLD 120  
 DB 61 GYCKQCLRLSKISYSEYRHYSVYGTTLGQYNKPLCDLLIRCIINXQKPLCEPKQRHLD 120  
 QY 121 KKQRFHNIRGRWTRGRCMSSCRSSRRTRRE 148  
 DB 121 KKQRFHNISNRWTRGRCVCMRPTQTQ 148

RESULT 60

ADO44083  
 ID ADO44083 standard; protein; 149 AA.

XX ADO44083;

DT 15-JUN-2004 (first entry)

XX Amino acid sequence of the E6 polypeptide of HPV58.

XX E6 protein; E7 protein; fusion protein; HPV; HPV-associated cancer;

KW cervical cancer; immune response; lower gastrointestinal tract cancer;

XX anal cancer; reproductive system cancer; penile cancer; vulvar cancer.

OS Human papillomavirus type 58.

XX WO2004030636-A2.

XX 15-APR-2004.

PF 02-OCT-2003; 2003WO-US031726.

XX 03-OCT-2002; 2002US-0415929P.

PA (AMHP ) WYETH HOLDINGS CORP.

XX Smith L, Casasetti MC;

DR MPI; 2004-316328/29.

XX N-PSDB; ADO44110.

XX New polypeptide comprising human papillomavirus E6 and E7 polypeptides,  
 PT useful for treating or preventing human papillomavirus (HPV)-associated  
 PT cancers, e.g. cervical cancer.  
 XX

PS Disclosure; Page 84-85; 101pp; English.

XX ADO44074-ADO44085 represent E6 polypeptides from human papillomaviruses.

CC ADO44088 is the consensus sequence derived from these polypeptides. The

CC specification describes human papillomavirus E6 and E7 polypeptides.

CC where the E7 polypeptide has mutations at any one or more of the amino

CC acids corresponding to amino acids 24, 26 or 91 of the sequence given in

CC ADO44073 and the E6 polypeptide has no mutations or has mutations at any

CC one or more of the amino acids corresponding to amino acids 63 or 106 of

CC the sequence given in ADO44072. The polypeptides of the invention are

CC useful for treating or preventing human papillomavirus (HPV)-associated

CC cancers, such as cervical cancer. The fusion proteins and nucleic acids

CC encoding the fusion proteins are useful for generating immune responses  
 CC against HPV. They are also useful for treating lower gastrointestinal  
 CC tract cancers, e.g. anal cancer, and other cancers of the reproductive  
 CC system, including penile and vulvar cancer.  
 XX

XX Sequence 149 AA;

Query Match 59.8%; Score 496; DB 8; Length 149;

Best Local Similarity 61.6%; Pred. No. 3.9e-47;  
 Matches 93; Conservative 20; Mismatches 36; Indels 2; Gaps 1;

QY 1 MFQDQEPKRLPOLCTELQTTIHDIIECVYCKQQLRRRYDPAFRLCIVRDGMPY 60  
 DB 1 MFQDDEKPRNLHDCQALFETVHEISLPVQCKTLRNEVYDFLFDLKLIVYRDGMPY 60  
 QY 61 AVXDKLKFYSKISEYRHYSVYGTTLGQYNKPLCDLLIRCIINXQKPLCEPKQRHLD 120  
 DB 61 AVCKVCGLRLSKISYSEYRHYSVYGTTLGQYNKPLCDLLIRCIINXQKPLCEPKQRHLD 120  
 QY 121 KKQRFHNIRGRWTRGRCMSSCRSSRRTRRE 151  
 DB 121 LKQRFHNISGRWTRGRCVCMRPTQTQ 149

RESULT 61

AEA98534  
 ID AEA98534 standard; protein; 149 AA.

XX AEA98534;

DT 08-SEP-2005 (first entry)

XX HPV (oncogenic strain) E6 amino acid sequence SEQ ID 15.

KW Papillomavirus infection; virucide; E6 protein; diagnosis; antibody;

XX cancer; cervix tumor; cytostatic.

OS Human papillomavirus; strain 58.

XX US2005142541-A1.

XX 30-JUN-2005.

PF 23-DEC-2004; 2004US-00021949.

XX 23-DEC-2003; 2003US-0532373P.

PA (ARBO-) ARBOR VITA CORP.

XX Lu PS, Garman JD, Belmares MP, Somoza DC, Schweizer J;

DR MPI; 2005-457781/46.

XX New antibody composition comprising a mixture of monoclonal antibodies  
 PT for oncogenic strains of human papilloma virus, useful for diagnosing  
 PT cancer.  
 XX

PS Disclosure; SEQ ID NO 15; 161pp; English.

XX The invention relates to an antibody composition comprising a mixture of

CC monoclonal antibodies that specifically bind to E6 proteins of human

CC papilloma virus (HPV) strains 16, 18, 31, 33 and 45, where at least one

CC of the monoclonal antibodies specifically binds to E6 proteins of at

CC least three different oncogenic HPV strains. Also included are a

CC diagnostic kit (for detecting an HPV E6 polypeptide in a sample,

CC comprising the antibody composition above), a method of detecting an HPV

CC E6 protein in a sample, a method of detecting the presence of an

CC oncogenic HPV E6 protein in a sample and a system for detecting the

CC presence of an oncogenic HPV E6 polypeptide in a sample (comprising a

CC first and a second binding partner for an oncogenic HPV E6 polypeptide,

CC where the first binding partner is a PDZ domain protein and the second

CC binding partner is an antibody that specifically binds to the E6 proteins

CC of at least three different oncogenic HPV strains). The antibody



XX Cheenut R, Newman MJ, Moche B, Baker D, Southwood S, Babe LM;  
 PI Chen Y, Deyoung LM, Huang MTF, Power SD;  
 XX WPI; 2005-658982/67.  
 DR  
 XX  
 PT New polynucleotide comprises a multi-epitope construct comprising nucleic  
 PT acids encoding the human papillomavirus (HPV) cytotoxic T lymphocyte  
 PT (CTL) epitopes, useful in preparing a vaccine against HPV.  
 PS  
 XX Disclosure; Page 66; 518pp; English.  
 XX  
 CC The invention relates to a new polynucleotide comprising a multi-epitope  
 CC construct comprising nucleic acids encoding the human papillomavirus  
 CC (HPV) cytotoxic T lymphocyte (CTL) epitopes e.g., HPV16.E1.214, and that  
 CC are directly or indirectly joined to one another in the same reading  
 CC frame, a vaccine minigene. Also included are a vector comprising the  
 CC multi-epitope construct, a polypeptide comprising an amino acid sequence  
 CC encoded by the polynucleotide, a composition (comprising the  
 CC polynucleotide, vector and/or polypeptide and a carrier), a cell  
 CC (comprising the polynucleotide, vector or polypeptide), inducing an  
 CC immune response against human papillomavirus virus (HPV) and making the  
 CC polynucleotide, vector or polypeptide. The epitopes are derived from  
 CC different strains of HPV and are from the E1, E2, E6 and E7 proteins. The  
 CC epitopes may be linked via a GP-anchor/spacer peptide. The order of the  
 CC epitopes in the vaccine protein are disclosed in the tables referred to  
 CC in the claims of the specification. The polynucleotide, vector or  
 CC polypeptide is useful in preparing a composition for inducing an immune  
 CC response against human papillomavirus virus (HPV) and thus providing a  
 CC defense against HPV infection and HPV-related cancers. The present  
 CC sequence is an HPV protein used to derive epitopes for the vaccine of the  
 CC invention.  
 XX  
 SQ Sequence 149 AA;

Query Match 59.8%; Score 496; DB 9; Length 149;  
 Best Local Similarity 61.6%; Pred. No. 3.9e-47;  
 Matches 93; Conservative 20; Mismatches 36; Indels 2; Gaps 1;  
 QY 1 MFQDPERPRKLPOCTELQTTIHDIIECYCKQQLRREYDPAFRLDCTVYDGNPY 60  
 DB 1 MFQDAEKRRTLHDCQALETSVHEIEIKVCCKTLQSEVYDFVFADLRIVYRDGNPF 60  
 QY 61 AVXDCKLFYSKISRYRHYCVSVGTLEQOYNKPLCDLLIRICINXQKPLCEBKQRHD 120  
 DB 61 AVCKVCLRLSKISRYRHYCVSVGTLEQTLKCLMELIRICICQRLCEBKQRHD 120  
 QY 121 KKORFHNIRGRWTCGMSCCRSSRTRETOI 151  
 DB 121 LMKRFHNISGRWTCGCAVCWRP--RRRQTOV 149

RESULT 64  
 ADO44081  
 ID ADO44081 standard; protein; 148 AA.  
 XX  
 AC ADO44081;  
 XX  
 DT 15-JUL-2004 (first entry)  
 XX  
 DE Amino acid sequence of the E6 polypeptide of HPV52.  
 XX  
 KW E6 protein; E7 protein; fusion protein; HPV; HPV-associated cancer;  
 KW cervical cancer; immune response; lower gastrointestinal tract cancer;  
 KW anal cancer; reproductive system cancer; penile cancer; vulvar cancer.  
 XX  
 OS Human papillomavirus type 52.  
 XX  
 PN WO2004030636-A2.  
 XX  
 PD 15-APR-2004.  
 XX  
 PF 02-OCT-2003; 2003WO-US031726.

XX  
 PR 03-OCT-2002; 2002US-0415929P.  
 XX  
 PA (AMHP ) WYETH HOLDINGS CORP.  
 XX  
 PI Smith L, Casaretti MC;  
 XX  
 DR WPI; 2004-316328/29.  
 DR N-PSDB; ADO44108.  
 XX  
 PT New polypeptide comprising human papillomavirus E6 and E7 polypeptides,  
 PT useful for treating or preventing human papillomavirus (HPV)-associated  
 PT cancers, e.g. cervical cancer.  
 PS  
 XX Disclosure; Page 83; 101pp; English.  
 XX  
 CC ADO44074-ADO44085 represent E6 polypeptides from human papillomaviruses.  
 CC ADO44098 is the consensus sequence derived from these polypeptides. The  
 CC specification describes human papillomavirus E6 and E7 polypeptides,  
 CC where the E7 polypeptide has mutations at any one or more of the amino  
 CC acids corresponding to amino acids 24, 26 or 91 of the sequence given in  
 CC ADO44073 and the E6 polypeptide has no mutations or has mutations at any  
 CC one or more of the amino acids corresponding to amino acids 63 or 106 of  
 CC the sequence given in ADO44072. The polypeptides of the invention are  
 CC useful for treating or preventing human papillomavirus (HPV)-associated  
 CC cancers, such as cervical cancer. The fusion proteins and nucleic acids  
 CC encoding the fusion proteins are useful for generating immune responses  
 CC against HPV. They are also useful for treating lower gastrointestinal  
 CC tract cancers, e.g. anal cancer, and other cancers of the reproductive  
 CC system, including penile and vulvar cancer.  
 XX  
 SQ Sequence 148 AA;

Query Match 58.7%; Score 487; DB 8; Length 148;  
 Best Local Similarity 61.7%; Pred. No. 3.9e-46;  
 Matches 87; Conservative 19; Mismatches 35; Indels 0; Gaps 0;  
 QY 1 MFQDPERPRKLPOCTELQTTIHDIIECYCKQQLRREYDPAFRLDCTVYDGNPY 60  
 DB 1 MFEDATPRRLTLEHCEVLESVHEIRLQCVQCKKELRREYKFLFTDLRIYVYDNNPY 60  
 QY 61 AVXDCKLFYSKISRYRHYCVSVGTLEQOYNKPLCDLLIRICINXQKPLCEBKQRHD 120  
 DB 61 GVCIMCLRFLSKISRYRHYCVSVGTLEQYKPLSEITTRICICQRLCEBKQRHD 120  
 QY 121 KKORFHNIRGRWTCGMSCCR 141  
 DB 121 ANKRFHNIMGRWTCGSCCWR 141

RESULT 65  
 AEA98536  
 ID AEA98536 standard; protein; 148 AA.  
 XX  
 AC AEA98536;  
 XX  
 DT 08-SEP-2005 (first entry)  
 XX  
 DE HPV (oncogenic strain) E6 amino acid sequence SEQ ID 17.  
 XX  
 KW Papillomavirus infection; virucide; E6 protein; diagnosis; antibody;  
 KW cancer; cervix tumor; cytostatic.  
 XX  
 OS Human papillomavirus; strain 52.  
 XX  
 PN US2005142541-A1.  
 XX  
 PD 30-JUN-2005.  
 XX  
 PF 23-DEC-2004; 2004US-00021949.  
 XX  
 PR 23-DEC-2003; 2003US-0532373P.

PA (ARBO-) ARBOR VITA CORP.  
 XX  
 PI Lu PS, Garman JD, Belmares MP, Somoza DC, Schweizer J;  
 XX  
 DR WPI; 2005-457781/46.  
 XX  
 PT New antibody composition comprising a mixture of monoclonal antibodies  
 PT for oncogenic strains of human papilloma virus, useful for diagnosing  
 PT cancer.  
 XX  
 PS Disclosure; SEQ ID NO 17, 161pp; English.  
 XX  
 CC The invention relates to an antibody composition comprising a mixture of  
 CC monoclonal antibodies that specifically bind to E6 proteins of human  
 CC papilloma virus (HPV) strains 16, 18, 31, 33 and 45, where at least one  
 CC of the monoclonal antibodies specifically binds to E6 proteins of at  
 CC least three different oncogenic HPV strains. Also included are a  
 CC diagnostic kit (for detecting an HPV E6 polypeptide in a sample,  
 CC comprising the antibody composition above), a method of detecting an HPV  
 CC E6 protein in a sample, a method of detecting the presence of an  
 CC oncogenic HPV E6 protein in a sample and a system for detecting the  
 CC presence of an oncogenic HPV E6 polypeptide in a sample (comprising a  
 CC first and a second binding partner for an oncogenic HPV E6 polypeptide,  
 CC where the first binding partner is a pDZ domain protein and the second  
 CC binding partner is an antibody that specifically binds to the E6 proteins  
 CC of at least three different oncogenic HPV strains). The antibody  
 CC composition, kit, methods, and system are useful for diagnosing cancer,  
 CC particularly cervical cancer. The present sequence is an HPV E6 protein.  
 XX  
 SQ Sequence 148 AA;  
 XX  
 Query Match 58.7%; Score 487; DB 9; Length 148;  
 Best Local Similarity 61.7%; Pred. No. 3.9e-46;  
 Matches 87; Conservative 19; Mismatches 35; Indels 0; Gaps 0;  
 QY 1 MFQDPOERRPKLPOLCTELQTTIHDIIECVYCKQQLRREYVDFAPRDLCTIVRDGMPY 60  
 DB 1 MFEDPATRPRTLHELCEVLESVHEIRLQCVQCKELQREYVKLFDTLRIVYDNNPY 60  
 QY 61 AVXDKLKFYSKISSEYRHVYCSVYGTLEQOYNKPLCDLLIRGINXQKPLCEEKORHLD 120  
 DB 61 GVCIMCLRFSLKISSEYRHVYSLYGTLEBRYKPLSEITIRICITQPLCEEKERHVN 120  
 QY 121 KKQRFHNIRGRWTGRCSCCR 141  
 DB 121 ANKRPFNIMGRWTGRCSCECMR 141  
 RESULT 66  
 AEC98868  
 ID AEC98868 standard; protein; 148 AA.  
 XX  
 AC AEC98868;  
 XX  
 DT 01-DEC-2005 (first entry)  
 XX  
 DE HPV\_52 Envelope protein E6.  
 XX  
 KW Human papilloma virus infection; virucide; cancer; cytostatic; vaccine;  
 KW epitope mapping; immune stimulation; cytotoxic T-lymphocyte.  
 XX  
 OS Human papillomavirus type 52.  
 XX  
 OS WO2005089164-A2.  
 XX  
 PN 29-SEP-2005.  
 PD  
 PF 03-JAN-2005; 2005WO-US000077.  
 PF  
 PR 31-DEC-2003; 2003US-0533211P.  
 PR 02-JUL-2004; 2004US-0584652P.  
 XX  
 PA (EPTM-) EPTIMUNE INC.  
 PA

PA (INNO-) INNOGENETICS NV.  
 PA (CHES/) CHESNUT R.  
 PA (NEWM/) NEWMAN M J.  
 PA (MOTH/) MOTHÉ B.  
 PA (BAKE/) BAKER D.  
 PA (SOOT/) SOUTHWOOD S.  
 PA (BABE/) BABE L M.  
 PA (CHEN/) CHEN Y.  
 PA (DEYO/) DEYOUNG L M.  
 PA (HUAN/) HUANG M T F.  
 PA (POWE/) POWER S D.  
 XX  
 PI Chesnut R, Newman MJ, Mothe B, Baker D, Southwood S, Babe LM;  
 PI Chen Y, Deyoung LM, Huang MTF, Power SD;  
 XX  
 DR WPI; 2005-658982/67.  
 XX  
 PT New polynucleotide comprises a multi-epitope construct comprising nucleic  
 PT acids encoding the human papillomavirus (HPV) cytotoxic T lymphocyte  
 PT (CTL) epitopes, useful in preparing a vaccine against HPV.  
 XX  
 PS Example 10; Page 349; 518pp; English.  
 XX  
 CC The invention relates to a new polynucleotide comprising a multi-epitope  
 CC construct comprising nucleic acids encoding the human papillomavirus  
 CC (HPV) cytotoxic T lymphocyte (CTL) epitopes e.g., HPV16 E1.214, and that  
 CC are directly or indirectly joined to one another in the same reading  
 CC frame, a vaccine minigene. Also included are a vector comprising the  
 CC multi-epitope construct, a polypeptide comprising an amino acid sequence  
 CC encoded by the polynucleotide, a composition (comprising the  
 CC polynucleotide, vector and/or polypeptide and a carrier), a cell  
 CC (comprising the polynucleotide, vector or polypeptide), inducing an  
 CC immune response against human papillomavirus virus (HPV) and making the  
 CC polynucleotide, vector or polypeptide. The epitopes are derived from  
 CC different strains of HPV and are from the E1, E2, E6 and E7 proteins. The  
 CC epitopes may be linked via a GP-anchor/spacer peptide. The order of the  
 CC epitopes in the vaccine protein are disclosed in the tables referred to  
 CC in the claims of the specification. The polynucleotide, vector or  
 CC polypeptide is useful in preparing a composition for inducing an immune  
 CC response against human papillomavirus virus (HPV) and thus providing a  
 CC defense against HPV infection and HPV-related cancers. The present  
 CC sequence is an HPV protein used to derive epitopes for the vaccine of the  
 CC invention.  
 XX  
 SQ Sequence 148 AA;  
 XX  
 Query Match 58.7%; Score 487; DB 9; Length 148;  
 Best Local Similarity 61.7%; Pred. No. 3.9e-46;  
 Matches 87; Conservative 19; Mismatches 35; Indels 0; Gaps 0;  
 QY 1 MFQDPOERRPKLPOLCTELQTTIHDIIECVYCKQQLRREYVDFAPRDLCTIVRDGMPY 60  
 DB 1 MFEDPATRPRTLHELCEVLESVHEIRLQCVQCKELQREYVKLFDTLRIVYDNNPY 60  
 QY 61 AVXDKLKFYSKISSEYRHVYCSVYGTLEQOYNKPLCDLLIRGINXQKPLCEEKORHLD 120  
 DB 61 GVCIMCLRFSLKISSEYRHVYSLYGTLEBRYKPLSEITIRICITQPLCEEKERHVN 120  
 QY 121 KKQRFHNIRGRWTGRCSCCR 141  
 DB 121 ANKRPFNIMGRWTGRCSCECMR 141  
 RESULT 67  
 AEC96424  
 ID AEC96424 standard; protein; 148 AA.  
 XX  
 AC AEC96424;  
 XX  
 DT 01-DEC-2005 (first entry)  
 XX  
 DE HPV protein E6 from HPV52.  
 XX

KM Human papilloma virus infection; virucide; cancer; cytostatic; vaccine;  
KW epitope mapping; immune stimulation; cytotoxic T lymphocyte.  
XX  
OS Human papillomavirus type 52.  
XX  
PN WO2005089164-A2.  
XX  
XX 29-SEP-2005.  
XX  
PD 03-JAN-2005; 2005WO-US000077.  
XX  
PF 31-DEC-2003; 2003US-0533211P.  
XX  
PR 02-JUL-2004; 2004US-0584652P.  
XX  
XX (EPIM-) EPIMUNE INC.  
PA (INNO-) INNOGENETICS NV.  
PA (CHES/) CHESNUT R.  
PA (NEMM/) NEMMAN M J.  
PA (MOTH/) MOTH B.  
PA (BAKE/) BAKER D.  
PA (SOUT/) SOUTWOOD S.  
PA (BABE/) BABE L M.  
PA (CHEN/) CHEN Y.  
PA (DEYO/) DEYOUNG L M.  
PA (HUAN/) HUANG M T F.  
PA (POME/) POWER S D.  
XX  
X1 Chesnut R, Newman MJ, Mothe B, Baker D, Southwood S, Babe LM;  
P1 Chen Y, Deyoung LM, Huang MTF, Power SD;  
XX  
XX WPI; 2005-658982/67.  
DR  
XX  
PT New polynucleotide comprises a multi-epitope construct comprising nucleic  
PT acids encoding the human papillomavirus (HPV) cytotoxic T lymphocyte  
PT (CTL) epitopes, useful in preparing a vaccine against HPV.  
PS  
XX Disclosure; Page 64; 518pp; English.  
XX  
XX The invention relates to a new polynucleotide comprising a multi-epitope  
CC construct comprising nucleic acids encoding the human papillomavirus  
CC (HPV) cytotoxic T lymphocyte (CTL) epitopes e.g., HPV16.E1.214, and that  
CC are directly or indirectly joined to one another in the same reading  
CC frame, a vaccine minigene. Also included are a vector comprising the  
CC multi-epitope construct, a polypeptide comprising an amino acid sequence  
CC encoded by the polynucleotide, a composition (comprising the  
CC polynucleotide, vector and/or polypeptide and a carrier), a cell  
CC (comprising the polynucleotide, vector or polypeptide), inducing an  
CC immune response against human papillomavirus virus (HPV) and making the  
CC polynucleotide, vector or polypeptide. The epitopes are derived from  
CC different strains of HPV and are from the E1, E2, E6 and E7 proteins. The  
CC epitopes may be linked via a gp-anchor/spacer peptide. The order of the  
CC epitopes in the vaccine protein are disclosed in the tables referred to  
CC in the claims of the specification. The polynucleotide, vector or  
CC polypeptide is useful in preparing a composition for inducing an immune  
CC response against human papillomavirus virus (HPV) and thus providing a  
CC defense against HPV infection and HPV-related cancers. The present  
CC sequence is an HPV protein used to derive epitopes for the vaccine of the  
CC invention.  
XX  
XX Sequence 148 AA;  
SQ

Query Match 58.7%; Score 487; DB 9; Length 148;  
Best Local Similarity 61.7%; Pred. No. 3.9e-46;  
Matches 87; Conservative 19; Mismatches 35; Indels 0; Gaps 0;

QY 1 MFQDQERPRKLPOLCTELQTTIHDIIECVYCKQQLRREYVDAFNDLCIVYDGNPY 60  
DB 1 MFEDPATPRTHLCEVLESVHEIRIQCVQCKELDRREVYKRLFTDLRIYVDDNNPY 60  
QY 61 AVXDKCLAFYSKISIRYHCYSVGTTLBEOQYNKRLCDLLIRCIKXKXPLCEEKORHLD 120  
DB 61 GVCIMCLAFLSKISIRYHCYSVGTTLBEOQYNKRLCDLLIRCIKXKXPLCEEKORHLD 120

QY 121 KKORFHNIRGRWTRCWSCCR 141  
DB 121 ANKRFHNIRGRWTRCWSCCR 141

RESULT 68  
AEA98878  
ID AEA98878 standard; protein, 148 AA.  
XX  
AC AEA98878;  
XX  
DT 08-SEP-2005 (first entry)  
XX  
DE HPV (oncogenic strain) E6 amino acid sequence SEQ ID 359.  
XX  
KW Papillomavirus infection; virucide; E6 protein; diagnosis; antibody;  
KM cancer; cervix tumor; cytostatic.  
XX  
OS Human papillomavirus; strain 34.  
XX  
PN US2005142541-A1.  
XX  
PD 30-JUN-2005.  
XX  
XX 23-DEC-2004; 2004US-00021949.  
XX  
PF 23-DEC-2003; 2003US-0532373P.  
XX  
PR 23-DEC-2003; 2003US-0532373P.  
XX  
PA (ARBO-) ARBOR VITA CORP.  
XX  
PI Lu PS, Garman JD, Belmares MP, Somoza DC, Schweizer J;  
XX  
XX WPI; 2005-457781/46.  
DR  
XX  
PT New antibody composition comprising a mixture of monoclonal antibodies  
PT for oncogenic strains of human papilloma virus, useful for diagnosing  
PT cancer.  
XX  
XX Disclosure; SEQ ID NO 359; 161pp; English.  
XX  
XX The invention relates to an antibody composition comprising a mixture of  
CC monoclonal antibodies that specifically bind to E6 proteins of human  
CC papilloma virus (HPV) strains 16, 18, 31, 33 and 45, where at least one  
CC of the monoclonal antibodies specifically binds to E6 proteins of at  
CC least three different oncogenic HPV strains. Also included are a  
CC diagnostic kit (for detecting an HPV E6 polypeptide in a sample,  
CC comprising the antibody composition above), a method of detecting an HPV  
CC E6 protein in a sample, a method of detecting the presence of an  
CC oncogenic HPV E6 protein in a sample and a system for detecting the  
CC presence of an oncogenic HPV E6 polypeptide in a sample (comprising a  
CC first and a second binding partner for an oncogenic HPV E6 polypeptide,  
CC where the first binding partner is a PD2 domain protein and the second  
CC binding partner is an antibody that specifically binds to the E6 proteins  
CC of at least three different oncogenic HPV strains). The antibody  
CC composition, kit, methods, and system are useful for diagnosing cancer,  
CC particularly cervical cancer. The present sequence is an HPV E6 protein.  
XX  
XX Sequence 148 AA;  
SQ

Query Match 58.3%; Score 484; DB 9; Length 148;  
Best Local Similarity 60.4%; Pred. No. 8.4e-46;  
Matches 87; Conservative 17; Mismatches 40; Indels 0; Gaps 0;

QY 2 FQDQERPRKLPOLCTELQTTIHDIIECVYCKQQLRREYVDAFNDLCIVYDGNPY 61  
DB 3 FPNDEERPRKLPALCEEVNISIHIEIDCVYCEQOLRVCEYDPIFDLCIVYKXKPLG 62  
QY 62 VXDCKLAFYSKISIRYHCYSVGTTLBEOQYNKRLCDLLIRCIKXKXPLCEEKORHLD 121  
DB 63 VQDCLLAFYSKISIRYHCYSVGTTLBEOQYNKRLCDLLIRCIKXKXPLCEEKORHLD 122  
QY 122 KORFHNIRGRWTRCWSCCR 145



XX Amino acid sequence of the E6 polypeptide of HPV68.  
DE  
XX E6 protein; E7 protein; fusion protein; HPV; HPV-associated cancer;  
XX cervical cancer; immune response; lower gastrointestinal tract cancer;  
XX anal cancer; reproductive system cancer; penile cancer; vulvar cancer.  
XX  
OS Human papillomavirus type 68.  
XX  
XX WO2004030636-A2.  
XX  
XX 15-APR-2004.  
XX  
XX 02-OCT-2003; 2003WO-US031726.  
XX  
XX 03-OCT-2002; 2002US-0415929P.  
XX  
XX (AMHP ) WYETH HOLDINGS CORP.  
XX  
XX Smith L, Cassetti MC;  
XX  
XX WPI; 2004-316328/29.  
XX  
XX N-PSDB; ADO44112.  
XX  
XX New polypeptide comprising human papillomavirus E6 and E7 polypeptides,  
XX useful for treating or preventing human papillomavirus (HPV)-associated  
XX cancers, e.g. cervical cancer.  
XX  
XX Disclosure; Page 85-86; 101pp; English.  
XX  
XX ADO44074-ADO44085 represent E6 polypeptides from human papillomaviruses.  
XX ADO44098 is the consensus sequence derived from these polypeptides. The  
XX specification describes human papillomavirus E6 and E7 polypeptides,  
XX where the E7 polypeptide has mutations at any one or more of the amino  
XX acids corresponding to amino acids 24, 26 or 91 of the sequence given in  
XX ADO44073 and the E6 polypeptide has no mutations or has mutations at any  
XX one or more of the amino acids corresponding to amino acids 63 or 106 of  
XX the sequence given in ADO44072. The polypeptides of the invention are  
XX useful for treating or preventing human papillomavirus (HPV)-associated  
XX cancers, such as cervical cancer. The fusion proteins and nucleic acids  
XX encoding the fusion proteins are useful for generating immune responses  
XX against HPV. They are also useful for treating lower gastrointestinal  
XX tract cancers, e.g. anal cancer, and other cancers of the reproductive  
XX system, including penile and vulvar cancer.  
XX  
XX Sequence 158 AA:  
SQ  
Query Match 56.4%; Score 468.5; DB 8; Length 158;  
Best Local Similarity 55.1%; Pred. No. 5e-44;  
Matches 86; Conservative 23; Mismatches 42; Indels 5; Gaps 1;  
QY 1 MFQDQERPRKLPOLCTELQTTIHDIIECYCKQQLRREYVDFAFRDLCTVYRDGNPY 60  
DB 3 LFHNPERRPYKLPDLCTLDITLHDITIDCVYCRQLOQTEVEYEFADLCTVYRDGVF 62  
QY 61 AVXKCKEYKISBYRHYCVSVGTLEQYKNRPLCDLLRCINXQKPLCPBEKQRHLD 120  
DB 63 AACQCKTFYAKIRLRYSSVYATLTETITNTKLYNLIRCMSCLKPLCPAEKLRHVT 122  
QY 121 KQRFNIRGRWTCRMSCCRSS-----RTRRETQL 151  
DB 123 TKRLHKIAGNFTGQCRHCHTCKREDRRIRRETQV 158  
RESULT 72  
AEA98880  
ID AEA98880 standard; protein; 158 AA.  
XX  
XX AEA98880;  
XX  
XX AC  
XX 08-SEP-2005 (first entry)  
XX  
XX HPV (oncogenic strain) E6 amino acid sequence SEQ ID 361.

XX Papillomavirus infection; virucide; E6 protein; diagnosis; antibody;  
XX cancer; cervix tumor; cytostatic.  
XX  
XX Human papillomavirus; strain 70.  
XX  
XX US2005142541-A1.  
XX  
XX 30-JUN-2005.  
XX  
XX 23-DEC-2004; 2004US-00021949.  
XX  
XX 23-DEC-2003; 2003US-0532373P.  
XX  
XX (ARBO-) ARBOR VITA CORP.  
XX  
XX Lu PS, Garman JD, Belmares MP, Somoza DC, Schweizer J;  
XX  
XX WPI; 2005-457781/46.  
XX  
XX New antibody composition comprising a mixture of monoclonal antibodies  
XX for oncogenic strains of human papilloma virus, useful for diagnosing  
XX cancer.  
XX  
XX Disclosure; SEQ ID NO 361; 161pp; English.  
XX  
XX The invention relates to an antibody composition comprising a mixture of  
XX monoclonal antibodies that specifically bind to E6 proteins of human  
XX papilloma virus (HPV) strains 16, 18, 31, 33 and 45, where at least one  
XX of the monoclonal antibodies specifically binds to E6 proteins of at  
XX least three different oncogenic HPV strains. Also included are a  
XX diagnostic kit (for detecting an HPV E6 polypeptide in a sample,  
XX comprising the antibody composition above), a method of detecting an HPV  
XX E6 protein in a sample, a method of detecting the presence of an  
XX oncogenic HPV E6 protein in a sample and a system for detecting the  
XX presence of an oncogenic HPV E6 polypeptide in a sample (comprising a  
XX first and a second binding partner for an oncogenic HPV E6 polypeptide,  
XX where the first binding partner is a PDZ domain protein and the second  
XX binding partner is an antibody that specifically binds to the E6 proteins  
XX of at least three different oncogenic HPV strains). The antibody  
XX composition, kit, methods, and system are useful for diagnosing cancer,  
XX particularly cervical cancer. The present sequence is an HPV E6 protein.  
XX  
XX Sequence 158 AA:  
SQ  
Query Match 56.4%; Score 468.5; DB 9; Length 158;  
Best Local Similarity 56.8%; Pred. No. 5e-44;  
Matches 88; Conservative 21; Mismatches 41; Indels 5; Gaps 1;  
QY 2 FQDQERPRKLPOLCTELQTTIHDIIECYCKQQLRREYVDFAFRDLCTVYRDGNPY 61  
DB 4 FPNPERRPYKLPDLCTLDITLHDITIDCVYCKTLOQTEVEYEFADLCTVYRDGVF 63  
QY 62 VXDCKLFYSKISBYRHYCVSVGTLEQYKNRPLCDLLRCINXQKPLCPBEKQRHLD 121  
DB 64 ACQCKTFYAKIRLRYSSVYATLTETITNTKLYNLIRCMSCLKPLCPAEKLRHVT 123  
QY 122 KQRFNIRGRWTCRMSCCRSS-----RTRRETQL 151  
DB 124 KRFPHQIAGSYTQGRHCHTCKREDRRIRRETQV 158  
RESULT 73  
AAR97562  
ID AAR97562 standard; protein; 172 AA.  
XX  
XX AAR97562;  
XX  
XX AC  
XX 27-AUG-2003 (revised)  
XX  
XX 11-JAN-1997 (first entry)  
XX  
XX Human papilloma virus E6/E7 protein variant.

KM Human Papilloma virus; E6; E7; deletion mutant; HPV; immune response;  
KM humoral immune response; cellular immune response; vaccine.  
XX  
OS Human papillomavirus.  
XX  
PN MO9619496-A1.  
XX  
PD 27-JUN-1996.  
XX  
PF 20-DEC-1995; 95MO-AU000868.  
XX  
PR 20-DEC-1994; 94AU-00000157.  
XX  
PA (CSLC-) CSL LTD.  
XX (UYOU ) UNIV QUEENSLAND.  
XX  
PI Edwards SJ, Cox J, Webb EA, Frazer I;  
XX  
DR WPI; 1996-309518/31.  
DR N-PSDB; AAT31834.  
XX  
PT Vaccine variants of human papilloma virus antigens - contain variants of  
PT E6 and/or E7 protein, pref. deletion mutants, and are used to treat or  
PT prevent HPV infection.  
XX  
PS Example 3; Page 17; 37pp; English.  
XX  
CC A variant of the human papilloma virus (HPV) E6 or E7 protein which  
CC elicits a humoral and/or cellular immune response against HPV can be used  
CC in vaccines against HPV or to treat HPV infection. The variant is  
CC preferably a deletion mutant comprising at least half, and preferably two  
CC thirds of full length E6 or E7 protein starting from the N- or C-  
CC terminus, or is a full length E6 moiety fused to a full length E7 moiety.  
CC The variant optionally has a linkage moiety and a foreign protein or  
CC peptide which facilitates the purification of, and enhances the  
CC immunogenicity of, the fusion protein. This is a fusion protein of the C-  
CC terminal end of E6 and the N-terminal end of E7. The protein is also a  
CC deletion mutant generated from the sequence described in AAT31833.  
CC (Updated on 27-AUG-2003 to correct OS field.)  
XX  
SQ Sequence 172 AA;  
XX  
Query Match 56.4%; Score 468; DB 2; Length 172;  
Best Local Similarity 86.1%; Pred. No. 6.3e-44;  
Matches 87; Conservative 1; Mismatches 1; Indels 12; Gaps 2;  
QY 57 GNPVAVXDKCLFYSKISEYRHVCYVGTTLTLEQO-----YMKPLCDLLIRCNXQKPL 110  
DB 2 GNPVAVCDKCLFYSKISEYRHVCYVGTTLTLEQOINCKPKNKPLCDLLIRC-----L 55  
QY 111 CPEEKORHLDKQRFNIRGRWTCRCMSCCRSSRTRETOL 151  
DB 56 CPEEKORHLDKQRFNIRGRWTCRCMSCCRSSRTRETOL 96  
XX  
RESULT 74  
ADO44080  
ID ADO44080 standard; protein; 151 AA.  
XX  
AC ADO44080;  
XX  
DT 15-JUL-2004 (first entry)  
XX  
DE Amino acid sequence of the E6 polypeptide of HPV51.  
XX  
KM E6 protein; E7 protein; fusion protein; HPV; HPV-associated cancer;  
KM cervical cancer; immune response; lower gastrointestinal tract cancer;  
KM anal cancer; reproductive system cancer; penile cancer; vulvar cancer.  
XX  
OS Human papillomavirus type 51.  
XX  
PN MO2004030636-A2.  
XX

PD 15-APR-2004.  
XX  
XX 02-OCT-2003; 2003WO-US031726.  
PF  
XX 03-OCT-2002; 2002US-0415929P.  
PR  
XX (AMHP ) WYETH HOLDINGS CORP.  
PA  
XX Smith L, Cassetti MC;  
XX  
XX WPI; 2004-316328/29.  
DR  
DR N-PSDB; ADO44107.  
XX  
XX New polypeptide comprising human papillomavirus E6 and E7 polypeptides,  
PT useful for treating or preventing human papillomavirus (HPV)-associated  
PT cancers, e.g. cervical cancer.  
XX  
XX Disclosure; Page 82; 101pp; English.  
XX  
CC ADO44074-ADO44085 represent E6 polypeptides from human papillomaviruses.  
CC ADO44098 is the consensus sequence derived from these polypeptides. The  
CC specification describes human papillomavirus E6 and E7 polypeptides,  
CC where the E7 polypeptide has mutations at any one or more of the amino  
CC acids corresponding to amino acids 24, 26 or 91 of the sequence given in  
CC ADO44073 and the E6 polypeptide has no mutations or has mutations at any  
CC one or more of the amino acids corresponding to amino acids 63 or 106 of  
CC there sequence given in ADO44072. The polypeptides of the invention are  
CC useful for treating or preventing human papillomavirus (HPV)-associated  
CC cancers, such as cervical cancer. The fusion proteins and nucleic acids  
CC encoding the fusion proteins are useful for generating immune responses  
CC against HPV. They are also useful for treating lower gastrointestinal  
CC tract cancers, e.g. anal cancer, and other cancers of the reproductive  
CC system, including penile and vulvar cancer.  
XX  
SQ Sequence 151 AA;  
XX  
Query Match 55.4%; Score 460; DB 8; Length 151;  
Best Local Similarity 57.0%; Pred. No. 4.2e-43;  
Matches 86; Conservative 24; Mismatches 41; Indels 0; Gaps 0;  
QY 1 MFQDPQERPRKLPOLCTELQTTIHDIIECYCKQQLRREYDPAFPLDLCVYRDNQPY 60  
DB 1 MFEDKREPRRTLHELCEALNVSMHNIQVVCYCKELCRADYVNAFTEIKIVYDNNPY 60  
QY 61 AYXDKCLFYSKISEYRHVCYVGTTLTLEQYKNRPLCDLLIRCNXQKPLCPEEKORHL 120  
DB 61 AYXDKCLFYSKISEYRHVCYVGTTLTLEQYKNRPLCDLLIRCNXQKPLCPEEKORHL 120  
QY 121 KKORFHNIRGRWTCRCMSCCRSSRTRETOL 151  
DB 121 KKORFHNIRGRWTCRCMSCCRSSRTRETOL 151  
XX  
RESULT 75  
AEA98543  
ID AEA98543 standard; protein; 151 AA.  
XX  
AC AEA98543;  
XX  
DT 08-SEP-2005 (first entry)  
XX  
DE HPV (oncogenic strain) E6 amino acid sequence SEQ ID 24.  
XX  
KM Papillomavirus infection; virucide; E6 protein; diagnosis; antibody;  
KM cancer; cervix tumor; cytostatic.  
XX  
OS Human papillomavirus; strain 51.  
XX  
PN US2005142541-A1.  
XX  
XX 30-JUN-2005.  
PD  
XX 23-DEC-2004; 2004US-00021949.  
PF

XX 23-DEC-2003; 2003US-0532373P.  
 PR (ARBO-) ARBOR VITA CORP.  
 XX  
 XX Lu PS, Garman JD, Belmares MP, Somoza DC, Schweizer J,  
 DR WPI; 2005-457781/46.  
 XX  
 XX New antibody composition comprising a mixture of monoclonal antibodies  
 PT for oncogenic strains of human papilloma virus, useful for diagnosing  
 PT cancer.  
 XX  
 PS Disclosure: SEQ ID NO 24; 161pp; English.  
 XX  
 CC The invention relates to an antibody composition comprising a mixture of  
 CC monoclonal antibodies that specifically bind to E6 proteins of human  
 CC papilloma virus (HPV) strains 16, 18, 31, 33 and 45, where at least one  
 CC of the monoclonal antibodies specifically binds to E6 proteins of at  
 CC least three different oncogenic HPV strains. Also included are a  
 CC diagnostic kit (for detecting an HPV E6 polypeptide in a sample,  
 CC comprising the antibody composition above), a method of detecting an HPV  
 CC E6 protein in a sample, a method of detecting the presence of an  
 CC oncogenic HPV E6 protein in a sample and a system for detecting the  
 CC presence of an oncogenic HPV E6 polypeptide in a sample (comprising a  
 CC first and a second binding partner for an oncogenic HPV E6 polypeptide,  
 CC where the first binding partner is a PDZ domain protein and the second  
 CC binding partner is an antibody that specifically binds to the E6 proteins  
 CC of at least three different oncogenic HPV strains). The antibody  
 CC composition, kit, methods, and system are useful for diagnosing cancer,  
 CC particularly cervical cancer. The present sequence is an HPV E6 protein.  
 CC  
 SQ Sequence 151 AA;

Query Match 55.4%; Score 460; DB 9; Length 151;  
 Best Local Similarity 57.0%; Pred. No. 4.2e-43;  
 Matches 86; Conservative 24; Mismatches 41; Indels 0; Gaps 0;  
 QY 1 MFQDPERPRKLPOLCTELQTTIHIIIECVYCKQQLREYVDFAFRDLCTVYRDGNPY 60  
 DB 1 MFEDRREPRRLTLECEALNVSMHNIQVVCYCKKELRADVYVNAFTEIKIVYRDNNPY 60  
 QY 61 AVXDKLKFYSKISEYRHVYCSVGTTLQOYNKPLCDLLIRCIYNXOKPLCEBEKQRHLD 120  
 DB 61 AVXKQCLFYSKIRYRYSVYGTTLBATTKSKSLVPLSIRCHRCORPLGEBEKQLVD 120  
 QY 121 KQRFHNIRGRWTCRCMCCRSSRTRRETOL 151  
 DB 121 EKRFHEIAGRWTGOCANCMQRTRORETQV 151

RESULT 76  
 ADO44079  
 ID ADO44079 standard; protein; 158 AA.  
 XX  
 AC ADO44079;  
 XX  
 DT 15-JUL-2004 (first entry)  
 XX  
 DE Amino acid sequence of the E6 polypeptide of HPV45.  
 XX  
 KW E6 protein; E7 protein; fusion protein; HPV; HPV-associated cancer;  
 KW cervical cancer; immune response; lower gastrointestinal tract cancer;  
 KW anal cancer; reproductive system cancer; penile cancer; vulvar cancer.  
 XX  
 OS Human papillomavirus type 45.  
 XX  
 PN WO2004030636-A2.  
 XX  
 PD 15-APR-2004.  
 XX  
 PR 02-OCT-2003; 2003WO-US0311726.  
 XX

PR 03-OCT-2002; 2002US-0415929P.  
 XX (AMHP ) WYETH HOLDINGS CORP.  
 PA  
 XX Smith L, Casasetti MC;  
 PI  
 XX WPI; 2004-316328/29.  
 DR N-P8DB; ADO44106.  
 XX  
 XX New polypeptide comprising human papillomavirus E6 and E7 polypeptides,  
 PT useful for treating or preventing human papillomavirus (HPV)-associated  
 PT cancers, e.g. cervical cancer.  
 XX  
 PS Disclosure: Page 81-82; 101pp; English.  
 XX  
 CC ADO44074-ADO44085 represent E6 polypeptides from human papillomaviruses.  
 CC ADO44098 is the consensus sequence derived from these polypeptides. The  
 CC specification describes human papillomavirus E6 and E7 polypeptides,  
 CC where the E7 polypeptide has mutations at any one or more of the amino  
 CC acids corresponding to amino acids 24, 26 or 91 of the sequence given in  
 CC ADO44073 and the E6 polypeptide has no mutations or has mutations at any  
 CC one or more of the amino acids corresponding to amino acids 63 or 106 of  
 CC the sequence given in ADO44072. The polypeptides of the invention are  
 CC useful for treating or preventing human papillomavirus (HPV)-associated  
 CC cancers, such as cervical cancer. The fusion proteins and nucleic acids  
 CC encoding the fusion proteins are useful for generating immune responses  
 CC against HPV. They are also useful for treating lower gastrointestinal  
 CC tract cancers, e.g. anal cancer, and other cancers of the reproductive  
 CC system, including penile and vulvar cancer.  
 CC  
 SQ Sequence 158 AA;

Query Match 55.4%; Score 459.5; DB 8; Length 158;  
 Best Local Similarity 56.1%; Pred. No. 5.1e-43;  
 Matches 87; Conservative 22; Mismatches 41; Indels 5; Gaps 1;  
 QY 2 FQDPERPRKLPOLCTELQTTIHIIIECVYCKQQLREYVDFAFRDLCTVYRDGNPYA 61  
 DB 4 FDDKQRPYKLPDLCTELNTSLQDVSTACVYCKATLETEYVQRFKDLCTVYRDCTIAYA 63  
 QY 62 VXDKCLKFYSKISEYRHVYCSVGTTLQOYNKPLCDLLIRCIYNXOKPLCEBEKQRHLD 121  
 DB 64 ACHKCIDYSHIRRELARYSNSVYGTTLKINTTELNYLLIRCLRQKPLNPKERKRLKD 123  
 QY 122 KQRFHNIRGRWTCRCMCCRSS-----RTRRETOL 151  
 DB 124 KRRFHSINGQYRGQCNCTCCDQARQERLRRRRETQV 158

RESULT 77  
 AEA98548  
 ID AEA98548 standard; protein; 158 AA.  
 XX  
 AC AEA98548;  
 XX  
 DT 08-SEP-2005 (first entry)  
 XX  
 DE HPV (oncogenic strain) E6 amino acid sequence SEQ ID 29.  
 XX  
 KW Papillomavirus infection; virucide; E6 protein; diagnosis; antibody;  
 KW cancer; cervix tumor; cytostatic.  
 XX  
 OS Human papillomavirus; strain 45.  
 XX  
 PN US2005142541-A1.  
 XX  
 PD 30-JUN-2005.  
 XX  
 PF 23-DEC-2004; 2004US-00021949.  
 XX  
 PR 23-DEC-2003; 2003US-0532373P.  
 XX  
 PA (ARBO-) ARBOR VITA CORP.

XX PI Lu PS, Garman JD, Belmares MP, Somoza DC, Schweizer J;  
 XX DR WPI, 2005-457781/46.  
 XX PT New antibody composition comprising a mixture of monoclonal antibodies  
 PT for oncogenic strains of human papilloma virus, useful for diagnosing  
 PT cancer.  
 XX PS Disclosure; SEQ ID NO 29; 161pp; English.  
 XX CC The invention relates to an antibody composition comprising a mixture of  
 CC monoclonal antibodies that specifically bind to E6 proteins of human  
 CC papilloma virus (HPV) strains 16, 18, 31, 33 and 45, where at least one  
 CC of the monoclonal antibodies specifically binds to E6 proteins of at  
 CC least three different oncogenic HPV strains. Also included are a  
 CC diagnostic kit (for detecting an HPV E6 polypeptide in a sample,  
 CC comprising the antibody composition above), a method of detecting an HPV  
 CC E6 protein in a sample, a method of detecting the presence of an  
 CC oncogenic HPV E6 protein in a sample and a system for detecting the  
 CC presence of an oncogenic HPV E6 polypeptide in a sample (comprising a  
 CC first and a second binding partner for an oncogenic HPV E6 polypeptide,  
 CC where the first binding partner is a PDZ domain protein and the second  
 CC binding partner is an antibody that specifically binds to the E6 proteins  
 CC of at least three different oncogenic HPV strains). The antibody  
 CC composition, kit, methods, and system are useful for diagnosing cancer,  
 CC particularly cervical cancer. The present sequence is an HPV E6 protein.  
 SO Sequence 158 AA;  
 Query Match 55.4%; Score 459.5; DB 9; Length 158;  
 Best Local Similarity 56.1%; Pred. No. 5.1e-43;  
 Matches 87; Conservative 22; Mismatches 41; Indels 5; Gaps 1;  
 QY 2 FDDPGRPKLPOLCTELQTHIDILIECVCKQQLRREYVDFAFRDLCTIVYRDGNPYA 61  
 DB 4 FDDPKORPKLPDLCTELMTSLQDVSIACVYKATLEREVQFAFKDCTIVYRDGINA 63  
 QY 62 VXDCKLKFYSKISEVRYHCYSYVGTTLLEQYNNKPLCDLLIRNCINXOKPLCPBEKQRHLDK 121  
 DB 64 ACHKCIDFYSRIRELRYNSVYGETLEKITETELYNLLIRLCRCQKPLNPAEKRRHLDK 123  
 QY 122 KORFNIRGRMTGRMCCSRSS-----RRRETQL 151  
 DB 124 KRFFSIAGQYRGQCNTCCDQARQERLRRRRRETQV 158  
 RESULT 78  
 AEC98867 standard; protein; 158 AA.  
 AC AEC98867;  
 XX 01-DEC-2005 (first entry)  
 XX DB HPV\_45 Envelope protein E6.  
 XX KW Human papilloma virus infection; virucide; cancer; cytostatic; vaccine;  
 XX KM epitope mapping; immune stimulation; cytotoxic T-lymphocyte.  
 XX OS Human papillomavirus type 45.  
 XX PN WO2005089164-A2.  
 XX PD 29-SEP-2005.  
 XX PF 03-JAN-2005; 2005MO-US000077.  
 XX PR 31-DEC-2003; 2003US-0533211P.  
 XX PR 02-JUL-2004; 2004US-0584652P.  
 XX PA (EPIIM-) EPIIMUNE INC.  
 XX PA (INNO-) INNOGENETICS NV.

PA (CHES/) CHESNUT R.  
 PA (NEMM/) NEMMAN M J.  
 PA (MOTH/) MOTH B.  
 PA (BAKE/) BAKER D.  
 PA (SOUT/) SOUTWOOD S.  
 PA (BABE/) BABE L M.  
 PA (CHEN/) CHEN Y.  
 PA (DEYO/) DEYOING L M.  
 PA (HUNAN/) HUANG M T F.  
 PA (POWER/) POWER S D.  
 XX PI Chesnut R, Newman MJ, Mothe B, Baker D, Southwood S, Babe LM;  
 PI Chen Y, Deyoung LM, Huang MTF, Power SD;  
 DR WPI, 2005-658982/67.  
 XX PT New polynucleotide comprises a multi-epitope construct comprising nucleic  
 PT acids encoding the human papillomavirus (HPV) cytotoxic T lymphocyte  
 PT (CTL) epitopes, useful in preparing a vaccine against HPV.  
 XX PS Example 10; Page 349; 518pp; English.  
 XX CC The invention relates to a new polynucleotide comprising a multi-epitope  
 CC construct comprising nucleic acids encoding the human papillomavirus  
 CC (HPV) cytotoxic T lymphocyte (CTL) epitopes e.g., HPV16.E1.214, and that  
 CC are directly or indirectly joined to one another in the same reading  
 CC frame, a vaccine minigene. Also included are a vector comprising the  
 CC multi-epitope construct, a polypeptide comprising an amino acid sequence  
 CC encoded by the polynucleotide, a composition (comprising the  
 CC polynucleotide, vector and/or polypeptide and a carrier), a cell  
 CC (comprising the polynucleotide, vector or polypeptide), inducing an  
 CC immune response against human papillomavirus virus (HPV) and making the  
 CC polynucleotide, vector or polypeptide. The epitopes are derived from  
 CC different strains of HPV and are from the E1, E2, E6 and E7 proteins. The  
 CC epitopes may be linked via a GP-anchor/spacer peptide. The order of the  
 CC epitopes in the vaccine protein are disclosed in the tables referred to  
 CC in the claims of the specification. The polynucleotide, vector or  
 CC polypeptide is useful in preparing a composition for inducing an immune  
 CC response against human papillomavirus virus (HPV) and thus providing a  
 CC defense against HPV infection and HPV-related cancers. The present  
 CC sequence is an HPV protein used to derive epitopes for the vaccine of the  
 CC invention.  
 SO Sequence 158 AA;  
 Query Match 55.4%; Score 459.5; DB 9; Length 158;  
 Best Local Similarity 56.1%; Pred. No. 5.1e-43;  
 Matches 87; Conservative 22; Mismatches 41; Indels 5; Gaps 1;  
 QY 2 FDDPGRPKLPOLCTELQTHIDILIECVCKQQLRREYVDFAFRDLCTIVYRDGNPYA 61  
 DB 4 FDDPKORPKLPDLCTELMTSLQDVSIACVYKATLEREVQFAFKDCTIVYRDGINA 63  
 QY 62 VXDCKLKFYSKISEVRYHCYSYVGTTLLEQYNNKPLCDLLIRNCINXOKPLCPBEKQRHLDK 121  
 DB 64 ACHKCIDFYSRIRELRYNSVYGETLEKITETELYNLLIRLCRCQKPLNPAEKRRHLDK 123  
 QY 122 KORFNIRGRMTGRMCCSRSS-----RRRETQL 151  
 DB 124 KRFFSIAGQYRGQCNTCCDQARQERLRRRRRETQV 158  
 RESULT 79  
 AAR63866 standard; protein; 158 AA.  
 ID AAR63866;  
 XX 16-OCT-2003 (revised)  
 XX DT 25-MAR-2003 (revised)  
 XX DT 28-JUN-1995 (first entry)  
 XX DE HPV18 E6/E7 proteins.



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PR 27-MAY-1994; 94US-00250795.
PR 13-SEP-1994; 94US-00305520.
PA (MITO-) MITOTIX INC.
PI Chiu MI, Cottarel G, Berlin V, Damagnez V, Draetta G, Rolfe M;
XX WPI; 1999-590402/50.
DR N-PSDB; AA227568.
XX
PT Identifying ubiquitination inhibitors using novel ubiquitin conjugating
XX enzyme.
XX
PS Example 2; Col 89-92; 61pp; English.
XX
XX This sequence is the human papillomavirus E6 protein. The invention
XX relates to assays for identifying an inhibitor of ubiquitin-mediated
XX proteolysis of a cell-cycle regulatory protein comprising contacting a
XX candidate agent with an ubiquitin-conjugating system and measuring the
XX level of ubiquitination. The ubiquitin-conjugating system comprises: (a)
XX a reconstituted protein mixture including a ubiquitin conjugating enzyme
XX (UBC) produced by the expression of a nucleic acid which hybridizes
XX under high stringency conditions to human UBC, Candida albicans UBC, or
XX Schizosaccharomyces pombe UBC coding sequences; (b) a regulatory protein
XX, and (c) ubiquitin. The polynucleotides are useful for identifying
XX ubiquitination inhibitors. The polynucleotides, polypeptides, antisense
XX compounds and antibodies against them may also be useful for the
XX treatment and/or diagnosis of proliferative disorders (e.g. cancer,
XX atherosclerosis, or restenosis), tissue connective disorders, rheumatoid
XX arthritis, insulin dependent diabetes mellitus, glomerulonephritis,
XX cirrhosis, and scleroderma)
XX
SQ Sequence 158 AA;
XX
Query Match 54.9%; Score 455.5; DB 2; Length 158;
Best Local Similarity 56.1%; Pred. No. 1.4e-42;
Matches 87; Conservative 21; Mismatches 42; Indels 5; Gaps 1;
XX
QY 2 FODPOERPKLPOLCTELOTTHDITLLECYCKOQLRREVVDPFARDCIYRDGNPYA 61
DB 4 FEPTRRPYKLPDLCTELMTSLQDIEITVCYKTVLETFEVPFAKDFVYVYRDSIPRA 63
XX
QY 62 VADKCLKFYSKISEVRYHCYVYGTTLLEQOYNKPLCDLLIRCNXOKPLCPREKORHLK 121
DB 64 ACHKCIDFYSRIRELRYHSDYVGDPLEKLTWGLYNLIRCLRCOKPLNPAEKLRLHNE 123
XX
QY 122 KORFNIRGRWTCRCMSCRSSR-----TRRETOL 151
DB 124 KRFFNIAGHYRGQCHSCCNBAROERLORRETQV 158
XX
RESULT 82
AAB03176
ID AAB03176 standard; protein; 158 AA.
XX
AC AAB03176;
XX
DT 12-SEP-2003 (revised)
DT 23-OCT-2000 (first entry)
XX
DE HPV-18 E6 protein.
XX
KW HPV-18 E6; ubiquitin mediated proteolysis; human;
KW cellular protein half life; ubiquitination inhibitor; p53; cyclin;
KW cell cycle regulator; myc deregulation; human papillomavirus;
KW HPV-18 E6 protein; cervical cancer; skin cancer; epidermal hyperplasia;
KW epidermal neoplasia; psoriasis; connective tissue disorder;
KW wound healing; cytoskeletal; antiproliferative; anticancer; antipsoriatic.
XX
OS Human papillomavirus; 18.
XX
PN US0608982-A.

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XX 30-MAY-2000.
PD 17-DEC-1996; 96US-00767942.
XX
PF 04-JAN-1994; 94US-00176937.
XX
PR 23-MAY-1994; 94US-00247904.
PR 27-MAY-1994; 94US-00250795.
PR 13-SEP-1994; 94US-00305520.
PR 07-JUN-1995; 95US-00486663.
XX
PA (MITO-) MITOTIX INC.
XX
PI Chiu MI, Cottarel G, Berlin V, Draetta G, Damagnez V, Rolfe M;
XX WPI; 2000-410854/35.
DR N-PSDB; AAA61623.
XX
PT Identifying an inhibitor of ubiquitin mediated proteolysis of regulatory
PT protein for treating cancers involves measuring ubiquitination levels of
PT the protein in the presence of candidate agent in an eukaryotic cell.
XX
PS Example 2; Col 97-100; 73pp; English.
XX
XX The invention relates to a method of identifying an inhibitor of
XX ubiquitin-mediated proteolysis of a cell cycle regulatory protein
XX comprising contacting an engineered eukaryotic cell with a candidate
XX agent. The eukaryotic cell is engineered to express a recombinant human,
XX Candida albicans or Schizosaccharomyces pombe ubiquitin-conjugating
XX enzyme (AAB03169-B03171), a cell cycle regulatory protein (such as p53)
XX and ubiquitin. The specification also discloses novel Candida albicans
XX and Schizosaccharomyces pombe ubiquitin-conjugating enzymes, caubCE and
XX spUBC (AAB03170, AAB03171), and two novel human ubiquitin-conjugating
XX enzymes, hUBC and rapUBC (AAB03169, AAB03173). The ubiquitin-mediated
XX proteolysis system is the major pathway for the selective, controlled
XX degradation of intracellular proteins in eukaryotic cells, and is
XX this system controls the half-lives of cellular proteins, and is
XX important in controlling the levels of proteins involved in cell cycle
XX progression. Alterations in the ubiquitination of these proteins may
XX therefore play a role in the development of cancers. For example, human
XX papillomaviruses such as HPV-18 encode a transforming protein, E6
XX (AAB03176), which combines with a cellular E6-associated protein (E6-AP;
XX AAB03177) to stimulate the ubiquitination of p53, thus targeting it for
XX degradation. The ubiquitination inhibitors identified according to the
XX method of the invention are useful for treatment of cervical cancers and
XX connective tissue disorders and for controlling the wound healing
XX process. They are also useful in treatment of hyperplastic epidermal
XX conditions such as psoriasis, neoplastic epidermal conditions, skin
XX cancers e.g., basal cell carcinomas, squamous cell carcinomas. The
XX inhibitors are useful for deregulating myc expression and rendering the
XX cells sensitive to chemotherapeutic treatment or to upset the balance of
XX transformed cells and cause apoptosis to occur. Inhibitors of ubiquitin-
XX mediated degradation of cyclins are useful as antiproliferative agents.
XX The present sequence represents HPV-18 E6 protein. (Updated on 12-SEP-
XX 2003 to standardise OS field)
XX
SQ Sequence 158 AA;
XX
Query Match 54.9%; Score 455.5; DB 3; Length 158;
Best Local Similarity 56.1%; Pred. No. 1.4e-42;
Matches 87; Conservative 21; Mismatches 42; Indels 5; Gaps 1;
XX
QY 2 FODPOERPKLPOLCTELOTTHDITLLECYCKOQLRREVVDPFARDCIYRDGNPYA 61
DB 4 FEPTRRPYKLPDLCTELMTSLQDIEITVCYKTVLETFEVPFAKDFVYVYRDSIPRA 63
XX
QY 62 VADKCLKFYSKISEVRYHCYVYGTTLLEQOYNKPLCDLLIRCNXOKPLCPREKORHLK 121
DB 64 ACHKCIDFYSRIRELRYHSDYVGDPLEKLTWGLYNLIRCLRCOKPLNPAEKLRLHNE 123
XX
QY 122 KORFNIRGRWTCRCMSCRSSR-----TRRETOL 151
DB 124 KRFFNIAGHYRGQCHSCCNBAROERLORRETQV 158
XX

```

RESULT 83  
AAB98427 standard; protein; 158 AA.  
ID AAB98427  
XX  
AC AAB98427;  
XX  
DT 22-AUG-2001 (first entry)  
XX  
XX Human papillomavirus protein HPV18 E6.  
DE Human papillomavirus; human leukocyte antigen; HLA; immune response; HPV;  
XX epitope; T cell; identification; vaccine; infection; genital wart;  
XX neoplastic growth; antiviral.  
KM Human papillomavirus.  
XX  
OS WO200141799-A1.  
XX  
PN 14-JUN-2001.  
XX  
PD 11-DEC-2000; 2000WO-US033549.  
XX  
PF 10-DEC-1999; 99US-0172705P.  
XX  
PR 15-AUG-2000; 2000US-00641528.  
XX  
PA (EPI-M-) EPIMUNE INC.  
XX  
PI Sette A, Sidney J, Southwood S, Chesnut R, Celis E, Grey HM,  
XX WPI, 2001-381497/40.  
DR An isolated human papilloma virus (HPV) epitope, useful in vaccines for  
XX treating HPV infections.  
PT  
PT Disclosure; Page 22; 756pp; English.  
XX  
XX The present invention describes an isolated prepared human papillomavirus  
CC (HPV) epitope (I). (I) has antiviral activity, and can be used in vaccine  
CC production. Peptides and corresponding nucleic acid compositions from the  
CC present invention are useful for stimulating an immune response to HPV by  
CC stimulating the production of CTL or HTL responses, specifically in the  
CC treatment or prophylaxis of HPV infection, in persons who have not  
CC manifested symptoms e.g. genital warts or neoplastic growth. The peptides  
CC can also be used in a tetramer staining assay to assess peripheral blood  
CC mononuclear cells for the presence of antigen-specific CTLs following  
CC exposure to a pathogen or immunogen, and as reagents to evaluate immune  
CC recall responses or evaluate the efficacy of a vaccine. The vaccine  
CC compositions are useful for removing warts or treating HPV infections.  
CC The epitopes for inclusion in an epitope-base vaccine may be selected  
CC from conserved regions of viral or tumour-associated antigens, which  
CC reduce the likelihood of escape mutants, also immunosuppressive epitopes  
CC that may be present in whole antigens can be avoided with the use of  
CC epitope-base vaccines. An additional advantage is the ability to combine  
CC selected epitopes (CTL and HTL) and to modify the composition of the  
CC epitopes achieving enhanced immunogenicity, the major benefit of the  
CC vaccine is that is safe and efficacious. AAB98391 to AAB98477 represent  
CC polypeptide sequences used in the exemplification of the present  
CC invention  
XX  
XX Sequence 158 AA;  
SQ

Query Match 54.9%; Score 455.5; DB 4; Length 158;  
Best Local Similarity 56.1%; Pred. No. 1.4e-42;  
Matches 87; Conservative 21; Mismatches 42; Indels 5; Gaps 1;

QY 2 FODDERPRKLPOLCTELTTHDIILIECVYCKQQLAREYVDFAPRLDCTIVYRGNPYA 61  
DB 4 FEDPRRRPKLPDLCTELTNTSLQDIEITVCYCKVLELTFEFAFKDLFVYVDSITHA 63  
QY 62 VXDCKLKFYSKISEVRYHCYSVYGTTLLEQVYKPKLDLIRICINXQKPLCEBEKORHLDK 121  
DB 64 ACHKCIDFYSKIRIRLHYSDSVYGTLEKLTNTGIVNLLIRCLRQCKPLNPAEKRLHINE 123

DB 64 ACHKCIDFYSKIRIRLHYSDSVYGTLEKLTNTGIVNLLIRCLRQCKPLNPAEKRLHINE 123  
QY 122 KORFHNIRGNTGRCMSCCRSSR-----TRRETQI 151  
DB 124 KRFHNINAGHYRGQCHSCCNRAQERLORRRETQV 158

RESULT 84  
ADO44074 standard; protein; 158 AA.  
ID ADO44074  
XX  
AC ADO44074;  
XX  
DT 15-JUL-2004 (first entry)  
XX  
XX Amino acid sequence of the E6 polypeptide of HPV18.  
DE E6 protein; E7 protein; fusion protein; HPV; HPV-associated cancer;  
XX cervical cancer; immune response; lower gastrointestinal tract cancer;  
XX anal cancer; reproductive system cancer; penile cancer; vulvar cancer.  
KM Human papillomavirus type 18.  
XX  
OS WO2004030636-A2.  
XX  
PN 15-APR-2004.  
XX  
PD 02-OCT-2003; 2003WO-US0311726.  
XX  
PF 03-OCT-2002; 2002US-0415929P.  
XX  
PR (AMHP ) WYETH HOLDINGS CORP.  
XX  
PA Smith L, Casasetti MC;  
XX WPI, 2004-316328/29.  
XX  
DR N-PEDB; ADO444101.  
XX  
XX New polypeptide comprising human papillomavirus E6 and E7 polypeptides,  
PT useful for treating or preventing human papillomavirus (HPV)-associated  
PT cancers, e.g. cervical cancer.  
XX  
XX Disclosure; Page 78; 101pp; English.  
XX  
XX ADO44074-ADO44085 represent E6 polypeptides from human papillomaviruses.  
CC ADO44098 is the consensus sequence derived from these polypeptides. The  
CC specification describes human papillomavirus E6 and E7 polypeptides,  
CC where the E7 polypeptide has mutations at any one or more of the amino  
CC acids corresponding to amino acids 24, 26 or 91 of the sequence given in  
CC ADO44073 and the E6 polypeptide has no mutations or has mutations at any  
CC one or more of the amino acids corresponding to amino acids 63 or 106 of  
CC the sequence given in ADO44072. The polypeptides of the invention are  
CC useful for treating or preventing human papillomavirus (HPV)-associated  
CC cancers, such as cervical cancer. The fusion proteins and nucleic acids  
CC encoding the fusion proteins are useful for generating immune responses  
CC against HPV. They are also useful for treating lower gastrointestinal  
CC tract cancers, e.g. anal cancer, and other cancers of the reproductive  
CC system, including penile and vulvar cancer.  
XX  
XX Sequence 158 AA;  
SQ

Query Match 54.9%; Score 455.5; DB 8; Length 158;  
Best Local Similarity 56.1%; Pred. No. 1.4e-42;  
Matches 87; Conservative 21; Mismatches 42; Indels 5; Gaps 1;

QY 2 FODDERPRKLPOLCTELTTHDIILIECVYCKQQLAREYVDFAPRLDCTIVYRGNPYA 61  
DB 4 FEDPRRRPKLPDLCTELTNTSLQDIEITVCYCKVLELTFEFAFKDLFVYVDSITHA 63  
QY 62 VXDCKLKFYSKISEVRYHCYSVYGTTLLEQVYKPKLDLIRICINXQKPLCEBEKORHLDK 121  
DB 64 ACHKCIDFYSKIRIRLHYSDSVYGTLEKLTNTGIVNLLIRCLRQCKPLNPAEKRLHINE 123



QY 122 KORFNIRGWTGRMCSCRSSR-----TRRETOL 151  
 ||:|||||:|:|:|||||:|:|:|||||:  
 Db 124 KRRFNIAGHYRGQCHSCCNRAEROERLQRRRETQV 158

RESULT 87  
 AEC98864  
 ID AEC98864 standard; protein; 158 AA.  
 AC AEC98864;  
 DT 01-DEC-2005 (first entry)  
 DE HPV\_18 Envelope protein E6.  
 KW Human papilloma virus infection; virucide; cancer; cytostatic; vaccine;  
 KM epitope mapping; immune stimulation; cytotoxic T-lymphocyte.  
 OS Human papillomavirus type 18.  
 XX WO2005089164-A2.  
 FN 29-SEP-2005.  
 PD 03-JAN-2005; 2005WO-US000077.  
 PF 31-DEC-2003; 2003US-053211P.  
 PR 02-JUL-2004; 2004US-0584652P.  
 XX (EPIIM-) EPIIMUNE INC.  
 PA (INNO-) INNOGENETICS NV.  
 PA (CHES/) CHESNUT R.  
 PA (NEWM/) NEWMAN M J.  
 PA (MOTH/) MOTH B.  
 PA (BAKE/) BAKER D.  
 PA (SOUT/) SOUTHWOOD S.  
 PA (BABE/) BABE L M.  
 PA (CHEN/) CHEN Y.  
 PA (DEYO/) DEYOUNG L M.  
 PA (HUAN/) HUANG M T F.  
 PA (POWE/) POWER S D.  
 XX Cheanut R, Newman MJ, Moche B, Baker D, Southwood S, Babe LM;  
 PI Chen Y, Deyoung LM, Huang MTF, Power SD;  
 DR WPI; 2005-658982/67.  
 XX New polynucleotide comprises a multi-epitope construct comprising nucleic  
 PT acids encoding the human papillomavirus (HPV) cytotoxic T lymphocyte  
 PT (CTL) epitopes, useful in preparing a vaccine against HPV.  
 PS Example 10; Page 349; 518pp; English.  
 XX The invention relates to a new polynucleotide comprising a multi-epitope  
 CC construct comprising nucleic acids encoding the human papillomavirus  
 CC (HPV) cytotoxic T lymphocyte (CTL) epitopes e.g., HPV16.E1.214, and that  
 CC are directly or indirectly joined to one another in the same reading  
 CC frame, a vaccine minigene. Also included are a vector comprising the  
 CC multi-epitope construct, a polypeptide comprising an amino acid sequence  
 CC encoded by the polynucleotide, a composition (comprising the  
 CC polynucleotide, vector and/or polypeptide and a carrier), a cell  
 CC (comprising the polynucleotide, vector or polypeptide), inducing an  
 CC immune response against human papillomavirus virus (HPV) and making the  
 CC polynucleotide, vector or polypeptide. The epitopes are derived from  
 CC different strains of HPV and are from the E1, E2, E6 and E7 proteins. The  
 CC epitopes may be linked via a GP-anchor/spacer peptide. The order of the  
 CC epitopes in the vaccine protein are disclosed in the tables referred to  
 CC in the claims of the specification. The polynucleotide, vector or  
 CC polypeptide is useful in preparing a composition for inducing an immune  
 CC response against human papillomavirus virus (HPV) and thus providing a  
 CC defense against HPV infection and HPV-related cancers. The present  
 CC sequence is an HPV protein used to derive epitopes for the vaccine of the  
 CC invention.

XX SQ Sequence 158 AA;  
 Query Match 54.9%; Score 455.5; DB 9; Length 158;  
 Best Local Similarity 56.1%; Pred. No. 1.4e-42;  
 Matches 87; Conservative 21; Mismatches 42; Indels 5; Gaps 1;

QY 2 FODPERPRKLPOLCTEITQTIHDIILECYCKQQLAREVYDFAFRDLCTVYRGNPYA 61  
 ||:|||||:|:|:|||||:|:|:|||||:  
 Db 4 FEDPTRRPYPKLPDLCTEINTSLQDIETICVCKTLELTFEVEFAPKLPVYRDSIPHA 63

QY 62 VXDCKLKFYSKISEYRHYCVSGVGTTLBOQYNKPLCDLLIRICINXQKPLCEPEKORHLDK 121  
 ||:|||||:|:|:|||||:|:|:|||||:  
 Db 64 ACHKCIDPYSKIRLEIRHISDSVYGDITLTKLNTGTGLNLIICLRQCKRLNPAEKRLHINE 123

QY 122 KORFNIRGWTGRMCSCRSSR-----TRRETOL 151  
 ||:|||||:|:|:|||||:|:|:|||||:  
 Db 124 KRRFNIAGHYRGQCHSCCNRAEROERLQRRRETQV 158

RESULT 88  
 AEC96398  
 ID AEC96398 standard; protein; 158 AA.  
 AC AEC96398;  
 DT 01-DEC-2005 (first entry)  
 DE HPV protein E6 from HPV18.  
 KW Human papilloma virus infection; virucide; cancer; cytostatic; vaccine;  
 KM epitope mapping; immune stimulation; cytotoxic T-lymphocyte.  
 OS Human papillomavirus type 18.  
 XX WO2005089164-A2.  
 FN 29-SEP-2005.  
 PD 03-JAN-2005; 2005WO-US000077.  
 PF 31-DEC-2003; 2003US-053211P.  
 PR 02-JUL-2004; 2004US-0584652P.  
 XX (EPIIM-) EPIIMUNE INC.  
 PA (INNO-) INNOGENETICS NV.  
 PA (CHES/) CHESNUT R.  
 PA (NEWM/) NEWMAN M J.  
 PA (MOTH/) MOTH B.  
 PA (BAKE/) BAKER D.  
 PA (SOUT/) SOUTHWOOD S.  
 PA (BABE/) BABE L M.  
 PA (CHEN/) CHEN Y.  
 PA (DEYO/) DEYOUNG L M.  
 PA (HUAN/) HUANG M T F.  
 PA (POWE/) POWER S D.  
 XX Cheanut R, Newman MJ, Moche B, Baker D, Southwood S, Babe LM;  
 PI Chen Y, Deyoung LM, Huang MTF, Power SD;  
 DR WPI; 2005-658982/67.  
 XX New polynucleotide comprises a multi-epitope construct comprising nucleic  
 PT acids encoding the human papillomavirus (HPV) cytotoxic T lymphocyte  
 PT (CTL) epitopes, useful in preparing a vaccine against HPV.  
 PS Disclosure; Page 57; 518pp; English.  
 XX The invention relates to a new polynucleotide comprising a multi-epitope  
 CC construct comprising nucleic acids encoding the human papillomavirus  
 CC (HPV) cytotoxic T lymphocyte (CTL) epitopes e.g., HPV16.E1.214, and that  
 CC are directly or indirectly joined to one another in the same reading  
 CC frame, a vaccine minigene. Also included are a vector comprising the

CC multi-epitope construct, a polypeptide comprising an amino acid sequence  
CC encoded by the polynucleotide, a composition (comprising the  
CC polynucleotide, vector and/or polypeptide and a carrier), a cell  
CC (comprising the polynucleotide, vector or polypeptide), inducing an  
CC immune response against human papillomavirus virus (HPV) and making the  
CC polynucleotide, vector or polypeptide. The epitopes are derived from  
CC different strains of HPV and are from the E1, E2, E6 and E7 proteins. The  
CC epitopes may be linked via a GP-anchor/spacer peptide. The order of the  
CC epitopes in the vaccine protein are disclosed in the tables referred to  
CC in the claims of the specification. The polynucleotide, vector or  
CC polypeptide is useful in preparing a composition for inducing an immune  
CC response against human papillomavirus virus (HPV) and thus providing a  
CC defense against HPV infection and HPV-related cancers. The present  
CC sequence is an HPV protein used to derive epitopes for the vaccine of the  
CC invention.

XX S0 Sequence 158 AA;

Query Match 54.9%; Score 455.5; DB 9; Length 158;  
Best Local Similarity 56.1%; Pred. No. 1.4e-42;  
Matches 87; Conservative 21; Mismatches 42; Indels 5; Gaps 1;

QY 2 FDDPQERPKLPOLCTELQTTIHDIILECYCKQQLRREYDFAFRDLCIVYRDGNPYA 61  
DB 4 FEDPTRRPPYKLPDLCTELNTSLQDIEITCYCKTVLETFEPEFAFKDLFVYVYRDSIPHA 63  
QY 62 VADKCLKPFYSKISEYRHYCYSVYGTTLQOYNKPLCDLIRCNXOKPLCPREKORHLDK 121  
DB 64 ACHKCIDFYSRIELRHYSVSVDYGTLEKLTGTGLYNLIRCLRCQKPLNPAEKLRHINE 123

QY 122 KORFNNIRGRWTGRCMSCCRSSR-----TRRETOL 151  
DB 124 KRFFNIAGHYRGQCHSCCNRAQRERLQRRRETQV 158

RESULT 89  
AA022924  
ID AA022924 standard; protein; 172 AA.  
XX  
XX  
AC AA022924;  
XX  
XX 12-DEC-2002 (first entry)  
XX  
XX Human papillomavirus-18 (HPV18) E6E7-protein sequence.  
XX  
XX  
XX Virucide; cytostatic; E6; E7 fusion protein; HPV; immunogenic; vaccine;  
XX fusion partner; immunogenicity; HPV infection; neoplasia; HPV18;  
XX human papillomavirus-18; E6E7-sequence.  
XX  
XX Human papillomavirus.  
XX  
XX  
XX EP1243655-A1.  
XX  
XX  
XX 25-SEP-2002.  
XX  
XX  
XX 23-MAR-2001; 2001EP-00107271.  
XX  
XX  
XX 23-MAR-2001; 2001EP-00107271.  
XX  
XX  
XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
XX  
XX  
XX Cid-Arregui A, Zur Hausen H;  
XX  
XX  
XX WPI: 2002-724952/79.  
XX  
XX  
XX N-PSDB; AAL53422.  
XX  
XX  
XX A new DNA sequence encoding a fusion protein comprising a mutagenized HPV  
XX (human papillomavirus) E6 or E7 coding sequence and a sequence encoding a  
XX highly immunogenic fusion partner is useful to vaccinate against HPV  
XX infection.  
XX  
XX  
XX Disclosure; Fig 4; 34pp; English.  
XX

CC The invention relates to a new DNA sequence encodes an E6 or E7 fusion  
CC protein of HPV, where at least 20% of the original codons are replaced by  
CC codons which lead to enhanced translation in a mammalian cell, containing  
CC a mutation which results in production of a truncated non-functional  
CC protein, and encoding a highly immunogenic polypeptide fusion partner  
CC capable of enhancing immunogenicity of the E6 or E7 protein in the  
CC mammalian host. The invention is used as a vaccine for the prevention or  
CC treatment of an HPV infection or a neoplasia associated with HPV  
CC infection. This sequence represents the human papillomavirus-18 (HPV18)  
CC E6E7-protein sequence of the invention

XX S0 Sequence 172 AA;

Query Match 54.9%; Score 455.5; DB 5; Length 172;  
Best Local Similarity 56.1%; Pred. No. 1.6e-42;  
Matches 87; Conservative 21; Mismatches 42; Indels 5; Gaps 1;

QY 2 FDDPQERPKLPOLCTELQTTIHDIILECYCKQQLRREYDFAFRDLCIVYRDGNPYA 61  
DB 10 FEDPTRRPPYKLPDLCTELNTSLQDIEITCYCKTVLETFEPEFAFKDLFVYVYRDSIPHA 69  
QY 62 VADKCLKPFYSKISEYRHYCYSVYGTTLQOYNKPLCDLIRCNXOKPLCPREKORHLDK 121  
DB 70 ACHKCIDFYSRIELRHYSVSVDYGTLEKLTGTGLYNLIRCLRCQKPLNPAEKLRHINE 129  
QY 122 KORFNNIRGRWTGRCMSCCRSSR-----TRRETOL 151  
DB 130 KRFFNIAGHYRGQCHSCCNRAQRERLQRRRETQV 164

RESULT 90  
AAR27728  
ID AAR27728 standard; protein; 271 AA.  
XX  
XX  
XX AAR27728;  
XX  
XX  
XX 24-OCT-2003 (revised)  
XX  
XX 25-MAR-2003 (revised)  
XX  
XX 09-MAR-1993 (first entry)  
XX  
XX  
XX HPV 18 E6 protein fragment.  
XX  
XX  
XX Virus vector; vaccinia virus; papillomavirus; HPV; human; amplification;  
XX immunotherapeutic.  
XX  
XX  
XX Human papillomavirus; 18.  
XX  
XX  
XX Key Location/Qualifiers  
XX FT 2..259  
XX FT Peptide /note="HPV-18 E6 protein"  
XX  
XX  
XX WO9216636-A1.  
XX  
XX  
XX 01-OCT-1992.  
XX  
XX  
XX 10-MAR-1992; 92WO-GB000424.  
XX  
XX  
XX 14-MAR-1991; 91GB-00005383.  
XX  
XX  
XX (IMMU ) IMMUNOLOGY LTD.  
XX  
XX  
XX Boursnell MEG, Inglis SC, Munro AJ;  
XX  
XX  
XX WPI: 1992-349219/42.  
XX  
XX  
XX N-PSDB; AAO29390.  
XX  
XX  
XX Recombinant virus vectors encoding human papillomavirus proteins - for  
XX treating and vaccinating against HPV infections and conditions caused by  
XX them, such as cervical cancer.  
XX  
XX  
XX Disclosure; Fig 1b; 83pp; English.  
XX  
XX  
XX The fragment of DNA contg. the HPV-18 E6/E7 coding region was prepd. by  
CC



```

Query Match          54.9%; Score 455.5; DB 2; Length 278;
Best Local Similarity 56.1%; Pred. No. 2.8e-42;
Matches 87; Conservative 21; Mismatches 42; Indels 5; Gaps 1;

OY 2 FODPERPRKLPOLCTELQTTIHDIILBCVCKQOQLLRREYVDFAFRDLCTIYRDGNPYA 61
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 115 FEDPTRRPYKLPDLCTELNTSLQDIETVCYKTVLELVEFEPAFKDLFVYVRDSIPHA 174
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 62 VXDCKLKFYSKISEYRHYCYSVYGTTLBQOYNKPLCDLLIRNCINXQKPLCEBKORHLDK 121
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 175 ACHKCIDFYSRIRELRHYSDSVYGDPLEKLTNTGLYNLLIRCLRCQKPLNPAEKURLHNE 234
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

OY 122 KORFNNIRGRMTGRCMSCCRSSR-----TRRETOL 151
DB 235 KRPFNINAGHYRGQCHSCCNRAQERLQRRRETQV 269

RESULT 93
AED52653
ID AED52653 standard; protein; 278 AA.
XX
XX AED52653;
AC
XX
XX 29-DEC-2005 (first entry)
DT
XX
XX Fusion protein D1/3-E6-His (HPV18).
DE
XX
XX Fusion protein; vaccine; papilloma; cytostatic; papillomavirus infection;
KM viricide; uterine cervix tumor; E6; D protein.
XX
XX Haemophilus influenzae; strain 772.
OS
OS Human papillomavirus type 18.
OS Synthetic.
OS Chimeric.
XX
XX IN9801903-14.
XX
XX PD 04-MAR-2005.
XX
XX PF 24-AUG-1998; 98IN-CH001903.
XX
XX PR 22-AUG-1997; 97EP-00179535.
XX
XX PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
XX PI Tyrrell AMR;
XX
XX DR WPI; 2005-557648/57.
XX
XX DR N-PSDB; AED52652.
XX
XX PT Vaccine.
XX
XX PS Example 16; Fig 22; 96pp; English.
XX
XX CC The invention relates to human Papilloma virus (HPV) fusion proteins,
CC linked to an immunological fusion partner that provides T helper epitopes
CC to the HPV antigen. Vaccine formulations comprising the fusion proteins
CC are useful in the treatment or prophylaxis of HPV induced lesions
CC (papillomas, warts and cervical cancer). HPV 16 (and HPV 18) E6 and E7
CC proteins (singly, as an E6-E7 fusion or mutated) were fused to either
CC Haemophilus influenzae D protein (20-127), the C-terminus of
CC Streptococcus pneumoniae type 1 protein (cLysA) or thioredoxin. The present
CC sequence represents an HPV-H. influenzae D protein, fusion protein of the
CC invention.
XX
XX SQ Sequence 278 AA;

Query Match          54.9%; Score 455.5; DB 9; Length 278;
Best Local Similarity 56.1%; Pred. No. 2.8e-42;
Matches 87; Conservative 21; Mismatches 42; Indels 5; Gaps 1;

OY 2 FODPERPRKLPOLCTELQTTIHDIILBCVCKQOQLLRREYVDFAFRDLCTIYRDGNPYA 61
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

```

DB 115 FEDPTRRPYKLPDLCTELNTSLQDIETVCYKTVLELVEFEPAFKDLFVYVRDSIPHA 174
OY 62 VXDCKLKFYSKISEYRHYCYSVYGTTLBQOYNKPLCDLLIRNCINXQKPLCEBKORHLDK 121
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 175 ACHKCIDFYSRIRELRHYSDSVYGDPLEKLTNTGLYNLLIRCLRCQKPLNPAEKURLHNE 234
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 122 KORFNNIRGRMTGRCMSCCRSSR-----TRRETOL 151
DB 235 KRPFNINAGHYRGQCHSCCNRAQERLQRRRETQV 269

RESULT 94
AAV25386
ID AAV25386 standard; protein; 383 AA.
XX
XX AAV25386;
AC
XX
XX 06-SEP-1999 (first entry)
DT
XX
XX HPV fusion protein D1/3-E6/E7-His/HPV18.
DE
XX
XX Fusion protein; E6 protein; E7 protein; E6/E7; immunomodulator; tumour;
KM immunological fusion partner; CpG oligonucleotide; immune response;
KM HPV antigen; prevention; treatment.
XX
XX OS Synthetic.
OS Human papillomavirus.
XX
XX PN W09933868-A2.
XX
XX PD 08-JUL-1999.
XX
XX PF 18-DEC-1998; 98WO-EP008563.
XX
XX PR 24-DEC-1997; 97GB-00027262.
XX
XX PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
XX PI Dalemans WJL; Gerard CMG;
XX
XX DR WPI; 1999-405485/34.
XX
XX DR N-PSDB; AAX78801.
XX
XX PT Composition comprising an E6, E7 or E6/E7 fusion protein from HPV to
XX induce immune response to HPV.
XX
XX PS Example XII; Page 61-62; 62pp; English.
XX
XX CC AAX78791-X78801 represent nucleic acid sequences which encode novel
CC constructs comprising an E6 or E7 protein or E6/E7 fusion protein from
CC HPV (represented in AAV25375-Y25386). These constructs are optionally
CC linked to an immunological fusion partner and an immunomodulatory CpG
CC oligonucleotide. The products of the invention can be used to induce an
CC immune response in a patient to an HPV antigen. They can also be used for
CC preventing or treating HPV induced tumours
XX
XX SQ Sequence 383 AA;

Query Match          54.9%; Score 455.5; DB 2; Length 383;
Best Local Similarity 56.1%; Pred. No. 4.1e-42;
Matches 87; Conservative 21; Mismatches 42; Indels 5; Gaps 1;

OY 2 FODPERPRKLPOLCTELQTTIHDIILBCVCKQOQLLRREYVDFAFRDLCTIYRDGNPYA 61
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 115 FEDPTRRPYKLPDLCTELNTSLQDIETVCYKTVLELVEFEPAFKDLFVYVRDSIPHA 174
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 62 VXDCKLKFYSKISEYRHYCYSVYGTTLBQOYNKPLCDLLIRNCINXQKPLCEBKORHLDK 121
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 175 ACHKCIDFYSRIRELRHYSDSVYGDPLEKLTNTGLYNLLIRCLRCQKPLNPAEKURLHNE 234
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 122 KORFNNIRGRMTGRCMSCCRSSR-----TRRETOL 151
DB 235 KRPFNINAGHYRGQCHSCCNRAQERLQRRRETQV 269

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RESULT 95
AA02642
XX AA02642 standard; protein; 383 AA.
AC
XX AA02642;
XX
AC
XX 17-OCT-2003 (revised)
DT 22-JUN-1999 (first entry)
XX
DE Prot.D1/3-E6-E7-His/HPV18 protein.
XX
XX Chimeric; E6; E7; fusion protein; protein D; vaccine; immunotherapy;
KM tumour; lesion; benign; malignant; virus; infection.
XX
XX Human papillomavirus.
OS Haemophilus influenzae.
XX Chimeric.
XX
XX MO9910375-A2.
XX
XX 04-MAR-1999.
XX
XX 17-AUG-1998; 98MO-EP005285.
XX
XX 22-AUG-1997; 97GB-00017953.
XX
XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
XX Bruck C, Cabezon Silva T, Delisse AEF, Gerard CMG;
PI Lombardo-Bencheikh A;
XX
XX WPI; 1999-190587/16.
DR N-PSDB; AAX29790.
XX
XX Human Papilloma Virus (HPV) fusion proteins - useful in vaccines for
PT treatment or prophylaxis of HPV induced lesions.
XX
XX Disclousure; Fig 25; 95pp; English.
XX
XX This sequence represents a chimeric E6 or E7 protein or E6/E7 fusion
CC protein from Human papillomavirus (HPV) linked to an immunological fusion
CC partner, in this case, a fragment of the Haemophilus influenzae B protein
CC D. The sequence also contains a histidine tag at the C-terminus of the
CC encoded protein. The protein can be used in a vaccine, for immuno-
CC therapeutically treating HPV induced tumour lesions (benign or malignant)
CC and preventing HPV viral infection. (Updated on 17-Oct-2003 to
CC standardise OS field)
XX
XX
XX Sequence 383 AA;
SQ
Query Match 54.9%; Score 455.5; DB 2; Length 383;
Best Local Similarity 56.1%; Pred. No. 4.1e-42;
Matches 87; Conservative 21; Mismatches 42; Indels 5; Gaps 1;
QY 2 FODQERPRKLPQLCTELQTTIHDIIECVYKQQLRREYVDFAFRDLCTIVYRDGNPYA 61
DB 115 FEDPRRPRYKLPDLCTELNTSLQDIETVCYKTVLETFEFAFKDLFVYVRDSIPHA 174
QY 62 VXDCKLKYSKISSEYRHYCVSYGTTLEQYVKNKPLCDLIRGKINXOKPLCEPEKORHDK 121
DB 175 ACHKCTIDYSRIRELRHYSDSVYGDTLEKLTNTGLYNLLIRLCRCQKPLNPAEKURHNE 234
QY 122 KORFNINRGWTRGCMSCCRSSR-----TRRETOL 151
DB 235 KRRFNTAGHYRGQCHSCNBARQERLQRRRETQV 269
QY
DB
RESULT 96
AED52657
XX AED52657 standard; protein; 383 AA.
XX

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AC AED52657;
XX
XX 29-DEC-2005 (first entry)
DT
XX
XX Fusion protein D1/3-E6-E7-His/HPV18.
DE
XX
XX Fusion protein; vaccine; papilloma; cytostatic; papillomavirus infection;
KM virucide; uterine cervix tumor; E7; E6; D protein.
XX
XX Haemophilus influenzae; strain 772.
OS
XX Human papillomavirus type 18.
OS Synthetic.
XX Chimeric.
XX
XX IN9801903-14.
XX
XX 04-MAR-2005.
XX
XX 24-AUG-1998; 98IN-CH001903.
XX
XX 22-AUG-1997; 97EP-00179535.
XX
XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
XX Tyrtrell AWR;
XX
XX WPI; 2005-557648/57.
DR N-PSDB; AED52656.
XX
XX Vaccine.
XX
XX Example 17; Fig 25; 96pp; English.
XX
XX The invention relates to human Papilloma virus (HPV) fusion proteins,
CC linked to an immunological fusion partner that provides T helper epitopes
CC to the HPV antigen. Vaccine formulations comprising the fusion proteins
CC are useful in the treatment or prophylaxis of HPV induced lesions
CC (papillomas, warts and cervical cancer). HPV 16 (and HPV 18) E6 and E7
CC proteins (singly, as an E6-E7 fusion or mutated) were fused to either
CC Haemophilus influenzae D protein (20-127), the C-terminus of
CC Streptococcus pneumoniae LytA protein (cLytA) or chloroixin. The present
CC sequence represents an HPV-H. influenzae D protein, fusion protein of the
CC invention.
XX
XX
XX Sequence 383 AA;
SQ
Query Match 54.9%; Score 455.5; DB 9; Length 383;
Best Local Similarity 56.1%; Pred. No. 4.1e-42;
Matches 87; Conservative 21; Mismatches 42; Indels 5; Gaps 1;
QY 2 FODQERPRKLPQLCTELQTTIHDIIECVYKQQLRREYVDFAFRDLCTIVYRDGNPYA 61
DB 115 FEDPRRPRYKLPDLCTELNTSLQDIETVCYKTVLETFEFAFKDLFVYVRDSIPHA 174
QY 62 VXDCKLKYSKISSEYRHYCVSYGTTLEQYVKNKPLCDLIRGKINXOKPLCEPEKORHDK 121
DB 175 ACHKCTIDYSRIRELRHYSDSVYGDTLEKLTNTGLYNLLIRLCRCQKPLNPAEKURHNE 234
QY 122 KORFNINRGWTRGCMSCCRSSR-----TRRETOL 151
DB 235 KRRFNTAGHYRGQCHSCNBARQERLQRRRETQV 269
QY
DB
RESULT 97
AEA98550
XX AEA98550 standard; protein; 162 AA.
XX
XX AEA98550;
XX
XX 08-SEP-2005 (first entry)
DT
XX
XX HPV (oncogenic strain) E6 amino acid sequence SEQ ID 31.
XX

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GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

# OM protein - protein search, using sw model

Run on: May 27, 2006, 05:10:28 ; Search time 29.1084 Seconds  
(without alignments)  
499.124 Million cell updates/sec

Title: US-10-530-253-13ED  
Sequence score: 830  
1 MFQDDPQRRPKLPOLCTELQ.....WTGRCHMSCRSSRRRTQL 151

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : PIR 80:\*  
1: PIR1:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	823	99.2	158	1	protein E6 - human
2	578	69.6	149	1	B6 protein - human
3	523	63.0	149	1	B6 protein - human
4	520	62.7	149	1	B6 protein - human
5	496	59.8	149	1	B6 protein - human
6	487	58.7	148	2	B6 protein - human
7	484	58.3	148	2	B6 protein - human
8	460	55.4	151	1	B6 protein - human
9	459.5	55.4	158	2	B6 protein - human
10	455.5	54.9	158	1	B6 protein - human
11	451.5	54.4	158	1	B6 protein - human
12	449.5	54.2	158	1	B6 protein - human
13	438	52.8	191	1	B6 protein - human
14	436.5	52.6	150	2	B6 protein - human
15	426.5	51.4	155	1	B6 protein - human
16	426.5	51.4	155	2	B6 protein - human
17	385.5	46.4	153	2	B6 protein - human
18	379	45.7	154	2	B6 protein - human
19	372.5	44.9	155	2	B6 protein - human
20	326.5	39.3	155	1	B6 protein - human
21	304	36.6	153	1	B6 protein - human
22	303	36.3	153	1	B6 protein - human
23	301	35.8	159	1	B6 protein - human
24	297.5	35.4	150	1	B6 protein - human
25	294	35.0	159	2	B6 protein - human
26	292	35.0	154	2	B6 protein - human
27	290.5	34.8	154	2	B6 protein - human
28	288.5	34.7	150	1	B6 protein - human
29	288	34.7	150	1	B6 protein - human

30	283	34.1	142	2	S36509	B6 protein - human
31	273	32.9	150	1	M6WL13	B6 protein - human
32	268	32.3	150	1	M6WL42	B6 protein - human
33	268	28.8	148	2	S36532	B6 protein - human
34	231	27.8	152	2	S36550	B6 protein - human
35	154	18.6	138	2	S36567	B6 protein - human
36	143.5	17.3	141	2	S36479	B6 protein - human
37	137	16.5	156	1	M6WL41	B6 protein - human
38	136.5	16.4	140	1	M6WL	B6 protein - human
39	134.5	16.2	139	1	M6WL82	B6 protein - human
40	132	15.9	161	2	S36491	B6 protein - human
41	129.5	15.6	207	2	S28510	B6 protein - multi
42	128.5	15.5	141	2	S36473	B6 protein - human
43	127	15.3	57	2	IS6705	B6 protein - human
44	127	15.3	273	1	M6WL8	B6 protein - human
45	123	14.8	157	2	S36538	B6 protein - human
46	123	14.8	166	2	S36485	B6 protein - human
47	121.5	14.6	148	2	S36590	B6 protein - human
48	119	14.3	137	1	M6WL8	B6 protein - human
49	118	14.2	155	1	M6WL8	B6 protein - human
50	118	14.2	157	1	M6WL8	B6 protein - human
51	116	14.0	157	1	M6WL8	B6 protein - human
52	113	13.6	157	1	M6WL8	B6 protein - human
53	86	10.4	154	2	S28509	B6 protein - Old W
54	83.5	10.1	135	1	M6WLDP	B6 protein - deer
55	83	10.0	32	2	S19906	B6-II protein - hu
56	83	10.0	35	2	S19909	B6-II protein - hu
57	83	10.0	35	2	S23825	B6-I protein - hum
58	79.5	9.6	471	2	T02749	G1/S transifion co
59	77.5	9.3	135	1	M6WL8	B6 protein - Euro
60	77.5	9.3	572	2	G02845	zyxin - human
61	77.5	9.3	1468	2	S11515	formin - mouse
62	77	9.3	699	2	T09483	Cys-rich protein R
63	76	9.2	400	2	S44810	outer dense fiber
64	75.5	9.1	250	2	S71522	hypothetical prote
65	75	9.0	303	2	T21125	outer dense fiber
66	74.5	9.0	262	2	S56100	alpha-fetoprotein
67	74.5	9.0	609	1	FRGO	alpha-fetoprotein
68	74.5	9.0	609	1	FRGO	alpha-fetoprotein
69	74.5	9.0	609	2	UC4258	alpha-fetoprotein
70	74	8.9	524	2	F96784	hypothetical prote
71	71	8.9	1379	2	T45119	FIM protein (Impor
72	73.5	8.9	357	2	A72220	conserved hypothet
73	73.5	8.9	549	2	T17525	proline-rich prote
74	73	8.8	284	2	UC7686	activator of CAMP-
75	73	8.8	557	2	A55933	paxillin - human
76	73	8.8	559	2	B55933	G1/S transifion co
77	72.5	8.7	866	2	T01171	conserved hypothet
78	72	8.7	270	2	G82108	hypothetical prote
79	72	8.7	422	2	T21820	protein P1504.19 (
80	71.5	8.6	565	2	H06477	DNA primase (EC 2.
81	71.5	8.6	375	1	A23689	limulus clotting e
82	71	8.6	1630	2	T40217	hypothetical prote
83	71	8.6	1638	2	D87749	protein unc-73b (i
84	71	8.6	1638	2	T42739	guanine nucleotide
85	71	8.6	2488	2	C97723	separate-trna lig
86	70.5	8.5	615	2	C86496	hypothetical prote
87	70	8.4	449	2	D72147	hypothetical prote
88	70	8.4	449	2	A81544	hypothetical prote
89	70	8.4	449	2	T3616	hypothetical prote
90	70	8.4	708	2	B81704	conserved hypothet
91	70	8.4	1436	2	T15519	hypothetical prote
92	69.5	8.4	314	2	B84474	hypothetical prote
93	69	8.3	298	2	T33884	hypothetical prote
94	69	8.3	327	2	A71928	cag island protein
95	69	8.3	1819	2	S56101	outer dense fiber
96	68.5	8.3	262	1	GQHUT1	tumor necrosis fac
97	68.5	8.3	455	1	T28250	hypothetical prote
98	68.5	8.3	519	2	A30817	sependility (ery h
99	68.5	8.3	868	2	G02741	skeletal muscle Li
100	68	8.2	280	2	G02741	

## ALIGNMENTS

## RESULT 1

M6WLH5 protein E6 - human papillomavirus type 16

C:Species: human papillomavirus type 16

C:Date: 28-May-1986 #sequence\_revision 28-May-1986 #text\_change 09-Jul-2004

A:Accession: A03682; J10427

R:Seedorf, K.; Krammer, G.; Durec, M.; Suhai, S.; Rowekamp, W.G.

Virology 145, 181-185, 1985

A:Title: Human papillomavirus type 16 DNA sequence.

A:Reference number: A22355; MUID:85246220; PMID:2990099

A:Accession: A03682

A:Molecule type: DNA

A:Residues: 1-158 &lt;SEB&gt;

A:Cross-references: UNIPROT:P03126; UNIPARC:UPI000000138B; GB:X02718; NID:G333031; PIDN:

R.Kennedy, I.M.; Haddock, J.K.; Clemente, J.B.

J. Virol. 65, 2093-2097, 1991

A:Title: A negative element in the human poapillomavirus type 16 genome acts at the level

A:Reference number: Z17014; MUID:91162763; PMID:1848319

A:Accession: T10427

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-158 &lt;KEN&gt;

A:Cross-references: UNIPARC:UPI000000138B; EMBL:X02718; NID:G333031; PIDN:AAA46939.1; PI

C:Genetics:

A:Gene: E6

C:Superfamily: papillomavirus E6 protein

C:Keywords: DNA binding; early protein; zinc finger

F:37-73/Region: zinc finger CCCC motif

F:110-146/Region: zinc finger CCCC motif

Query Match 99.2%; Score 823; DB 1; Length 158;

Best local similarity 98.0%; Pred. No. 2.7e-71;

Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFODPOERPRKLPOLCTELQTTIHIIIECVYCKQQLRREYDPAFRLDCIVYRDGPNY 60

DB 8 MFODPOERPRKLPOLCTELQTTIHIIIECVYCKQQLRREYDPAFRLDCIVYRDGPNY 67

QY 61 AVXDCKLFYSKISEYRHVCYVGTTLBQYKNRPLCDLIRICINXQKPLCPBEKQRHLD 120

DB 68 AVCDCKLFYSKISEYRHVCYVGTTLBQYKNRPLCDLIRICINXQKPLCPBEKQRHLD 127

QY 121 KKQRFHNIRGRWTCRSCSSSRTRETOL 151

DB 128 KKQRFHNIRGRWTCRSCSSSRTRETOL 158

RESULT 2

M6WLJ5 E6 protein - human papillomavirus type 35

C:Species: human papillomavirus type 35

A:Note: host Homo sapiens (man)

C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 09-Jul-2004

A:Accession: E40824; S36521

R:Marich, J.E.; Postelsier, A.V.; Rice, S.M.; McGraw, K.A.; Dubensky, T.W.

Virology 186, 770-776, 1992

A:Title: The phylogenetic relationship and complete nucleotide sequence of human papillom

A:Reference number: A40824; MUID:92124753; PMID:1310198

A:Accession: E40824

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-149 &lt;MAR&gt;

A:Cross-references: UNIPROT:P27228; UNIPARC:UPI00001383CF; GB:M74117; NID:G333050; PIDN:

R.Delius, H.; Hofmann, B.

submitted to the EMBL Data Library, August 1993

A:Description: Primer-directed sequencing of human papillomavirus types.

A:Reference number: S36469

A:Accession: S36521

A:Status: preliminary

A:Molecule type: DNA

A:Accession: S36521

A:Status: preliminary

A:Molecule type: DNA

A:Accession: S36521

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-149 &lt;DEL&gt;

A:Cross-references: UNIPARC:UPI00001383CF; EMBL:X74477; NID:G396997; PIDN:CAA52561.1; PI

A:Experimental source: strain 35H

C:Superfamily: papillomavirus E6 protein

C:Keywords: DNA binding; early protein; zinc finger

F:30-66/Region: zinc finger CCCC motif

F:103-139/Region: zinc finger CCCC motif

Query Match 69.6%; Score 578; DB 1; Length 149;

Best local similarity 71.5%; Pred. No. 5.7e-48;

Matches 108; Conservative 13; Mismatches 28; Indels 2; Gaps 1;

QY 1 MFODPOERPRKLPOLCTELQTTIHIIIECVYCKQQLRREYDPAFRLDCIVYRDGPNY 60

DB 1 MFODPOERPRKLPOLCTELQTTIHIIIECVYCKQQLRREYDPAFRLDCIVYRDGPNY 60

QY 61 AVXDCKLFYSKISEYRHVCYVGTTLBQYKNRPLCDLIRICINXQKPLCPBEKQRHLD 120

DB 61 GVCCKLFYSKISEYRHVCYVGTTLBQYKNRPLCDLIRICINXQKPLCPBEKQRHLD 120

QY 121 KKQRFHNIRGRWTCRSCSSSRTRETOL 151

DB 121 KKQRFHNIRGRWTCRSCSSSRTRETOL 149

RESULT 3

M6WLJ3

E6 protein - human papillomavirus type 31

C:Species: human papillomavirus type 31

A:Note: host Homo sapiens (man)

C:Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 09-Jul-2004

A:Accession: A32444

R:Goldsprough, M.D.; Disilvestre, D.; Temple, G.F.; Lorincz, A.T.

Virology 171, 306-311, 1989

A:Title: Nucleotide sequence of human papillomavirus type 31: a cervical neoplasia-associated

A:Reference number: A94398; MUID:89299478; PMID:2545036

A:Accession: A32444

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-149 &lt;GOL&gt;

A:Cross-references: UNIPROT:P17386; UNIPARC:UPI00001383CB; GB:J04353; NID:G333048; PIDN:

C:Comment: This protein may be involved in the oncogenic potential of this virus.

C:Superfamily: papillomavirus E6 protein

C:Keywords: DNA binding; early protein; zinc finger

F:30-66/Region: zinc finger CCCC motif

F:103-139/Region: zinc finger CCCC motif

Query Match 63.0%; Score 523; DB 1; Length 149;

Best local similarity 64.9%; Pred. No. 9.9e-43;

Matches 98; Conservative 18; Mismatches 33; Indels 2; Gaps 1;

QY 1 MFODPOERPRKLPOLCTELQTTIHIIIECVYCKQQLRREYDPAFRLDCIVYRDGPNY 60

DB 1 MFODPOERPRKLPOLCTELQTTIHIIIECVYCKQQLRREYDPAFRLDCIVYRDGPNY 60

QY 61 AVXDCKLFYSKISEYRHVCYVGTTLBQYKNRPLCDLIRICINXQKPLCPBEKQRHLD 120

DB 61 GVCCKLFYSKISEYRHVCYVGTTLBQYKNRPLCDLIRICINXQKPLCPBEKQRHLD 120

QY 121 KKQRFHNIRGRWTCRSCSSSRTRETOL 151

DB 121 KKQRFHNIRGRWTCRSCSSSRTRETOL 149

RESULT 4

M6WLJ3

E6 protein - human papillomavirus type 33

C:Species: human papillomavirus type 33

C:Date: 30-Jun-1987 #sequence\_revision 30-Jun-1987 #text\_change 09-Jul-2004

A:Accession: A03683

R:Coile, S.T.; Strebeck, R.E.

J. Virol. 56, 991-995, 1986

A:Title: Genome organization and nucleotide sequence of human papillomavirus type 33, wh

A:Accession: A03683

A:Status: preliminary

A:Molecule type: DNA

A:Accession: A03683

A:Status: preliminary

A:Molecule type: DNA

A:Accession: A03683

A:Status: preliminary

A:Molecule type: DNA

A:Accession: A03683

A:Status: preliminary

A:Molecule type: DNA

A:Accession: A03683

A:Status: preliminary

A:Molecule type: DNA







C:Species: human papillomavirus type 56  
C:Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 09-Jul-2004  
C:Accession: A33377; S36579  
R:Location: A.T.; Quinn, A.P.; Goldsborough, M.D.; McAllister, P.; Temple, G.F.  
J. Gen. Virol. 70, 3099-3104, 1989  
J. Title: Human papillomavirus type 56: a new virus detected in cervical cancers.  
A:Reference number: A33377; PMID:9063558; PMID:2555440  
A:Accession: A33377  
A:Molecule type: DNA  
A:Residues: 1-155 <LOB>  
A:Cross-references: UNIPROT:P24836; UNIPARC:UPI00001383E0  
R:Delius, H.; Hofmann, B.  
submitted to the EMBL Data Library, August 1993  
A:Description: Primer-directed sequencing of human papillomavirus types.  
A:Reference number: S36469  
A:Accession: S36579  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-155 <DEU>  
A:Cross-references: UNIPARC:UPI00001383E0; EMBL:X74483; NID:G397053; PIDN:CA52596.1; PI  
C:Superfamily: papillomavirus E6 protein  
C:Keywords: DNA binding; early protein; transforming protein; zinc finger  
F:106-142/Region: zinc finger CCCC motif

Query Match 51.4%; Score 426.5; DB 1; Length 155;  
Best Local Similarity 56.4%; Pred. No. 1.6e-33;  
Matches 84; Conservative 17; Mismatches 47; Indels 1; Gaps 1;

Qy 2 FQDQPERPKLPOLCTELQTTIHDIIECYCKQQLAREVYDPAFRDLCTVYRDGNPY 61  
Db 5 FNNFOERPRSLHNLSEVLEIPLDLRLSCYCKKELTAEVYVFACTELKLVYRDGPYA 64

Qy 62 VXDCKLKFYSKISEYHNYCYVGTTLLEQYNNKPLCDLLIRCTNKKQKPLCEPEKQRLDK 121  
Db 65 VCRVCLLFYSKVRKRYDYVSGATLESITRKQKQCDLLIRCYRCQSPLTPEEKQLHCDR 124

Qy 122 KQRFHNRGRWTGRCMSCCR--SSRTRET 149  
Db 125 KRRFHLAHGWTGSCLCGWRQTSREPRRS 153

RESULT 17  
S36503

E6 protein - human papillomavirus type 30

C:Species: human papillomavirus type 30

C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004

C:Accession: S36503

R:Delius, H.; Hofmann, B.

submitted to the EMBL Data Library, August 1993

A:Description: Primer-directed sequencing of human papillomavirus types.

A:Reference number: S36469

A:Accession: S36503

A:Molecule type: DNA

A:Residues: 1-153 <DEU>

A:Cross-references: UNIPROT:P36809; UNIPARC:UPI00001383CA; EMBL:X74474; NID:G396973; PID

C:Superfamily: papillomavirus E6 protein

C:Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match 46.4%; Score 385.5; DB 2; Length 153;  
Best Local Similarity 50.0%; Pred. No. 1.3e-29;  
Matches 74; Conservative 26; Mismatches 47; Indels 1; Gaps 1;

Qy 2 FQDQPERPKLPOLCTELQTTIHDIIECYCKQQLAREVYDPAFRDLCTVYRDGNPY 61  
Db 5 FENGERRRTVHNLCEVQSTLLEQLQCVCKLSSSEVYNFACKQLRVYRDSYA 64

Qy 62 VXDCKLKFYSKISEYHNYCYVGTTLLEQYNNKPLCDLLIRCTNKKQKPLCEPEKQRLDK 121  
Db 65 VCNFCCLLFYSKVRKRYDYVSGATLESITRKQKQCDLLIRCYRCQSPLTPEEKQLHCDR 124

Qy 122 KQRFHNRGRWTGRCMSCCRSSRTRET 149  
Db 125 KRRFHLAHGWTGSCLCGWRQTSREPRRS 153

Db 125 KRRFHLAHGWTGSCLCGWRQTSREPRRS 151  
RESULT 18  
S36527  
E6 protein - human papillomavirus type 53  
C:Species: human papillomavirus type 53  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
C:Accession: S36527  
R:Delius, H.; Hofmann, B.  
submitted to the EMBL Data Library, August 1993  
A:Description: Primer-directed sequencing of human papillomavirus types.  
A:Reference number: S36469  
A:Accession: S36527  
A:Molecule type: DNA  
A:Residues: 1-154 <DEU>  
A:Cross-references: UNIPROT:P36815; UNIPARC:UPI00001383DE; EMBL:X74482; NID:G397046; PIDN  
C:Superfamily: papillomavirus E6 protein  
C:Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match 45.7%; Score 379; DB 2; Length 154;  
Best Local Similarity 51.1%; Pred. No. 5.4e-29;  
Matches 72; Conservative 20; Mismatches 49; Indels 0; Gaps 0;

Qy 1 MFQDQPERPKLPOLCTELQTTIHDIIECYCKQQLAREVYDPAFRDLCTVYRDGNPY 60  
Db 5 LFENGERRRTVHNLCEVQSTLLEQLQCVCKLSSSEVYNFACTELKLVYRDGPYA 64

Qy 61 AVXDCKLKFYSKISEYHNYCYVGTTLLEQYNNKPLCDLLIRCTNKKQKPLCEPEKQRLDK 120  
Db 65 GVCKFCCLLFYSKVRKRYDYVSGATLESITRKQKQCDLLIRCYRCQSPLTPEEKQLHCDR 124

Qy 121 KQRFHNRGRWTGRCMSCCR 141  
Db 125 YKRFHNRGRWTGRCMSCCR 145

RESULT 19  
A44890

E6 protein - human papillomavirus type 66

C:Species: human papillomavirus type 66

C:Date: 31-Mar-1993 #sequence\_revision 31-Mar-1993 #text\_change 09-Jul-2004

C:Accession: A44890

R:Tawheed, A.R.; Beaudenon, S.; Favre, M.; Orth, G.

J. Clin. Microbiol. 29, 2656-2660, 1991

A:Title: Characterization of human papillomavirus type 66 from an invasive carcinoma of

A:Reference number: A44890; PMID:92128556; PMID:1663515

A:Accession: A44890

A:Molecule type: DNA

A:Residues: 1-155 <TAM>

A:Cross-references: UNIPROT:Q80955; UNIPARC:UPI00001383E6

A>Note: sequence extracted from NCBI backbone (NCBI:78637, NCBI:P:78638)

C:Superfamily: papillomavirus E6 protein

C:Keywords: DNA binding; early protein; transforming protein; zinc finger

F:106-142/Region: zinc finger CCCC motif

Query Match 44.9%; Score 372.5; DB 2; Length 155;  
Best Local Similarity 50.7%; Pred. No. 2.2e-28;  
Matches 76; Conservative 20; Mismatches 53; Indels 1; Gaps 1;

Qy 1 MFQDQPERPKLPOLCTELQTTIHDIIECYCKQQLAREVYDPAFRDLCTVYRDGNPY 60  
Db 4 IFSTQGERPRSLHNLSEVLEIPLDLRLSCYCKKELTAEVYVFACTELKLVYRDGPYA 63

Qy 61 AVXDCKLKFYSKISEYHNYCYVGTTLLEQYNNKPLCDLLIRCTNKKQKPLCEPEKQRLDK 120  
Db 64 AVCNFCCLLFYSKVRKRYDYVSGATLESITRKQKQCDLLIRCYRCQSPLTPEEKQLHCDR 123

Qy 121 KQRFHNRGRWTGRCMSCCRSSRTRETQ 150  
Db 124 KRRFHLAHGWTGSCLCGWRQTSREPRRS 152

RESULT 20

E6 protein - human papillomavirus type 43  
C:Species: human papillomavirus type 43  
A:Note: host Homo sapiens (man)  
C:Date: 30-Sep-1990 #sequence\_revision 30-Sep-1990 #text\_change 09-Jul-2004  
C:Accession: A34144  
R:Loerincz, A.T.; Quinn, A.P.; Goldsborough, M.D.; Schmidt, B.J.; Temple, G.F.  
J. Virol. 63, 2825-2834, 1989  
A:Title: Cloning and partial DNA sequencing of two new human papillomavirus types associ  
A:Reference number: A34144; MUID:89259065; PMID:2542593  
A:Accession: A34144  
A:Molecule type: DNA  
A:Residues: 1-155 <LOE>  
A:Cross-references: UNIPROT:P19709; UNIPARC:UPI00001383D6; GB:M27022; NID:G341596; PIDN:  
C:Superfamily: papillomavirus E6 protein  
C:Keywords: DNA binding; early protein; transforming protein; zinc finger  
F:31-67/Region: zinc finger CCCC motif  
F:104-140/Region: zinc finger CCCC motif

Query Match	39.3%	Score 326.5	DB 1	Length 155
Best Local Similarity	41.8%	Pred. No. 5.4e-24		
Matches 61; Conservative	27;	Mismatches 55;	Indels 3;	Gaps 1

7 ERPRKLPOLCTELQTTIHDIILECVYCKQQLRREVYDFAFRDLCIVYRDGNPYAVXDKC 66

Db 8 QNARTIFELDECNITLPTLQIGCIFCKKWLTTTEVLSFAFRDLRVWRDGYPPAACLAC 67

67 LKFYSKISEYRHYCYSVYGTLEQYNKPLCDLLIRCINXQKPLCPBEKQRLDKKQRFH 126

Db 68 LQFHGKISQYRHFYAAAYADTVEEETKQTVFDLCIRCKCHKPLSPVEKVQHIVQKQFF 127

127 NRGWGTGRCMSC---CRSSRTRRET 145

Db 128 KIHSTWKGYCLHCTWKSCKEKRRSET 153

## RESULT 21

E6 protein - human papillomavirus type 6b  
 C:Species: human papillomavirus type 6b  
 C:Date: 30-Sep-1987 #sequence\_revision 30-Sep-1987 #text\_change 09-Jul-2004  
 C:Accession: E20558  
 R:Schwarz, E.; Duvrst, M.; Demankowski, C.; Lattermann, O.; Zech, R.; Wolfesperger, E.; St  
 EMBO J. 2, 2341-2348, 1983  
 A:Title: DNA sequence and genome organization of genital human papillomavirus type 6b.  
 A:Reference number: A90975; MUID:84131949; PMID:6321162  
 A:Accession: E20558  
 A:Molecule type: DNA  
 A:Reads: 1-150 <SCH>  
 A:Cross-references: UNIPROT:P06462; UNIPARC:UPI00000028A; GB:X00203; NID:960955; PIDN:C  
 C:Superfamily: papillomavirus E6 protein  
 C:Keywords: DNA binding; early protein; zinc finger  
 F:31-67/Region: zinc finger CCCC motif  
 F:104-140/Region: zinc finger CCCC motif

Query Match	36.6%	Score 304	DB 1.2	Length 150
Best Local Similarity	39.8%	Pred. No. 7.3e-22		
Matches 51	Conservative 29	Mismatches 48	Indels 0	Gaps 0

12 LPOLCTELQTTIHDIILECVCKQQLRREVYDFAFRDLCIVRRDGNPYAVXDKCLKFYS 71

Db 13 IDQLCKTFNLSMHTLQINCVPCKNALTTAEIYSAYKHKLKLFRRGGYPYACACCLEFHG 72

72 KISEYRHYCYSVGTLEQYNKPLCDLLIRCNXOKPLCPBEKORHLDDKKORFNIRGR 131

Db 73 KINQYRHFDYAGYATTVEEETKODILDLVLRCYLCHKPLCEVEKVHILTKARFIKLNCT 132

QY	132	WTGRCMSC	139
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Db 133 WKGRCLHC 140

RESULT 22

E6 protein - human papillomavirus type 57  
C:Species: human papillomavirus type 57  
A:Note: host Homo sapiens (man)  
C:Date: 17-Feb-1994 #sequence\_revision 17-Feb-1994 #text\_change 09-Jul-2004  
C:Accession: S15621  
R:Hirsch-Behnam, A.; Delius, H.; de Villiers, E.M.  
Virus Res. 18, 81-98, 1990  
A:Title: A comparative sequence analysis of two human papillomavirus (HPV) types 2a and 5  
A:Reference number: S15614; PMID:9118659; PMID:1964523  
A:Accession: S15621  
A:Molecule type: DNA  
A:Residues: 1-153 <HR>  
A:Cross-references: UNIPROT:E22158; UNIPARC:UPI00001383E1; EMBL:X55965; NID:G60882; PIDN  
C:Superfamily: Papillomavirus E6 protein  
C:Keywords: DNA binding; early protein; transforming protein; zinc finger  
P:29-65/Region: zinc finger CCCC motif  
P:102-138/Region: zinc finger CCCC motif

Query Match	36.5%;	Score 303;	DB 1;	Length 153;
Best Local Similarity	43.5%;	Pred. No. 9.3e-22;		
Matches 57;	Conservative 23;	Mismatches 51;	Indels 0;	Gaps 0

9 PRKLPLCTELQTTIHDIILECVYCKQOLLREVDFAFRDLCIVYRDGNPYAVXDKCLK 68

Db 8 PRNIFLLCREYGLEJEDLRILCVYCKRPLSDADVLAFAVKELFVWRKGFPYGACEKCLI 67

69 FYSKISEYRHYCYSVYGTLEQOYNKPLCDLLIRCINXQKPLCPBEKQPHLDKKQRFHNI 126

Db 68 AAKLRQYRHHYSCYGDVETETGIRIPQLFMRICYCHKPLCWEEKKALLVGNKRFHKI 127

QY 129 RGRWTGRCMSC 139

Db 128 SGQWTGHCMNC 138

## RESULT 23

E6 protein - human papillomavirus type 44  
 C:Species: human papillomavirus type 44  
 A:Note: host Homo sapiens (man)  
 C:Date: 30-Sep-1990 #sequence\_\_revision 30-Sep-1990 #text change 09-Jul-2004  
 J:Accession: B34144  
 J:Location: A.T.; Quim, A.P.; Goldborough, M.D.; Schmidt, B.J.; Temple, G.F.  
 J:Virol. 63, 2829-2834, 1989  
 A:Title: Cloning and partial DNA sequencing of two new human papillomavirus types associated  
 A:Reference number: A34144; MUID:89259065; PMID:2542593  
 A:Accession: B34144  
 A:Molecule type: DNA  
 A:Residues: 1-150 <105>  
 A:Cross-references: UNIPROT:P19710; UNIPARC:UPI0000183D7; GB:M27023; NID:G341597; PIDN:P  
 C:Superfamily: Papillomavirus E6 protein  
 C:Keywords: DNA binding; early protein; transforming protein; zinc finger  
 F:31-67/Region: zinc finger CCCC motif  
 F:104-140/Region: zinc finger CCCC motif

Query Match	36.3%	Score 301	DB 1	length 150
Best Local Similarly	39.8%	Pred. No.	1.4e-21	
Matches 53, Conservative	28,	Mismatches	52,	Indels 0, Gaps 0

QY 10 RKLPOCTELOTTHDIILECVYCKQOLLREVVYDFAFRDLCIVRDGNPYAVXDKCLKF 69

Db 11 QSIDLCKECNIPMHNLIQILCVFCRKTLSAEVYSFAKQLYVVRGNFPFAACAICLEL 70

QY 70 YSKISEYRHYCVGTLEOQYNKPLCDLLIRCINXQKPLCPREEKORHLDDKKORFHNIR 129

Db 71 QGKVNQFRHFNAGYAVTVEETNKSILDVLR CYLCHKPLCHVEKVRHILDKARFIKLQ 130

QY	130	GRWTGRCMSCRS	142
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Db 131 DTWKGRCFHCWTS 143

## RESULT 24

S3614  
E6 protein - human papillomavirus type 2a  
C/Species: human papillomavirus type 2a  
A/Note: host Homo sapiens (man)  
C/Date: 17-Feb-1994 #sequence\_revision 17-Feb-1994 #text\_change 09-Jul-2004  
C/Accession: S15614  
R/Hirsch-Benham, A.; Delius, H.; de Villiers, E.M.  
Virus Res. 18, 81-98, 1990  
A/Title: A comparative sequence analysis of two human papillomavirus (HPV) types 2a and  
A/Reference number: S15614; MUID:91188699; PMID:1964523  
A/Accession: S15614  
A/Molecule type: DNA  
A/Residues: 1-159 <HR>  
A/Cross-references: UNIPROT:P25484; UNIPARC:UPI0000164A75; EMBL:X55964  
C/Superfamily: papillomavirus E6 protein  
C/Keywords: DNA binding; early protein; transforming protein; zinc finger  
F:35-71/Region: zinc finger CCCC motif  
F:108-144/Region: zinc finger CCCC motif

Query Match 35.8%; Score 297.5; DB 1; Length 159;  
Best Local Similarity 41.7%; Pred. No. 3.2e-21;  
Matches 60; Conservative 23; Mismatches 54; Indels 7; Gaps 1;

QY 9 PRKLPOLCTELQTTIHDIIECYCKOQLRREYDFAFRDLCIVYRDGNPYAVXDKCLK 68  
DB 14 PRNIFLLCKEYGLELDRLICVCRALSDADVAFAIKELSVWKRKGFPGACGKCLI 73  
QY 69 FYSKISEYRHVCYSVGTTLLEQOYNKPLCDLLIRICINXOKPLCEBKORHLDKQRFHNI 128  
DB 74 AAGKLRLQYRHHMHSYCGDTVETETGPIPLPOLFMRCYICHKPLSWEKXALLVGNKRPHNI 133  
QY 129 RGRWTRGCMSCCS-----SRT 145  
DB 134 SGRWTHGCMNCSSCTATDPASRT 157

## RESULT 25

M6WLL1  
E6 protein - human papillomavirus type 11  
C/Species: human papillomavirus type 11  
C/Date: 13-Aug-1986 #sequence\_revision 13-Aug-1986 #text\_change 09-Jul-2004  
C/Accession: A03684  
R/Dartmann, K.; Schwarz, E.; Gissmann, L.; zur Hausen, H.  
Virology 151, 124-130, 1986  
A/Title: The nucleotide sequence and genome organization of human papilloma virus type 1  
A/Reference number: A94338; MUID:86181601; PMID:3008427  
A/Accession: A03684  
A/Molecule type: DNA  
A/Residues: 1-150 <DAR>  
A/Cross-references: UNIPROT:P04019; UNIPARC:UPI00001383B7; GB:M14119; NID:G333026; PIDN:  
C/Superfamily: papillomavirus E6 protein  
C/Keywords: DNA binding; early protein; zinc finger  
F:31-67/Region: zinc finger CCCC motif  
F:104-140/Region: zinc finger CCCC motif

Query Match 35.4%; Score 294; DB 1; Length 150;  
Best Local Similarity 35.8%; Pred. No. 6.6e-21;  
Matches 49; Conservative 33; Mismatches 55; Indels 0; Gaps 0;

QY 3 ODPOERPRKLPOLCTELQTTIHDIIECYCKOQLRREYDFAFRDLCIVYRDGNPYAV 62  
DB 4 KDASTATSINQOLCKTFPLSLHTIQICVFCRNALTTETIAYAVKMLKVVWRDNFPFAA 63  
QY 63 XDKCLKYSKISEYRHVCYSVGTTLLEQOYNKPLCDLLIRICINXOKPLCEBKORHLDKK 122  
DB 64 CACCLELQSKINQYRHHMHSYCGDTVETETGPIPLPOLFMRCYICHKPLCEIEKLGHLGK 123  
QY 123 QRHNINRGRWTRGCMSC 139  
DB 124 ARFTKLNNQWGRCLHC 140

## RESULT 26

S36497  
E6 protein - human papillomavirus type 27  
C/Species: human papillomavirus type 27  
C/Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
C/Accession: S36497  
R/Delius, H.; Hofmann, B.  
submitted to the EMBL Data Library, August 1993  
A/Description: Primer-directed sequencing of human papillomavirus types.  
A/Reference number: S36469  
A/Accession: S36497  
A/Molecule type: DNA  
A/Residues: 1-159 <DEL>  
A/Cross-references: UNIPROT:P36808; UNIPARC:UPI00001383C6; EMBL:X74473; NID:G3396964; PIDN:  
C/Superfamily: papillomavirus E6 protein  
C/Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match 35.2%; Score 292; DB 2; Length 159;  
Best Local Similarity 42.7%; Pred. No. 1.1e-20;  
Matches 56; Conservative 21; Mismatches 54; Indels 0; Gaps 0;

QY 9 PRKLPOLCTELQTTIHDIIECYCKOQLRREYDFAFRDLCIVYRDGNPYAVXDKCLK 68  
DB 14 PRNIFLLCKEYGLELDRLICVCRALSDADVAFAIKELSVWKRKGFPGACGKCLI 73  
QY 69 FYSKISEYRHVCYSVGTTLLEQOYNKPLCDLLIRICINXOKPLCEBKORHLDKQRFHNI 128  
DB 74 AAGKLRLQYRHHMHSYCGDTVETETGPIPLPOLFMRCYICHKPLSWEKXALLVGNKRPHNI 133  
QY 129 RGRWTRGCMSC 139  
DB 134 SGRWTHGCMQC 144

## RESULT 27

S36584  
E6 protein - human papillomavirus type 7  
C/Species: human papillomavirus type 7  
C/Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
C/Accession: S36584  
R/Delius, H.; Hofmann, B.  
submitted to the EMBL Data Library, August 1993  
A/Description: Primer-directed sequencing of human papillomavirus types.  
A/Reference number: S36469  
A/Accession: S36584  
A/Molecule type: DNA  
A/Residues: 1-154 <DEL>  
A/Cross-references: UNIPROT:P36800; UNIPARC:UPI00001383B3; EMBL:X74463; NID:G3397060; PIDN:  
C/Superfamily: papillomavirus E6 protein  
C/Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match 35.0%; Score 290.5; DB 2; Length 154;  
Best Local Similarity 37.1%; Pred. No. 1.5e-20;  
Matches 53; Conservative 30; Mismatches 57; Indels 3; Gaps 1;

QY 10 RKLPLCTELQTTIHDIIECYCKOQLRREYDFAFRDLCIVYRDGNPYAVXDKCLKF 69  
DB 10 RTLELDCDCNITLPTQINICFNSILQTAEVLAFAFRILYVWRNDFFPAACVCKLEF 69  
QY 70 YSKISEYRHVCYSVGTTLLEQOYNKPLCDLLIRICINXOKPLCEBKORHLDKQRFHNI 129  
DB 70 YGKVNQYRHHMHSYCGDTVETETGPIPLPOLFMRCYICHKPLSWEKXALLVGNKRPHNI 129  
QY 130 GRWTRGCMSC---CRSRTRET 149  
DB 130 DSWTGYCICMCKCMKMGQRSET 152

## RESULT 28

S36555  
E6 protein - human papillomavirus type 40

C:Species: human papillomavirus type 40  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
C:Accession: J36555  
R:Delattre, H.; Holmann, B.  
Submitted to the EMBL Data Library, August 1993  
A:Description: Primer-directed sequencing of human papillomavirus types.  
A:Reference number: J36469  
A:Accession: J36555  
A:Molecule type: DNA  
A:Residues: 1-154 <DEL>  
A:Cross-references: UNIPROT:P36812; UNIPARC:UPI00001383D3; EMBL:X74478; NID:G397014; PIR  
C:Superfamily: Papillomavirus E6 protein  
C:Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match 34.8%; Score 288.5; DB 2; Length 154;  
Best Local Similarity 37.1%; Pred. No. 2.3e-20;  
Matches 53; Conservative 29; Mismatches 56; Indels 3; Gaps 1;

QY 10 RKLPLQCTELQTTIHDIILECYCKQKQLRREYVDFAFRDLCTIYRDGNPYAVXDKCLKF 69  
DB 10 RTVLVELCQCNITLPTLIDICVFKTVLKTAEVLAFAFRELIVYWRDDPFAACPRCLDL 69  
QY 70 YSKISEYRHVCYVGTLLBOQYNKPLCDLLIRCLNKKPLCPBEKQHLDKQRFHNIR 129  
DB 70 HGKVNQYNFRPAAAPVPEETGLTIIVIRCCCKRPLSPVEKTHIVKTIQFFKLK 129  
QY 130 GRWTGRCMSC---CRSRTRET 149  
DB 130 DSWTCYCLHCKWKCKMEKGRSET 152

RESULT 29  
WMLC1  
E6 protein - pygmy chimpanzee papillomavirus (type 1)  
C:Species: pygmy chimpanzee papillomavirus  
C:Date: 30-Jun-1993 #sequence\_revision 30-Jun-1993 #text\_change 16-Jul-1999  
C:Accession: J36818  
R:Van Ranst, M.; Fuse, A.; Fiten, P.; Beuken, E.; Pfister, H.; Burk, R.D.; Opdenakker, C  
A:Title: Human papillomavirus type 13 and pygmy chimpanzee papillomavirus type 1: Compar  
A:Reference number: A42955; MUID:92391075; PMID:1325697  
A:Accession: J36818  
A:Molecule type: DNA  
A:Residues: 1-150 <VAN>  
A:Cross-references: UNIPARC:UPI00001383ED; EMBL:X62844; NID:G61010; PIRN:CAA4655.1; PIR  
C:Superfamily: Papillomavirus E6 protein  
C:Keywords: DNA binding; early protein; transforming protein; zinc finger  
F:31-67/Region: zinc finger CCCC motif  
F:104-140/Region: zinc finger CCCC motif

Query Match 34.7%; Score 288; DB 1; Length 150;  
Best Local Similarity 38.3%; Pred. No. 2.5e-20;  
Matches 51; Conservative 28; Mismatches 54; Indels 0; Gaps 0;

QY 10 RKLPLQCTELQTTIHDIILECYCKQKQLRREYVDFAFRDLCTIYRDGNPYAVXDKCLKF 69  
DB 11 KTIIDPLCKEYNLCMSLDIQLCPCKRTISTABVAIFQYKDNLNIVYQGNFPFAACACCLDI 70  
QY 70 YSKISEYRHVCYVGTLLBOQYNKPLCDLLIRCLNKKPLCPBEKQHLDKQRFHNIR 129  
DB 71 QGKVNQYNFRPAAAPVPEETGLTIIVIRCCCKRPLSPVEKTHIVKTIQFFKLK 130  
QY 130 GRWTGRCMSCCRS 142  
DB 131 CEWKGRCFHCWTS 143

RESULT 30  
J36509  
E6 protein - human papillomavirus type 32  
C:Species: human papillomavirus type 32  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
C:Accession: J36509

R. Delius, H.; Hofmann, B.  
submitted to the EMBL Data Library, August 1993  
A.Description: Primer-directed sequencing of human papillomavirus types.  
A.Reference number: S36465  
A.Accession: S36509  
A.Molecule type: DNA  
A.Residues: 1-142 <DEL>  
A.Cross-references: UNIPROT:P36810; UNIPARC:UPI00001383CC; EMBL:X74475; NID:g396981; PID:  
C.Superfamily: papillomavirus B6 protein  
C.Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match            34.1%; Score 283; DB 2; Length 142;  
Best Local Similarity 40.9%; Pred. No. 7e-20;  
Matches 54; Conservative 22; Mismatches 56; Indels 0; Gaps 0;

Dy       8 RRRKLPOLCTELQTTIHDIILCEVCYCKOQLRREVDPAFRDLCTIYRDGNPYAVXDKLF 67  
         :|::||::||::||::||::||::||::||::||::||::||::||::||::||  
Db      9 QSTLYQLCKDGLTLRNLCICWCKNHLTSAEAYAHFKDXLVVWKGFPIYACAFCL 68  
         :|::||::||::||::||::||::||::||::||::||::||::||::||  
Dy     68 KFYKSISEVRHYCYSVYGTTLEQQYNKPPLCDLLIRGCINMOKPCLPEBKORHLDKKRFHN 127  
         ::||::||::||::||::||::||::||::||::||::||::||::||  
Db     69 EFYSKVCAALRHVDRAFMHTVEGETGELLEQTIFCALIQKPLSPSKDHIIYGRHFRF 128  
         ::||::||::||::||::||::||::||::||::||::||::||::||  
Dy     128 IRGWTCRCMSC 139  
         |||||||  
Db     129 ILNRWTGRCTQC 140  
         |||||||

RESULT 31  
MEM142  
B6 protein - human papillomavirus type 13  
C.Species: human papillomavirus type 13  
A.Note: host Homo sapiens (man)  
C.Date: 30-Jun-1993 #sequence\_revision 30-Jun-1993 #text\_change 09-Jul-2004  
C.Accession: A42955  
R.van Ranst, M.; Fuse, A.; Filten, P.; Beuken, E.; Pfister, H.; Burk, R.D.; Odenakker, G.  
Virolgy 190, 587-596, 1992  
A>Title: Human papillomavirus type 13 and pygmy chimpanzee papillomavirus type 1: Compar  
A.Reference number: A42955; MIDID:92391075; PMID:1325697  
A.Accession: A42955  
A.Molecule type: DNA  
A.Residues: 1-150 <VAN>  
A.Cross-references: UNIPROT:Q02269; UNIPARC:UPI00001383B9; EMBL:X62843; NID:g60295; PIDN  
C.Superfamily: papillomavirus B6 protein  
C.Keywords: DNA binding; early protein; transforming protein; zinc finger  
F.31-67/Region: zinc finger CCCC motif  
F.104-140/Region: zinc finger CCCC motif

Query Match            32.9%; Score 273; DB 1; Length 150;  
Best Local Similarity 36.8%; Pred. No. 6.6e-19;  
Matches 49; Conservative 29; Mismatches 55; Indels 0; Gaps 0;

Dy     10 RKLPOLCTELQTTIHDIILECVCKOQLRREVDPAFRDLCTIYRDGNPYAVXDKLF 69  
         :|::||::||::||::||::||::||::||::||::||::||::||::||  
Db     11 KTIDDLCKECNMSTMISLIQIVFCRKLTSTAETVAFOYKSLIYVMRGPPFAACACCIEI 70  
         :|::||::||::||::||::||::||::||::||::||::||::||::||  
Dy     70 YKSISEVRHYCYSVYGTTLEQQYNKPPLCDLLIRGCINMOKPCLPEBKORHLDKKRFHNIR 129  
         ::||::||::||::||::||::||::||::||::||::||::||::||  
Db     71 QCKINQFRFPDDAGFAVTEEDTKOSILDVLTRCYLCHKPLCEVEKLRLHQAKRFTKLN 130  
         :|::||::||::||::||::||::||::||::||::||::||::||::||  
Dy     130 GRWTGRCSGCCRS 142  
         |||||||  
Db     131 SSMKGRCFFCMSS 143  
         |||||||

RESULT 32  
MEM142  
B6 protein - human papillomavirus type 42  
C.Species: human papillomavirus type 42  
A>Note: host Homo sapiens (man)  
C.Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 09-Jul-2004  
C.Accession: E39451  
R.Philipp, W.; Honore, N.; Saap, M.; Cole, S.T.; Streack, R.E.

Virology 186, 331-334, 1992  
 Article: Human papillomavirus type 42: new sequence, conserved genome organization.  
 A:Reference number: A39451; MUID:92087479; PMID:1309278  
 A:Accession: E39451  
 A:Status: translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-150 <PHI>  
 A:Cross-references: UNIPROT:P27229; UNIPARC:UP100001383B5; GB:M73236  
 C:Superfamily: papillomavirus E6 protein  
 C:Keywords: DNA binding; early protein; zinc finger  
  
 Query Match 32.3%; Score 268; DB 1; Length 150;  
 Best Local Similarity 41.7%; Pred. No. 2e-18;  
 Matches 55; Conservative 20; Mismatches 57; Indels 0; Gaps 0;  
  
 QY 8 RPRKLPOLCTELQTTTHDIIIECYCKQQLRREYYDAFRPLCIYRGNPFAVXDKL 67  
 :||| ||| :  
 Db 9 QPRTLVQLCEPFGILTNNLQISCIWCKGHLGAEFLAVHFKDLVVMWRDFFYAAACAFCL 68  
 :||| ||| :  
 QY 66 KPFYSKISEVHYGCVYGTTLLEQYNNKPLCDLLRCINXQKPLCEPEKORHLDPKQRFNH 127  
 :||| ||| :  
 Db 69 EFNRSKICALNHYERSAFWYVEKETGLLLEEQIRICALCQKPLSQSEKNNHIDTGRFOR 128  
 :||| ||| :  
 QY 128 IRGRWTCRCMSC 139  
 :||| ||| :  
 Db 129 ILQMTGRCCTHC 140  
 :||| ||| :  
  
 RESULT 33  
 S36532  
 E6 protein - human papillomavirus type 10  
 C:Species: human papillomavirus type 10  
 C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
 C:Accession: S36532  
 R:Delius, H.; Hofmann, B.  
 submitted to the EMBL Data Library, August 1993  
 A:Description: Primer-directed sequencing of human papillomavirus types.  
 A:Reference number: S36469  
 A:Accession: S36532  
 A:Molecule type: DNA  
 A:Residues: 1-148 <DEL>  
 A:Cross-references: UNIPROT:P36802; UNIPARC:UP100001383B6; EMBL:X74465; NID:S396901; PILD  
 C:Superfamily: papillomavirus E6 protein  
 C:Keywords: DNA binding; early protein; nucleus; zinc finger  
  
 Query Match 28.8%; Score 239; DB 2; Length 148;  
 Best Local Similarity 34.6%; Pred. No. 1.1e-15;  
 Matches 46; Conservative 25; Mismatches 62; Indels 0; Gaps 0;  
  
 QY 7 ERRRKLPOLCTELQTTTHDIIIECYCKQQLRREYVDAFPDLCIYRDGNFYAVXDKC 66  
 :||| ||| :  
 Db 6 OEFRNTLLCRNGIPIEDRLICIFCTKQUTAAELAFALRELYLVWRAGVYGACARC 65  
 :||| ||| :  
 QY 67 LKEYSKISEVHYGCVYGTTLLEQYNNKPLCDLLRCINXQKPLCEPEKORHLDPKQRFH 126  
 :||| ||| :  
 Db 66 LLIQIVRLKLYNDYVVEGVEETKOSITYQLIRCYWCHKPLVREEDRRNRRLH 125  
 :||| ||| :  
 QY 127 NIRGRWTCRCMSC 139  
 :||| ||| :  
 Db 126 KISGYWRGSCCYC 138  
 :||| ||| :  
  
 RESULT 34  
 S36550  
 E6 protein - human papillomavirus type 3  
 C:Species: human papillomavirus type 3  
 C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
 C:Accession: S36550  
 R:Delius, H.; Hofmann, B.  
 submitted to the EMBL Data Library, August 1993  
 A:Description: Primer-directed sequencing of human papillomavirus types.  
 A:Reference number: S36469  
 A:Accession: S36550

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A:Molecule type: DNA
A:Residues: 1-152 <DEL>
A:Cross-References: UNIPROT:P36799, UNIPARC:UPI00001383B0; EMBL:X74462; NID:g397005; PIDD
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match          27.8%; Score 231; DB 2; Length 152;
Best Local Similarity 34.4%; Pred. No. 6,7e-15;
Matches 45; Conservative 23; Mismatches 63; Indels 0; Gaps 0;

Oy      9 PRKLQQLTELTOTTHDIIIECVYCKQOLLREVDPAFRDLCTVRRDGNPYAVXDKCLK 68
       :|::||::||::||::||::||::||::||::||::||::||::||::||::||
Db     12 PKNIPLFCRNTGIGEDDLRLHLCIFCTKQLTTTELQAFLRELINVMVRGGAPYGACARCLL 71

Oy      69 FFSKISSEVHYGVSVGTLEQQYNKPLCDLLIRCNIXKKPLCPREEKHRLDKORPHNI 128
       ::||::||::||::||::||::||::||::||::||::||::||::||::||
Db     72 VEGIARRLRKYMSYSVSGVEESTKOSIDTQOLRCYMKCHKPLVKEEKDRHRNEKRRLHKI 131

Oy      129 RGRWTRGRMSC 139
       |||||
Db     132 SGHWKSGCYOC 142

RESULT 35
S36567
E6 protein - human papillomavirus type 49
C:Species: human papillomavirus type 49
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S36567
R:Idellus, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36469
A:Accession: S36567
A:Molecule type: DNA
A:Residues: 1-138 <DEL>
A:Cross-References: UNIPROT:P36813, UNIPARC:UPI00001383DB; EMBL:X74480; NID:g397030; PIDD
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match          18.6%; Score 154; DB 2; Length 138;
Best Local Similarity 27.1%; Pred. No. 1,3e-07;
Matches 36; Conservative 30; Mismatches 65; Indels 2; Gaps 2;

Oy      8 RPRLPQLTELTOTTHTDIIECVYCKQOLLREVDPAFRDLCTVRRDGNPYAVXDKCL 67
       ||::||::||::||::||::||::||::||::||::||::||::||::||
Db     3 RPVKVCELAHNHNIPIMEVLTPCNFCTGFVTYOELLEFDYKDNLIMKGDFVGCCAAAC- 61

Oy      68 KRVSKISEVRHNYCS-VNGTTLEQQYNKPLCDLLIRCNIXKKPLCPREEKHRLDKORFH 126
       ::||::||::||::||::||::||::||::||::||::||::||::||::||
Db     62 AVRSAYHEFTNHQETLVGIEIGRAANIATIVRWCLICLKRLDLLEKLDICQHREFH 121

Oy      127 NIRGWTRGRMSC 139
       :|::||::||::||::||::||::||::||::||::||::||::||::||
Db     122 RVNRWKGVCRHC 134

RESULT 36
S36479
E6 protein - human papillomavirus type 17
C:Species: human papillomavirus type 17
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S36479
R:Idellus, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36469
A:Accession: S36479
A:Molecule type: DNA
A:Residues: 1-141 <DEL>
A:Cross-References: UNIPROT:P36805, UNIPARC:UPI00001383BC; EMBL:X74469; NID:g396932; PIDD
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; nucleus; zinc finger

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Qy      9 PRKLPOLCTELQTTIHDIIECVYCKQQLRREVYDFAFRDLCTIVRDGNPYAVXDKLK 68
Db      24 PATTDLAALLFIPLDDLVPCNFCGNFLTYLEIEFEPEKSLIKWLYVYACCCCT 83
Qy      69 FYSKISEYRHVCYSVYGTTLLEQYVKKPLCDLLIRICINXQKPLCEPEKORHLDKQRFNI 128
Db      84 ATATFEFNEFESVYTGREIEDVTKSIFDIDVRQCTCMKTLDAIEKLDICGRRRPFILV 143
Qy      129 RGRWTRGCMSC 139
Db      144 RGSWKGICRLC 154

RESULT 41
S28510
E6 protein - multimammate rat papillomavirus (fragment)
C/Species: multimammate rat papillomavirus
C/Date: 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 09-Jul-2004
C/Accession: S28510; S22956
R:van Ranst, M.A.
submitted to the EMBL Data Library, April 1992
A/Reference number: S28509
A/Accession: S28510
A/Molecule type: DNA
A/Residues: 1-207 <VAN>
A/Cross-references: UNIPROT:P30735; UNIPARC:UPI00001383BA; EMBL:X65201; NID:g60575; PIDN
A/Note: the source is designated as Mastomys natalensis papillomavirus
R:van Ranst, M.; Tachez, R.; Pruss, J.; Burk, R.D.
Nucleic Acids Res. 20, 2889, 1992
A/Title: Primary structure of the E6 protein of Microtus minutus papillomavirus and Mast
A/Reference number: S22955; MUID:92310995; PMID:1319576
A/Accession: S22956
A/Status: nucleic acid sequence not shown
A/Molecule type: DNA
A/Residues: 77-204 <VAN2>
A/Cross-references: UNIPARC:UPI0000178416; EMBL:X65201
A/Note: the source is designated as Mastomys natalensis papillomavirus
C/Superfamily: papillomavirus E6 protein
C/Keywords: DNA binding; early protein; nucleus; zinc finger
F:95-171/Region: zinc finger C3HC4 motif

Query Match      15.6%; Score 129.5; DB 2; Length 207;
Best Local Similarity 22.1%; Pred. No. 4.2e-05;
Matches 32; Conservative 26; Mismatches 54; Indels 33; Gaps 3;

Qy      17 TELQTTIH-----DIIIECVYCKQQLRREVYDFAFRDLCTIVRDGNPYAVXDK 65
Db      71 SRMRVYHSFVERLGIREDLLLPCTFCGRFLTOELTAFPFSAPNLWGRGCAHGICTA 130
Qy      66 CLKFYSKISEYRHVCYSVYGTTLLEQYVKKPLCDLL-----IRCINXQKPLCEPE 114
Db      131 CARVCASLDLFLH-----QNSRPLADYARDENLTLHGAKRCRCMKLSTSTE 179
Qy      115 KQRLHDKQRFNIRGRWTRGCMSC 139
Db      180 KLECAERGESFAKYRGQWRARCRIC 204

RESULT 42
S36473
E6 protein - human papillomavirus type 15
C/Species: human papillomavirus type 15
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C/Accession: S36473
R:Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A/Description: primer-directed sequencing of human papillomavirus types.
A/Reference number: S36469
A/Accession: S36473
A/Molecule type: DNA
A/Residues: 1-141 <DEL>
A/Cross-references: UNIPROT:P36804; UNIPARC:UPI00001383BB; EMBL:X74468; NID:g396924; PID

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C/Superfamily: papillomavirus E6 protein
C/Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match      15.5%; Score 128.5; DB 2; Length 141;
Best Local Similarity 27.1%; Pred. No. 3.6e-05;
Matches 36; Conservative 25; Mismatches 71; Indels 1; Gaps 1;

Qy      8 RPKLPOLCTELQTTIHDIIECVYCKQQLRREVYDFAFRDLCTIVRDGNPYAVXDKC 66
Db      5 KPFVQQLADLTCPLVDILLPCRFQGRFLTYIELVSLNKGILWTEEDPFACCSSC 64
Qy      67 LKFSKISEYRHVCYSVYGTTLLEQYVKKPLCDLLIRICINXQKPLCEPEKORHLDKQRFH 126
Db      65 AFATAQEFNSNFQSVCSWEIIVEQKPVGDIIIRCKFCIKLIDIEKIDICYBERQFH 124
Qy      127 NIRGRWTRGCMSC 139
Db      125 KVRNWKGLCRHC 137

RESULT 43
I56705
E6 protein - human papillomavirus type 18
C/Species: human papillomavirus type 18
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C/Accession: I56705
R:Inagaki, Y.; Tsunokawa, Y.; Takebe, N.; Nawa, H.; Nakanishi, S.; Terada, M.; Sugimura,
J. Virol. 62, 1640-1646, 1988
A/Title: Nucleotide sequences of cDNAs for human papillomavirus type 18 transcripts in He
A/Reference number: I56705; MUID:88188247; PMID:2833614
A/Accession: I56705
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-57 <RES>
A/Cross-references: UNIPROT:Q90133; UNIPARC:UPI00000EDDSF; GB:M20324; NID:g183933; PIDN:
C/Superfamily: papillomavirus E6 protein

Query Match      15.3%; Score 127; DB 2; Length 57;
Best Local Similarity 58.5%; Pred. No. 2.1e-05;
Matches 24; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

Qy      2 RQDPQERPKLPOLCTELQTTIHDIIECVYCKQQLRREV 42
Db      4 FEDPTRRPPYKLPDLCTELMTSLQDIEITCYVCKTVLELTV 44

RESULT 44
W6WLRB
E6 protein - cottontail rabbit papillomavirus
C/Species: cottontail rabbit papillomavirus
C/Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 16-Feb-1997
C/Accession: A03686
R:Garti, I.; Danos, O.; Yaniv, M.
Proc. Natl. Acad. Sci. U.S.A. 82, 1580-1584, 1985
A/Title: Genomic structure of the cottontail rabbit (Shope) papillomavirus.
A/Reference number: A94027; MUID:8516175; PMID:2984661
A/Accession: A03686
A/Molecule type: DNA
A/Residues: 1-273 <GIR>
A/Cross-references: UNIPARC:UPI0000000953
C/Superfamily: papillomavirus E6 protein
C/Keywords: DNA binding; early protein; zinc finger

Query Match      15.3%; Score 127; DB 1; Length 273;
Best Local Similarity 26.4%; Pred. No. 9.5e-05;
Matches 37; Conservative 21; Mismatches 68; Indels 14; Gaps 4;

Qy      9 PRKLPOLCTELQTTIHDIIECVYCKQQLRREVYDFAFRDLCTIVRDGNPYAVXDKLK 68
Db      6 PRSLEKIQOIIQISLEDPFCGICPGKTLGAERKLFKCTGLCTVHWKGMWGTGCRDCTV 65
Qy      69 FYSKISEYRHVCYSVYGTTLLEQYVKKPLCDLLIRICINXQKPLCEPE---KQRH-----L 119

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Db 66 LSCALDYCHLALAPALBAALVGEISSWFRCTVCGRRLLTPEKIELBARNCITLCI 125

Qy 120 DKXQRFHINRGWTRCMSG 139

Db 126 DKQGYF-----QWRGHCSSC 140

#### RESULT 45

S36538 E6 protein - human papillomavirus type 12

C/Species: human papillomavirus type 12

C/Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004

C/Accession: S36538

R/Delius, H.; Hofmann, B.

submitted to the EMBL Data Library, August 1993

A/Description: Primer-directed sequencing of human papillomavirus types.

A/Reference number: S36469

A/Accession: S36538

A/Molecule type: DNA

A/Residues: 1-157 <DEL>

A/Cross-references: UNIPROT:P36803; UNIPARC:UPI00001383B8; EMBL:X74466; NID:G396910; PII

C/Superfamily: papillomavirus E6 protein

C/Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match 14.8%; Score 123; DB 2; Length 157;  
Best Local Similarity 27.1%; Pred. No. 0.00014;  
Matches 36; Conservative 18; Mismatches 79; Indels 0; Gaps 0;

Qy 7 ERPRKLPOLCTELQTTIHDIIECVYCKQQLRREYVDFAFRDLCTVYRDGNPYAVXDKC 66

Db 16 ELPTTIELADLDLIPVDCIVNFCGKFLDFEVDGDKKQTLTKGHLFVACRSC 75

Qy 67 LKRYSKISEYRHYCVSYGTTLEQYNNKPLCDLLIRICINXQKPLCEBKORHLDKKQRF 126

Db 76 CAATATVEFNEFVQQTALGRDIEIATGKISIFDLKIRQCOTCLSPDITTEKLDSCGRGPFH 135

Qy 127 NIRGRWTRCMSG 139

Db 136 KVRDRWKIGICRQC 148

#### RESULT 46

S36485 E6 protein - human papillomavirus type 19

C/Species: human papillomavirus type 19

C/Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004

C/Accession: S36485

R/Delius, H.; Hofmann, B.

submitted to the EMBL Data Library, August 1993

A/Description: Primer-directed sequencing of human papillomavirus types.

A/Reference number: S36469

A/Accession: S36485

A/Molecule type: DNA

A/Residues: 1-166 <DEL>

A/Cross-references: UNIPROT:P36806; UNIPARC:UPI00001383BD; EMBL:X74470

C/Superfamily: papillomavirus E6 protein

C/Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match 14.8%; Score 123; DB 2; Length 166;  
Best Local Similarity 24.4%; Pred. No. 0.00014;  
Matches 32; Conservative 24; Mismatches 75; Indels 0; Gaps 0;

Qy 9 PRKLPOLCTELQTTIHDIIECVYCKQQLRREYVDFAFRDLCTVYRDGNPYAVXDKC 68

Db 29 PATAGLAALIEIPDLDCVNCFCGFLSHLEACEFDDKRLSLWKGLVYACCRWCCT 88

Qy 69 FYKISISRYHYCVSYGTTLEQYNNKPLCDLLIRICINXQKPLCEBKORHLDKKQRFH 128

Db 89 ATATFEFNEFVQQTALGRDIEIATGKISIFDLKIRQCOTCLSPDITTEKLDICGRRLPFH 148

Qy 129 RGRWTRCMSG 139

Db 149 RDSWKIGICRQC 159

#### RESULT 47

S36590 E6 protein - human papillomavirus type 9

C/Species: human papillomavirus type 9

C/Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004

C/Accession: S36590

R/Delius, H.; Hofmann, B.

submitted to the EMBL Data Library, August 1993

A/Description: Primer-directed sequencing of human papillomavirus types.

A/Reference number: S36469

A/Accession: S36590

A/Molecule type: DNA

A/Residues: 1-148 <DEL>

A/Cross-references: UNIPROT:P36801; UNIPARC:UPI00001383B5; EMBL:X74464; NID:G397068; PII

C/Superfamily: papillomavirus E6 protein

C/Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match 14.6%; Score 121.5; DB 2; Length 148;  
Best Local Similarity 24.6%; Pred. No. 0.00018;  
Matches 33; Conservative 31; Mismatches 67; Indels 3; Gaps 3;

Qy 8 RPRKLPOLCTELQTTIHDIIECVYCKQQLRREYVDFAFRDLCTVYRDGNPYAVXDKC 66

Db 12 KPRVIELADTLVPLDILIPCKFCNRFLSYBELNFKDLQLTWTEBDVYGLCSSC 71

Qy 67 LKRYSKISEYRHYCVSYGTTLEQYNNKPLCDLLIRICINXQKPLCEBKORHLDKKQRF 125

Db 72 -AVASQLEFTHFQFAVVGDIETVGTAGNIGICIRCYCFKLLDLVEKLTATCYKFEQF 130

Qy 126 NIRGRWTRCMSG 139

Db 131 YKRVNSWKIGICRQC 144

#### RESULT 48

W6MIEB

E6 protein - bovine papillomavirus type 1

C/Species: bovine papillomavirus type 1

C/Date: 30-Sep-1987 #sequence\_revision 30-Sep-1987 #text\_change 09-Jul-2004

C/Accession: C18151

R/Chen, E.Y.; Howley, P.M.; Levinson, A.D.; Seeburg, P.H.

Nature 299, 529-534, 1982

A/Title: The primary structure and genetic organization of the bovine papillomavirus typ

A/Reference number: A93289; PMID:83012974; PMID:6289124

A/Accession: C18151

A/Molecule type: DNA

A/Residues: 1-137 <CHE>

A/Cross-references: UNIPROT:P06931; UNIPARC:UPI0000033CF0; GB:X02346; GB:J02044; GB:M246

R/Danos, O.; Engel, L.W.; Chen, E.Y.; Yaniv, M.; Howley, P.M.

J. Virol. 46, 557-566, 1983

A/Title: Comparative analysis of the human type 1a and bovine type 1 papillomavirus geno

A/Reference number: A92993; PMID:83189357; PMID:6302319

A/Contents: annotation

R/Androphy, E.J.; Schiller, J.T.; Lowy, D.R.

Science 230, 442-445, 1985

A/Title: Identification of the protein encoded by the E6 transforming gene of bovine pap.

A/Reference number: A94282; PMID:86018841; PMID:2996134

A/Contents: annotation; identification of the protein

C/Comment: This protein is present in the cell nucleus and the cellular membrane.

C/Superfamily: papillomavirus E6 protein

C/Keywords: DNA binding; early protein; transforming protein; zinc finger

Query Match 14.3%; Score 119; DB 1; Length 137;  
Best Local Similarity 28.9%; Pred. No. 0.00029;  
Matches 35; Conservative 16; Mismatches 68; Indels 2; Gaps 2;

Qy 28 LECYCKQQLRREYVDFAFRDLCTVYRDGNPYAVXDKCLKFYKSKISEYRHYCVSYGTT 87

Db 15 LDCIMCREPLTEVDFACWYKDFHVVIRBGRGACTICLNCIATERRLMOGVPTVGE 74

Qy 88 LEOQYNNPLDILLIRICINXQKPLCEBKORHLDKKQRFHINRGWTRCMSGCR-SSRT 145

Db 75 AELHAGTLDRLCRCCGCGKLTNENGRVLFNEPECKTNRANIRRCYDCCRHGSR 134  
Oy 146 R 146  
Db 135 K 135

## RESULT 49

W6WL47  
E6 protein - human papillomavirus type 47  
C:Species: human papillomavirus type 47  
A:Note: host Homo sapiens (man)  
C:Date: 31-Mar-1991 #sequence\_revision 31-Mar-1991 #text\_change 09-Jul-2004  
C:Accession: A35324  
R:Kiyono, T.; Adachi, A.; Ishibashi, M.  
Virology 177, 401-405, 1990  
A:Title: Genome organization and taxonomic position of human papillomavirus type 47 infe  
A:Reference number: A35324; MUID:90281611; PMID:2162112  
A:Accession: A35324  
A:Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-156 <K1Y>  
A:Cross-references: UNIPROT:P22422; UNIPARC:UPI00001383D9; GB:M32305; NID:G333062; PIDN:  
C:Superfamily: papillomavirus E6 protein  
C:Keywords: DNA binding; early protein; transforming protein; zinc finger  
F:40-76/Region: zinc finger CCCC motif  
F:113-149/Region: zinc finger CCCC motif

Query Match 14.3%; Score 119; DB 1; Length 156;  
Best Local Similarity 24.8%; Pred. No. 0.00032;

Matches 34; Conservative 23; Mismatches 80; Indels 0; Gaps 0;

Oy 3 QDPQPRPKLPQLCTELQTTIHDIIEGVYCKQQLREVVYDPAFRDLCTVYRGNPYAV 62  
Db 13 EEKLELPTTIRGLQQLDIPVDCILPFCGRFDYVECFDKLTLLMKDYSVAC 72  
Oy 63 XDCKLKFYSKISEVRYHCYSVYGTLEQYNNKPLCDLLIRICINXQKPLCPREKORHLDK 122  
Db 73 CRLCGSATATYEFNPFVYQYTLGRDIELATGSLFEIDIRCHTCLSFIDIEKLDSCGRG 132  
Oy 123 QRFNIRGRWTGRCMSC 139  
Db 133 LPFHKVRNAMKGVCRQC 149

## RESULT 50

W6WL8  
E6 protein - human papillomavirus type 8  
C:Species: human papillomavirus type 8  
C:Date: 30-Jun-1987 #sequence\_revision 30-Jun-1987 #text\_change 09-Jul-2004  
C:Accession: A03685  
R:Fuchs, P.G.; Ittner, T.; Weninger, J.; Pfister, H.  
J. Virol. 58, 626-634, 1986  
A:Title: Epidermodyplasiea verruciformis-associated human papillomavirus 8: genomic sequ  
A:Reference number: A93019; MUID:86200410; PMID:3009874  
A:Accession: A03685  
A:Molecule type: DNA  
A:Residues: 1-155 <FUC>  
A:Cross-references: UNIPROT:P06428; UNIPARC:UPI00001383B4; GB:M12737; NID:G333074  
A:Note: this ORF is not annotated in GenBank entry PFH8CG  
C:Superfamily: papillomavirus E6 protein  
C:Keywords: DNA binding; early protein; zinc finger  
F:39-75/Region: zinc finger CCCC motif  
F:112-148/Region: zinc finger CCCC motif

Query Match 14.2%; Score 118; DB 1; Length 155;  
Best Local Similarity 25.0%; Pred. No. 0.0004;

Matches 34; Conservative 27; Mismatches 69; Indels 6; Gaps 3;

Oy 7 ERPRKLPLQCLTELQTTIHDIIEGVYCKQQLREVVYDPAFRDLCTVYRGNPYAVXD-- 64  
Db 16 ELPSITVELAALAIPILODCSVPCNFCGNFIDPELCEFDKRLCLIKWN--YVVTACC 72

Oy 65 KCLKFYSKISEY-RHYCYSVYGTLEQYNNKPLCDLLIRICINXQKPLCPREKORHLDKQ 123  
Db 73 RCCCVATATPEFNEVYEQYTLGRDIELATGSLFEIDVRKONCLSFIDIEKLDCCGRG 132  
Oy 124 RFFNIRGRWTGRCMSC 139  
Db 133 PFHKGVRNAMKGVCRQC 148

## RESULT 51

W6WL5  
E6 protein - human papillomavirus type 5b  
C:Species: human papillomavirus type 5b  
A:Note: host Homo sapiens (man)  
C:Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 09-Jul-2004  
C:Accession: E40480  
R:Yabe, Y.; Sakai, A.; Hitsumoto, T.; Kato, H.; Ogura, H.  
Virology 183, 793-798, 1991  
A:Title: A subtype of human papillomavirus 5 (HPV-5b) and its subgenomic segment amplifie  
A:Reference number: A40480; MUID:91306467; PMID:1649510  
A:Accession: E40480  
A:Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-157 <YAB>  
A:Cross-references: UNIPROT:P26556; UNIPARC:UPI00000060C6; GB:D90252; NID:G222395; PIDN:  
C:Superfamily: papillomavirus E6 protein  
C:Keywords: DNA binding; early protein; zinc finger  
F:41-77/Region: zinc finger CCCC motif  
F:114-150/Region: zinc finger CCCC motif

Query Match 14.0%; Score 116; DB 1; Length 157;  
Best Local Similarity 24.8%; Pred. No. 0.00063;

Matches 34; Conservative 22; Mismatches 81; Indels 0; Gaps 0;

Oy 3 QDPQPRPKLPQLCTELQTTIHDIIEGVYCKQQLREVVYDPAFRDLCTVYRGNPYAV 62  
Db 14 KDKALEPSTIRDLAETIGIPLDICIIPNFCGRFLNLYLCEFPYKLSLWKDYCVFAC 73  
Oy 63 XDCKLKFYSKISEVRYHCYSVYGTLEQYNNKPLCDLLIRICINXQKPLCPREKORHLDK 122  
Db 74 CRVCCGATATYEFNPFQYTLGRDIELASGLSFIDIRCHTCLAFDLIEKLDCCGRG 133  
Oy 123 QRFNIRGRWTGRCMSC 139  
Db 134 LPFHKVRNAMKGVCRQC 150

## RESULT 52

W6WL5  
E6 protein - human papillomavirus type 5  
C:Species: human papillomavirus type 5  
C:Date: 30-Sep-1987 #sequence\_revision 30-Sep-1987 #text\_change 16-Feb-1997  
C:Accession: F26277  
R:Zachow, K.R.; Ostrow, R.S.; Paras, A.J.  
Virology 158, 251-254, 1987  
A:Title: Nucleotide sequence and genome organization of human papillomavirus type 5.  
A:Reference number: A94360; MUID:87207670; PMID:3033892  
A:Accession: F26277  
A:Molecule type: DNA  
A:Residues: 1-157 <ZAC>  
A:Cross-references: UNIPARC:UPI000017495B  
C:Superfamily: papillomavirus E6 protein  
C:Keywords: DNA binding; early protein; zinc finger  
F:41-77/Region: zinc finger CCCC motif  
F:114-150/Region: zinc finger CCCC motif

Query Match 13.6%; Score 113; DB 1; Length 157;  
Best Local Similarity 24.1%; Pred. No. 0.0012;

Matches 33; Conservative 22; Mismatches 82; Indels 0; Gaps 0;

Oy 3 QDPQPRPKLPQLCTELQTTIHDIIEGVYCKQQLREVVYDPAFRDLCTVYRGNPYAV 62  
Db 16 ELPSITVELAALAIPILODCSVPCNFCGNFIDPELCEFDKRLCLIKWN--YVVTACC 72

Db 14 KDKAEPLSLIRDLAEALGIPVIDCLIPCNPCGNFLNTLAECEPHYKRLSLIMKQCYFAC 73  
 QY 63 XDKCLKRYKSISEYRHYCYSVYGTTLQOYNKPLCDLLIRNCINXQKPLCPEEKORHLDDK 122  
 Db 74 CRVCCGATATYEFQFYEQVTLGRDILASGLSIFDIDIRCQTGLAFLDITKLDCCGRG 133  
 QY 123 QRFNIRGRWTRGCMSC 139  
 Db 134 LPFHKVRNWKIGICRQC 150

## RESULT 53

S28509

E6 protein - Old World harvest mouse papillomavirus (fragment)

C/Species: Old World harvest mouse papillomavirus  
 C/Date: 12-Mar-1993 #sequence\_revision 12-Mar-1993 #text\_change 09-Jul-2004  
 C/Accession: S28509; S22955  
 R:van Ranst, M.A.  
 Submitted to the EMBL Data Library, April 1992  
 A/Reference number: S28509  
 A/Accession: S28509  
 A/Molecule type: DNA  
 A/Residues: 1-154 <VAN2>  
 A/Cross-references: UNIPROT:P30734; UNIPARC:UPI0000170P1E; EMBL:X65200; NID:G60571; PIDN  
 A/Note: the source is designated as Microgms minutus papillomavirus  
 R:van Ranst, M.; Tachezy, R.; Fruse, J.; Burk, R.D.  
 Nucleic Acids Res. 20, 2889, 1992  
 A/Title: Primary structure of the E6 protein of Microgms minutus papillomavirus and Mast  
 A/Reference number: S22955; MUID:92310995; PMID:1319576  
 A/Accession: S22955  
 A/Status: nucleic acid sequence not shown  
 A/Molecule type: DNA  
 A/Residues: 20-147 <VAN2>  
 A/Cross-references: UNIPARC:UPI0000178417; EMBL:X65200  
 A/Note: the source is designated as Microgms minutus papillomavirus  
 C/Superfamily: papillomavirus E6 protein  
 C/Keywords: DNA binding; early protein; zinc finger  
 F:38-74/Region: zinc finger  
 F:11-147/Region: zinc finger

Query Match 10.4%; Score 86; DB 2; Length 154;  
 Best Local Similarity 23.2%; Pred. No. 0.45;  
 Matches 35; Conservative 19; Mismatches 75; Indels 22; Gaps 6;  
 QY 5 PQ-ERPKLPLQCTE-----LQTTIDHIIIECYCKQQLIRREYDFAFDLCIVY 54  
 Db 3 POPRPYPSPMELCREYTLBQLKFLANTLDTLMPCHFCSSFMDLNKASYLASQLKVIY 62  
 QY 55 RDGNPVAVXDKCKLFYKISFYRHVCYSV--YGTTLQOYNKPLCDLLIRNCINXQKPLC 111  
 Db 63 KD---CCFKGACIKRRRLAFAEROKYQVCGEADLVEANVGVSHVNLTVRCSECLALLT 119  
 QY 112 PEKORHLDDK---QRFNIRGRWTRGCMSC 139  
 Db 120 ASEK---LDAKCEIQTLIVRHMRTSCRCAC 147

## RESULT 54

W6WLDP

E6 protein - deer papillomavirus

C/Species: deer papillomavirus  
 C/Date: 28-May-1986 #sequence\_revision 28-May-1986 #text\_change 09-Jul-2004  
 C/Accession: A03687  
 R:Groff, D.E.; Lancaster, W.D.  
 J. Virol. 56, 85-91, 1985  
 A/Title: Molecular cloning and nucleotide sequence of deer papillomavirus.  
 A/Reference number: A93013; MUID:85293253; PMID:2993669  
 A/Accession: A03687  
 A/Molecule type: DNA  
 A/Residues: 1-135 <GRO>  
 A/Cross-references: UNIPROT:P03128; UNIPARC:UPI00001383EB; GB:M11910; NID:G333021; PIDN:  
 C/Superfamily: papillomavirus E6 protein  
 C/Keywords: DNA binding; early protein; zinc finger

Query Match 10.1%; Score 83.5; DB 1; Length 135;  
 Best Local Similarity 28.6%; Pred. No. 0.68;  
 Matches 34; Conservative 17; Mismatches 57; Indels 11; Gaps 4;

QY 28 LECYCKQQLLR---REYDFAFDLCIVYRDGNPVAVXDKCKLFYKISFYRHVCYSVY 84  
 Db 9 LYCVFCYLGKAEKARCYDKIR--TVVRGLRCVACTACLEKGYLERYVANAPOPVY 65  
 QY 85 GTTLQO--QYNKPLCDLLIRNCINXQKPLCPEEKORHLDDKQRFNIRGRWTRGCMSCCR 141  
 Db 66 QGSIIEBDFPIQKAC---IRCWCGGILTRDEKDRHRYPFELYVIFRNOVLGRCYCTCTR 121

## RESULT 55

S19906

E6-II protein - human papillomavirus type 33 (fragment)

C/Species: human papillomavirus type 33  
 C/Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 09-Jul-2004  
 C/Accession: S19906  
 R:Snijders, P.J.F.; van den Brule, A.J.C.; Schrijnemakers, H.F.J.; Raaphorst, P.M.C.; Me  
 submitted to the EMBL Data Library, January 1992  
 A/Description: HPV type 33 in a tonsillar carcinoma generates its putative E7 mRNA via t  
 A/Reference number: S19906  
 A/Accession: S19906  
 A/Molecule type: mRNA  
 A/Residues: 1-32 <SN1>  
 A/Cross-references: UNIPROT:Q81885; UNIPARC:UPI00000F932A; EMBL:X64086; NID:G60282; PIDN  
 C/Superfamily: papillomavirus E6 protein  
 C/Keywords: early protein

Query Match 10.0%; Score 83; DB 2; Length 32;  
 Best Local Similarity 59.3%; Pred. No. 0.19;  
 Matches 16; Conservative 4; Mismatches 7; Indels 0; Gaps 0;  
 QY 15 LCTELQTTIDHIIIECYCKQQLLRRE 41  
 Db 3 LQALETTHINIELQCECKKPLORSE 29

## RESULT 56

S19909

E6-III protein - human papillomavirus type 33 (fragment)

C/Species: human papillomavirus type 33  
 C/Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 09-Jul-2004  
 C/Accession: S19909  
 R:Snijders, P.J.F.; van den Brule, A.J.C.; Schrijnemakers, H.F.J.; Raaphorst, P.M.C.; Me  
 submitted to the EMBL Data Library, January 1992  
 A/Description: HPV type 33 in a tonsillar carcinoma generates its putative E7 mRNA via t  
 A/Reference number: S19906  
 A/Accession: S19909  
 A/Molecule type: mRNA  
 A/Residues: 1-35 <SN1>  
 A/Cross-references: UNIPROT:Q81887; UNIPARC:UPI00000EBD75; EMBL:X64087; NID:G60286; PIDN  
 C/Superfamily: papillomavirus E6 protein  
 C/Keywords: early protein

Query Match 10.0%; Score 83; DB 2; Length 35;  
 Best Local Similarity 59.3%; Pred. No. 0.21;  
 Matches 16; Conservative 4; Mismatches 7; Indels 0; Gaps 0;  
 QY 15 LCTELQTTIDHIIIECYCKQQLLRRE 41  
 Db 3 LQALETTHINIELQCECKKPLORSE 29

## RESULT 57

S23825

E6-I protein - human papillomavirus type 33 (fragment)

C/Species: human papillomavirus type 33  
 C/Date: 20-Feb-1995 #sequence\_revision 30-Jan-1998 #text\_change 09-Jul-2004  
 C/Accession: S23825; S23829  
 R:Snijders, P.J.F.; van den Brule, A.J.C.; Schrijnemakers, H.F.J.; Raaphorst, P.M.C.; Me



Db 535 YKC 537

# RESULT 61

111515

formin - mouse

C/Species: Mus musculus (house mouse)

C/Date: 22-Jan-1994 #sequence\_revision 10-Nov-1995 #text\_change 09-Jul-2004

C/Accession: S11515

R/Woychik, R.P.; Maas, R.L.; Zeller, R.; Vogt, T.F.; Leder, P.

Nature 346, 850-853, 1990

A/Title: 'Formin': protein deduced from the alternative transcripts of the limb deform

A/Reference number: S11515; MUID:90363291; PMID:2352150

A/Accession: S11515

A/Molecule type: mRNA

A/Residues: 1-1468 <NOY>

A/Cross-references: UNIPROT:Q05860; UNIPARC:UPI0000027927; EMBL:X53599; NID:g52877; PIDN

Query Match 9.3%; Score 77.5; DB 2; Length 1468;

Best Local Similarity 27.4%; Pred. No. 25;

Matches 34; Conservative 14; Mismatches 47; Indels 29; Gaps 5;

QY 16 CTEIQTTHDIIIECVCKQQLLRREYVDFAFRLDGIYRDGNPYAVXDKLKFYSKISE 75

Db 6 CT-LQ--LHNPALCYISFYLKGVGRGYSKGTVTLDRSNNAF----- 47

QY 76 YRHYSYVVG---TTLEQYNRPLCDLLRINCXQKPL-----CPEKORHLDKKQRFH 126

Db 48 --NHCVQVRGPDITSLSQDPENHPGDIFFKQPTKNILTYLTAKEKRLDSLRS 105

QY 127 NING 130

Db 106 NITG 109

# RESULT 62

T09483

Cys-rich protein RAMP - human

C/Species: Homo sapiens (man)

C/Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999

C/Accession: T09483

R/Smedley, D.P.; Hamoudi, R.; Clark, J.; Warren, W.; Abdul-Rauf, M.; Somers, G.; Venter,

submitted to the EMBL Data Library, November 1997

A/Description: RAMP, a novel gene encoding a Cys-rich protein.

A/Reference number: Z16688

A/Accession: T09483

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-699 <SME>

A/Cross-references: UNIPARC:UPI0000169706; EMBL:AF035374; NID:g2665702; PID:g2665703

A/Genetic:

A/Map position: 13q11-12

Query Match 9.3%; Score 77; DB 2; Length 699;

Best Local Similarity 22.2%; Pred. No. 14;

Matches 37; Conservative 17; Mismatches 49; Indels 64; Gaps 10;

QY 25 DILIECVCKQQLLR-----EYVDFAFRLDGIYRDGNPYAVXDKLKFYSKISE 76

Db 362 DIQKKNYCKNSPFCSPKLEIEMENKVFQFCK-----TCSDDYKXLAHI 405

QY 77 RHVC-YSVYGTLEQYN---KPLCD-----LIIRCI--NXQKPLCPPEE 114

Db 406 VTYEYCOEKEKTHETVNFSGVKRPFSEGGKLYKODFARLGLRCVTCNYCSQLCKG 465

QY 115 KQRLDKK-----QRFNIRGRW---TGRCMGCRSSRTRE 148

Db 466 ATKELDGVNRDPCSEDCCKKFD---WYKPARC-DCKSKQTLKE 507

# RESULT 63

T21125

hypothetical protein F19H8.2 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Sep-1997

C/Accession: S44810

R/Antonacci-Fulton, L.

submitted to the EMBL Data Library, September 1993

A/Description: Sequence of the C. elegans cosmid F44B9.

A/Reference number: S44807

A/Accession: S44810

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-400 <ANT>

A/Cross-references: UNIPARC:UPI000017B6C2; EMBL:L23648; NID:g388585; PID:g388589

C/Genetics:

A/Introns: 49/2, 124/3, 188/3, 233/2, 274/2, 321/1, 358/2

Query Match 9.2%; Score 76; DB 2; Length 400;

Best Local Similarity 17.2%; Pred. No. 10;

Matches 27; Conservative 35; Mismatches 57; Indels 38; Gaps 4;

QY 4 DPERPRKLPQ-----LCTELQTTIHDIIECVCK--QQLRREYVDFAFR 48

Db 196 EPOSHIRESPQKETNLEKYSTGEICLYRELVNDLVNTKSTYSLTKKMERKPLN---- 251

QY 49 DLCTVARDGNPYAVXDKLKFYSKISEYRHYSYVGTLEQYNRPLCDLLRINCXQK 108

Db 252 -----QGENPNLDADCKNALQRMDSIDROIIEKREPTKRMGTGEYIELMDSELUK 305

QY 109 PLCEEKORHLDKKQRFNI-----RGRW 112

Db 306 PMDERQKRAELEQRALVISTPPVESHVWGKW 342

# RESULT 64

S71522

outer dense fiber protein 2 - human

C/Species: Homo sapiens (man)

C/Date: 09-Dec-1997 #sequence\_revision 09-Dec-1997 #text\_change 09-Jul-2004

C/Accession: S71522; I38074

R/Hoffeibert, S.; Burfield, P.; Hoyer-Fender, S.; Lange, R.; Haidl, G.; Engel, W.

Hum. Mol. Genet. 2, 2167-2170, 1993

A/Title: A homozygous deletion of 27 basepairs in the coding region of the human outer d

A/Reference number: I38074; MUID:94154698; PMID:8111388

A/Accession: S71522

A/Status: nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-250 <HOF>

A/Cross-references: UNIPROT:Q14990; UNIPARC:UPI0000130BD2; EMBL:X74614; NID:g474425; PID

A/Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1993

C/Genetics:

A/Map position: 8

A/Introns: 107/2

C/Function:

A/Description: provides the sperm tail with stabilizing and zinc binding properties

A/Note: one of the main component of the sperm tail

Query Match 9.1%; Score 75.5; DB 2; Length 250;

Best Local Similarity 27.5%; Pred. No. 7.1;

Matches 33; Conservative 14; Mismatches 36; Indels 37; Gaps 7;

QY 40 REYVDFAFRLDGIYRDGNPYAVXDKLKFYSKISEYRHYSYVGTLEQYNRK 94

Db 26 RCIDFESTRLCDLYM--HPYCCDLHPYCL-----KRSRC 65

QY 95 PLCDLLRINCXQKPLCEEKORHLD-----DKKORFHNIRGRWTCM--SCRRS 143

Db 66 GLCDLYPCCLDYKLYLRSLASLSERKARALAEDEGRALKAR-RITNPIILASSCCSSN 124

# RESULT 65

T21125

hypothetical protein F19H8.2 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans  
C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C/Accession: J21125  
R/Steward, C.  
Submitted to the EMBL Data Library, March 1997  
A/Reference number: Z19379  
A/Accession: J21125  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-303 <MIL>  
A/Cross-references: UNIPROT:O45378, UNIPARC:UPI0000075882, EMBL:Z93378, PIDN:CA807582.1,  
A/Experimental source: clone F19H8  
C/Genetics:  
A/Gene: CESP:F19H.2  
A/Map position: 2  
A/Introns: 27/2; 96/3; 147/3; 201/3

Query Match 9.0%; Score 75; DB 2; Length 303;  
Best Local Similarity 19.1%; Pred. No. 9.5;  
Matches 36; Conservative 29; Mismatches 49; Indels 74; Gaps 10;

Oy 6 QERRKLPOLCTELQ-----TTHDITLCEVCCKOQLLREYVD---FA 46  
Db 70 ESQGRLCPSWCGHKSNETIVNIGAVGNSTTDLQDVSFECDDLKNCCLAVKXNGHCYF 129  
Oy 47 FRDLC-----IYRDSG-----NRYAVXDKCLKFSKISE-----YRHCVSYVGT 86  
Db 130 FKKRCEDDAISKXGSKTSRNP-KTAGECIAKQKCKQKRGYACTFRHC----- 182  
Oy 87 TLEQYNNPLCDL-----LIRCNXOKPLCPPEKORHLDDKORFHNIRG 130  
Db 183 ---RKYMLPEIEVNNSTLTNSHTVQVSPLEQCLNFQK-ICAAKYKGFACRQ----- 231  
Oy 131 RWTGRCMS 138  
Db 232 -YRKKCL 238

RESULT 66  
S56100  
outer dense fiber protein - pig  
C/Species: Sus scrofa domestica (domestic pig)  
C/Date: 10-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 09-Jul-2004  
C/Accession: S56100  
R/Kim, Y.; Adham, I.M.; Haack, T.; Krenning, H.; Engel, W.  
Biol. Chem. Hoppe-Seyler 376, 431-435, 1995  
A/Title: Molecular cloning and characterization of the bovine and porcine outer dense fi  
A/Reference number: S56100; MUID:9606278; PMID:7576240  
A/Accession: S56100  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-262 <KIM>  
A/Cross-references: UNIPROT:Q29077, UNIPARC:UPI0000130BD3, GB:X65513, NID:G1165146; PIDN:

Query Match 9.0%; Score 74.5; DB 2; Length 262;  
Best Local Similarity 27.5%; Pred. No. 9.2;  
Matches 33; Conservative 14; Mismatches 36; Indels 37; Gaps 7;

Oy 40 REVVDPAFRDLCIYVRDNPYAVD-----KCLAFYSKISRYRHCVSYVGTLEQYNNK 94  
Db 26 RCIDFSTRCLCDLYM-HFYCCCDLHYPYCL-----CYS-----KRSRSC 65  
Oy 95 PLCDLLIRCNXOKPLCPPEKORHL-----DKORFHNIRGRMTGRGM-SCCRSS 143  
Db 66 GLCDLIPCLCDVLYLCIRPSLRSEKRAIRAIDEKELAKLR-KITNRIIASCCSSN 124

RESULT 67  
PFGO  
alpha-fetoprotein precursor - gorilla  
C/Species: Gorilla gorilla (gorilla)  
C/Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004  
C/Accession: A37970

R/Ryan, S.C.; Zielinski, R.; Dugaiczky, A.  
Genomics 9, 60-72, 1991  
A/Title: Structure of the gorilla alpha-fetoprotein gene and the divergence of primates.  
A/Reference number: A37970; MUID:91165517; PMID:11706310  
A/Accession: A37970  
A/Molecule type: DNA  
A/Residues: 1-609 <RYA>  
A/Cross-references: UNIPROT:P28050, UNIPARC:UPI000012A6F8, GB:M38272; NID:G817963; PIDN:  
C/Genetics:  
A/Map position: 4q11-12  
A/Introns: 29/1; 46/2; 90/3; 161/2; 205/3; 238/2; 281/3; 353/2; 397/3; 430/2; 476/3; 551/  
C/Superfamily: serum albumin; serum albumin repeat homology  
C/Keywords: embryo; fetus; globulin; glycoprotein; metal binding; plasma  
F.1-18/Domain: signal sequence #status predicted <SIG>  
F.19-609/Product: alpha-fetoprotein #status predicted <MAT>  
F.29-202/Domain: serum albumin repeat homology <SA1>  
F.221-394/Domain: serum albumin repeat homology <SA2>  
F.413-592/Domain: serum albumin repeat homology <SA3>  
F.22/Binding site: copper (His) #status predicted  
F.99-114,113-124,148-193,192-201,224-270,269-303,302-313,384-393,416-462,461-472,  
F.249/Binding site: bilirubin (Lys) #status predicted  
F.251/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 9.0%; Score 74.5; DB 1; Length 609;  
Best Local Similarity 23.4%; Pred. No. 21;  
Matches 34; Conservative 26; Mismatches 44; Indels 41; Gaps 8;

Oy 6 QERRKLPOLCTELQTTIHDIIECVYCKOQLLREYVDFAFRDLCTV----- 54  
Db 279 QDGKIMSYVCSQ-QDPLSNKITEC--CKLTLE-----KQCIIHANEDEKPEGLS 327  
Oy 55 -----BDGNFYAVXDKCLKFSKISEY--RHYCVSYVGTTLQOYNNPLCDLLIR 103  
Db 328 PNLNRFIDGRDHFQFSSGKRNIFLASFVHEYSRRHQLAV---SVLRVAKGYELLEKC 384  
Oy 104 INXOKPL-C-----PEEKORHLDDKQ 123  
Db 385 FQTEPNLECODKGEELQKYIOESQ 409

RESULT 68  
FPHU  
alpha-fetoprotein precursor [validated] - human  
N/Alternate names: AFP; alpha-1-fetoprotein; alpha-fetoglobulin  
C/Species: Homo sapiens (man)  
C/Date: 19-Feb-1984 #sequence\_revision 19-Feb-1984 #text\_change 09-Jul-2004  
C/Accession: A26624; S37655; A33961; A91497; A23699; A61460; A90624; A90757; A93042; A03;  
R/Gibbs, P.E.M.; Zielinski, R.; Boyd, C.; Dugaiczky, A.  
Biochemistry 26, 1332-1343, 1987  
A/Title: Structure, polymorphism, and novel repeated DNA elements revealed by a complete  
A/Reference number: A26624; MUID:87185438; PMID:2436661  
A/Accession: A26624  
A/Molecule type: DNA  
A/Residues: 1-609 <GIB>  
A/Cross-references: UNIPROT:P02771; UNIPARC:UPI0000012A9; GB:M4110; NID:G773678; PIDN:  
R/McVey, J.H.; Michaelides, K.; Hansen, L.P.; Ferguson-Smith, M.; Tilghman, S.; Krumlauf  
Hum. Mol. Genet. 2, 379-384, 1993  
A/Title: A G->A substitution in an HNF I binding site in the human alpha-fetoprotein gen  
A/Reference number: S37655; MUID:93278385; PMID:7684942  
A/Accession: S37655  
A/Molecule type: DNA  
A/Residues: 1-28 <MCV>  
A/Cross-references: UNIPARC:UPI000016A4D; EMBL:Z19532; NID:G28527; PIDN:CAA79592.1; PID  
A/Note: the authors translated the codon TAT for residue 26 as Thr  
R/Moringa, T.; Sakai, M.; Wegmann, T.G.; Tamachi, T.  
Proc. Natl. Acad. Sci. U.S.A. 80, 4604-4608, 1983  
A/Title: Primary structures of human alpha-fetoprotein and its mRNA.  
A/Reference number: A93961; MUID:83273664; PMID:6192439  
A/Accession: A93961  
A/Molecule type: mRNA  
A/Residues: 1-609 <MOR>  
A/Cross-references: UNIPARC:UPI00000012A9; GB:J00077; NID:G311348; PIDN:CAA24758.1; PID:  
R/Beattie, W.G.; Dugaiczky, A.

Gene 20, 415-422, 1982  
 A>Title: Structure and evolution of human alpha-fetoprotein deduced from partial sequenc  
 A/Reference number: A91497; MUID:85158778; PMID:6187626  
 A/Accession: A91497  
 A/Molecule type: mRNA  
 A/Residues: 429-556 <BEA>  
 A/Cross-references: UNIPARC:UPI0000174421; GB:J00076  
 R/Pucci, P.; Siciliano, R.; Malorni, A.; Marino, G.; Tecce, M.F.; Ceccarini, C.; Terrana  
 Biochemistry 30, 5061-5066, 1991  
 A>Title: Human alpha-fetoprotein primary structure: a mass spectrometric study.  
 A/Reference number: A23699; MUID:91242409; PMID:1709810  
 A/Accession: A23699  
 A/Molecule type: protein  
 A/Residues: 19-45;60-97;102-107;122-184;187-249;255-489;507-609 <PUC>  
 A/Cross-references: UNIPARC:UPI0000174422; UNIPARC:UPI0000174424; UNIPARC:UPI0000174424;  
 R/Tecce, M.F.; Terrana, B.; Giuliani, M.M.; Ceccarini, C.  
 J. Nucl. Med. Allied Sci. 34, 213-216, 1990  
 A>Title: Characterization of in vitro expressed human alpha-fetoprotein as highly repro  
 A/Reference number: A61480; MUID:91225826; PMID:1709209  
 A/Accession: A61480  
 A/Molecule type: protein  
 A/Residues: 19-45;63-97;102-107;122-184;187-249;255-489;507-609 <TEC>  
 A/Cross-references: UNIPARC:UPI0000174422; UNIPARC:UPI0000174424; UNIPARC:UPI0000174425;  
 R/Vachnin, S.; Hsu, R.; Helmricks, R.L.; Miller, J.B.  
 Biochim. Biophys. Acta 493, 418-428, 1977  
 A>Title: Studies on human alpha-fetoprotein. Isolation and characterization of monomeric  
 A/Reference number: A90624; MUID:77242506; PMID:70228  
 A/Accession: A90624  
 A/Molecule type: protein  
 A/Residues: 'S', 20-22, 'S', 24-35 <YAC>  
 A/Cross-references: UNIPARC:UPI0000174424  
 A/Note: dimeric and trimeric forms have been found in addition to the monomeric form  
 R/Aoyagi, Y.; Ikenaka, T.; Ichida, F.  
 Cancer Res. 37, 3663-3667, 1977  
 A>Title: Comparative chemical structure of human alpha-fetoproteins from fetal serum and  
 A/Reference number: A90757; MUID:78001760; PMID:71198  
 A/Accession: A90757  
 A/Molecule type: protein  
 A/Residues: 'S', 20-30, 'A', 32-37, 'A', <NOY>  
 A/Cross-references: UNIPARC:UPI000017442B  
 R/Ruoslahti, E.; Pihko, H.; Vaheri, A.; Seppala, M.; Virolainen, M.; Kontinen, A.  
 Johns Hopkins Med. J. Suppl. 3, 249-255, 1974  
 A>Title: 20. Alpha fetoprotein: structure and expression in man and inbred mouse strains  
 A/Reference number: A93042; MUID:75018719; PMID:4118095  
 A/Accession: A93042  
 A/Molecule type: protein  
 A/Residues: 'S', 20-24, 'Q', 26-30, 'A', 32-35, 'E', 37-39 <RUO>  
 A/Cross-references: UNIPARC:UPI000017442C  
 R/Sakai, M.; Morinaga, T.; Urano, Y.; Watanabe, K.; Wegmann, T.G.; Tamaoki, T.  
 J. Biol. Chem. 260, 5055-5060, 1985  
 A>Title: The human alpha-fetoprotein gene. Sequence organization and the 5' flanking reg  
 A/Reference number: A92520; MUID:85182629; PMID:2580830  
 A/Contents: annotation; gene, exons and introns  
 R/Aoyagi, Y.; Ikenaka, T.; Ichida, F.  
 Cancer Res. 38, 3483-3486, 1978  
 A>Title: Copper(II)-binding ability of human alpha-fetoprotein.  
 A/Reference number: A90758; MUID:79001617; PMID:80265  
 A/Contents: annotation; metal binding  
 R/Aoyagi, Y.; Ikenaka, T.; Ichida, F.  
 Cancer Res. 39, 3571-3574, 1979  
 A>Title: alpha-fetoprotein as a carrier protein in plasma and its bilirubin-binding abil  
 A/Reference number: A90759; MUID:80001710; PMID:89900  
 A/Contents: annotation; bilirubin binding  
 C/Comment: AFP is synthesized by the fetal liver and yolk sac. It occurs in the plasma  
 C trace amounts after birth. The serum level in adults is usually less than 40 ng/ml. Af  
 C/Comment: Human AFP binds copper, nickel, and fatty acids as well as, and the bilirubin  
 properties.  
 C/Genetics:  
 A/Gene: GDB:AFP  
 A/Cross-references: GDB:119660; OMIM:104150  
 A/Map position: 4q11-q13  
 A/Introns: 29/1; 46/2; 90/3; 161/2; 205/3; 238/2; 281/3; 353/2; 397/3; 430/2; 476/3; 551  
 C:Superfamily: serum albumin, serum albumin repeat homology

C:Keywords: embryo; fetus; globulin; glycoprotein; metal binding; plasma  
 F:1-18/Domain: signal sequence #status predicted <SIG>  
 F:19-609/Product: alpha-fetoprotein #status predicted experimental <MAT>  
 F:129-202/Domain: serum albumin repeat homology <SA1>  
 F:221-394/Domain: serum albumin repeat homology <SA2>  
 F:413-592/Domain: serum albumin repeat homology <SA3>  
 F:22/Binding site: copper (His) #status experimental  
 F:99-114, 113-124, 148-193, 199-201, 224-270, 269-277, 289-303, 302-313, 384-393, 416-462, 461-472  
 F:249/Binding site: bilirubin (Lys) #status predicted  
 F:251/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 Query Match 9.0%; Score 74.5; DB 1; Length 609;  
 Best Local Similarity 23.4%; Pred. No. 21;  
 Matches 34; Conservative 26; Mismatches 44; Indels 41; Gaps 8;  
 Oy 6 QERRKLPOLCTELQTTIHDIIECVYCKQQLRREYDFAPRLCTIVY----- 54  
 Db 279 QDGEKIMSYICSQ-QDTLSNKTTC--CKLTTL-----RQCITHAENDEKPEGLS 327  
 Oy 55 -----RDGNRYAVXDKCLKFKYSKISEY--RHYCVYGTTLLEQGYNKPLCDLLIRC 103  
 Db 328 PNLNRFGLGDDPFGFSSGEGKNIFLASVHEYSRRHPOLAV---SVILRVAKGYOELLKCK 384  
 Oy 104 INXOKPL-C-----PEEKORHLDDKKQ 123  
 Db 385 FQTEPNPLECDQKGEELQKVIQESQ 409  
 RESULT 69  
 JC4258  
 alpha-fetoprotein precursor - chimpanzee  
 C/Species: Pan troglodytes (chimpanzee)  
 C/Date: 27-Nov-1995 #sequence, rev1a10n 08-Feb-1996 #text, change 09-Jul-2004  
 C/Accession: JC4258  
 R:Nishio, H.; Gibbs, P.E.M.; Minghetti, P.P.; Zielinski, R.; Dugalczyk, A.  
 Gene 162, 213-220, 1995  
 A>Title: The chimpanzee alpha-fetoprotein-encoding gene shows structural similarity to t  
 A/Reference number: JC4258; MUID:96032345; PMID:7557431  
 A/Accession: JC4258  
 A/Molecule type: DNA  
 A/Residues: 1-609 <NS>  
 A/Cross-references: UNIPROT:Q28789; UNIPARC:UPI000012A6FA; GB:U21916; MID:G841311; PIDN  
 C/Comment: This protein is a plasma protein produced in the fetal and neonatal liver and  
 C similar properties and structure.  
 C/Genetics:  
 A/Gene: afp  
 A/Map position: 3p  
 A/Introns: 29/1; 46/2; 90/3; 161/2; 205/3; 238/2; 281/3; 353/2; 397/3; 430/2; 476/3; 551  
 C:Superfamily: serum albumin, serum albumin repeat homology  
 C/Keywords: glycoprotein  
 F:1-19/Domain: signal sequence #status predicted <SIG>  
 F:20-609/Product: alpha-fetoprotein #status predicted <MAT>  
 F:129-202/Domain: serum albumin repeat homology <SA1>  
 F:221-394/Domain: serum albumin repeat homology <SA2>  
 F:413-592/Domain: serum albumin repeat homology <SA3>  
 F:42,251/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 Query Match 9.0%; Score 74.5; DB 2; Length 609;  
 Best Local Similarity 23.4%; Pred. No. 21;  
 Matches 34; Conservative 26; Mismatches 44; Indels 41; Gaps 8;  
 Oy 6 QERRKLPOLCTELQTTIHDIIECVYCKQQLRREYDFAPRLCTIVY----- 54  
 Db 279 QDGEKIMSYICSQ-QDTLSNKTTC--CKLTTL-----RQCITHAENDEKPEGLS 327  
 Oy 55 -----RDGNRYAVXDKCLKFKYSKISEY--RHYCVYGTTLLEQGYNKPLCDLLIRC 103  
 Db 328 PNLNRFGLGDDPFGFSSGEGKNIFLASVHEYSRRHPOLAV---SVILRVAKGYOELLKCK 384  
 Oy 104 INXOKPL-C-----PEEKORHLDDKKQ 123  
 Db 385 FQTEPNPLECDQKGEELQKVIQESQ 409

## RESULT 70

F96784

hypothetical protein F1B16.6 [imported] - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004

C/Accession: F96784

R/Theologian: A.; Becker, J.R.; Palm, C.J.; Federici, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A/Authors: Salberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A/Reference number: A86141; MUID:21016719; PMID:11130712

A/Accession: F96784

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-524 &lt;STO&gt;

A/Cross-references: UNIPROT:Q9FWS9; UNIPARC:UPI00000A25AD; GB:AE005173; NID:g10120440; F

C/Genetics:

A/Gene: F1B16.6

A/Map position: 1

Query Match 8.9%; Score 74; DB 2; Length 524;

Best Local Similarity 24.3%; Pred. No. 20;

Matches 27; Conservative 17; Mismatches 41; Indels 26; Gaps 4;

OY 43 YDPAFRLC--IVYRGNPYAVXD--KCLFYSKISE-----YRHY 79

DB 98 FQHYQNSLSTVNNLSTMSDENGKSLVHGHNSQILPSSVYNNNGNGVFYNNY 157

OY 80 CYSYVG--TTLEQYKRLCDLIRCIKXOKPCREKQKRLDKKQFHN 127

DB 158 RYETSGFVSVLRSLRYLKTQQLDEYVSVKDLKLGKMKMKMDKQDFHN 208

RESULT 71

T45119

FIM protein [imported] - human

C/Species: Homo sapiens (man)

C/Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 09-Jul-2004

C/Accession: T45119

R/Popovici, C.; Adelaide, J.; Ollendorff, V.; Chaffenet, M.; Guasch, G.; Jacrot, M.; Ler

Proc. Natl. Acad. Sci. U.S.A. 95, 5712-5717, 1998

A/Title: Fibroblast growth factor receptor 1 is fused to FIM in stem-cell myeloprolifera

A/Reference number: Z22919; MUID:98245146; PMID:9576949

A/Accession: T45119

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-1379 &lt;FOP&gt;

A/Cross-references: UNIPROT:Q9UBW7; UNIPARC:UPI000016AF9A; EMBL:Y13472; NID:g3135791; PI

C/Genetics:

A/Gene: FIM

Query Match 8.9%; Score 74; DB 2; Length 1379;

Best Local Similarity 22.2%; Pred. No. 51;

Matches 37; Conservative 16; Mismatches 50; Indels 64; Gaps 10;

OY 25 DILECVYCKQQLARR-----EYDFAFRDLCTIVRDGNPYAVXDKLKFYSKISEY 76

DB 636 DIOLKKNCKKSPKSPKLEMEKNVHOFCK-----TCDNDYKKAHCI 679

OY 77 RHYC-YSYVGTTLLEQYV---KPLCD-----LLIRCI--NXQKPLCPBE 114

DB 680 VTVEYECCEKTLHTETVNFSGVKRPFCEGCKLYKODFARLIGRLCTVCYCSOLCKGG 739

OY 115 KQRLDKK-----QRFHNIRGR---TGRMCSCRSRTRE 148

DB 740 ATKELDGVVRDFCEBCKCKFOD---WYKAARC-DCKSGGTIKE 781

## RESULT 72

A72220

conserved hypothetical protein - Thermotoga maritima (strain MSB)

C/Species: Thermotoga maritima

C/Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 31-Dec-2004

C/Accession: A72220

R/Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwin, M.L.; Dodson, R.J.; Haft, D.H.; Hickey

Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;

C.M.

Nature 399, 323-329, 1999

A/Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq

A/Reference number: A72200; MUID:99287316; PMID:10360571

A/Accession: A72220

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-357 &lt;ARN&gt;

A/Cross-references: UNIPROT:Q9X221; UNIPARC:UPI00000C1227; GB:AE001810; GB:AE000512; NID

A/Experimental source: strain MSB

C/Genetics:

A/Gene: TM1695

Query Match 8.9%; Score 73.5; DB 2; Length 357;

Best Local Similarity 28.7%; Pred. No. 15;

Matches 29; Conservative 12; Mismatches 43; Indels 17; Gaps 4;

OY 6 QERPRKLPOLCTELQTTIHDIIECYCK-----OQLRRE--VYDF-----AFRDL 50

DB 46 KENIMKEVOTCEKLEKVVH--LDETVPEPLIFPEFOEWLRENTTPKDFKAVSLKGLYDL 103

OY 51 CIVYRDGNPYAVXDKLKFYSKISEYRHYCYSGYGTLEQ 91

DB 104 ALEYADNRLVDIADHDIKFMMDIDENYAPAYELKSLLEQ 144

RESULT 73

T17525

proline-rich protein A35L - Chlorella virus PBCV-1

C/Species: Chlorella virus PBCV-1

C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

C/Accession: T17525

R/Graves, M.V.; Van Etten, J.L.

submitted to the EMBL Data Library, May 1999

A/Reference number: Z18806

A/Accession: T17525

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-549 &lt;GBA&gt;

A/Cross-references: UNIPROT:Q89370; UNIPARC:UPI00000F6AD8; EMBL:U42580; NID:94028896; PI

A/Experimental source: specific host Chlorella strain NC64A

C/Genetics:

A/Gene: A35L

Query Match 8.9%; Score 73.5; DB 2; Length 549;

Best Local Similarity 21.4%; Pred. No. 23;

Matches 33; Conservative 30; Mismatches 62; Indels 29; Gaps 7;

OY 17 TELQTTIHDIIEC--VYCKQQLARRVYDFAF-----DLCIYRDGNPYAVXDKC 66

DB 36 TEEQTLTYQYCKATDTPKOTWESKCEBDLAYRPELKLHDMCNLMQDFPGMRDN 95

OY 67 LKFSKISEYRHYCYSGYGTLEQYKPLCDLI-----RCINXOKPLCPBEKQRLDK 121

DB 96 EQLPERS-----YCIDSDGNIDKQ---PFCVTKCTTPGKISQAE---AEERKQREK 145

OY 122 KQFHNIRGR---WTGRMCSCRSSTRTRETQL 151

DB 146 ROIQAEAGKAAAEFOGSEYRCLYSRYKEPPQV 179

## RESULT 74

JC7686

activator of cAMP-responsive element modulator, testis - human  
 C:Species: Homo sapiens (man)  
 C:Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 09-Jul-2004  
 C:Accession: J07686  
 R:Palermo, I., Litrico, L.; Emmanuele, G.; Giuffrida, V.; Saabone-Corsi, P.; De Cesare, R.  
 Biochem. Biophys. Res. Commun. 283, 406-411, 2001  
 A:Title: Cloning and expression of activator of CREM in testis in human testicular tissue  
 A:Reference number: J07686; MUID:21226154; PMID:11327716  
 A:Contents: Testis  
 A:Accession: J07686  
 A:Molecule type: mRNA  
 A:Residues: 1-284 <PAL>  
 A:Cross-references: UNIPROT:O9N0U2; UNIPROT:O8W21; UNIPARC:UPI000017CB67; GB:AF278541  
 C:Comment: This protein activates cAMP-responsive element modulator in a phosphorylation  
 of human spermatogenesis.  
 C:Genetic8:  
 C:Gene: act  
 A:Map position: 6q  
 A:Introns: 53/3; 112/3; 168/3; 231/3  
 C:Keywords: spermatogenesis; testis

[illegible]

RESULT 75  
A55933  
paxillin - human  
N/Alternate names: peroxisomal membrane protein 3  
C/Species: Homo sapiens (man)  
C/Date: 23-Mar-1995 #sequence\_revision 05-Apr-1995 #text\_change 09-Jul-2004  
C/Accession: A55933  
J/Saigai, R.; Li, J.L.; Lo, S.H.; Brunkhorst, B.; Kansae, G.S.; Sobhany, E.S.; Sun, Y.;  
J. Biol. Chem. 270, 5039-5047, 1995  
A/Title: Molecular cloning of human paxillin, a focal adhesion protein phosphorylated by  
A/Reference number: A55933, PMID:7534286  
A/Accession: A55933  
A/Molecule type: mRNA  
A/Residues: 1-557 <SAL>  
A/Cross-references: UNIPROT:P49023; UNIPARC:UPI0000280A7; GB:U14588; NID:G704347; PIDN:  
C/Genetics:  
A/Gene: GDB:PXN  
A/Cross-references: GDB:702105  
A/Map position: 12q24-12q24  
C/Keywords: cell adhesion; cytoskeleton; peroxisome; phosphoprotein; zinc finger  
F/46-55/Region: proline-rich  
F/324-374/Domain: LIM metal-binding repeat homology <LM1>  
F/388-433/Domain: LIM metal-binding repeat homology <LM2>  
F/444-492/Domain: LIM metal-binding repeat homology <LM3>  
F/501-551/Domain: LIM metal-binding repeat homology <LM4>  
F/31,116,181/Binding site: phosphate (Tyr) (covalent) #status predicted

```

Query Match 8.8% Score 73. DB 2. Length 557.
Best Local Similarity 20.7%: Pred. No. 26.
Matches 19. Conservative 18. Mismatches 29. Indels 26. Gaps 3

OY      14 QLTGLQTTIHDIIEECYCKQOOLIREVYDPAFPLDCLVYRDNPNVAVXDKCLFYSKI 73
DB      334 QVAVTMGKTWPEHFVCTHCEIISNPF-----RDGGPYCEKD-----YNNLF 379

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QY      74 SEIRHYCYSVGTLEQYNKRLCDLLIRCN 105
          ||      ||:|:::
Db      380 SPRCYC-----NGPILDKVVTALD 399

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RESULT 76  
B55933  
paxillin - chicken  
C.Species: Gallus gallus (chicken)  
C.Date: 23-Mar-1995 #sequence\_revision 05-Apr-1995 #ext\_change 09-Jul-2004  
C.Accession: B55933  
R.Saiga, R.; Li, J.L.; Lo, S.H.; Brunkhorst, B.; Karsae, G.S.; Sobhany, E.S.; Sun, Y.; I  
J. Biol. Chem. 270, 5039-5047, 1995  
A.Title: Molecular cloning of human paxillin, a focal adhesion protein phosphorylated by  
A.Reference number: A55933; MUID:95197488; PMID:7534286  
A.Accession: B55933  
A.Molecule type: mRNA  
A.Retadues: 1-559 <SAL>  
A.Cross-References: UNIPROT:P49024; UNIPARC:UPI0000131378; GB:U14589; NID:9704349; PIDN:4  
C.Keywords: cell adhesion; cytoskeleton; phosphoprotein; zinc finger  
F:46-55/Region: LIM metal-binding repeat rich  
F:326-376/Domain: LIM metal-binding repeat homology <LIM1>  
F:385-435/Domain: LIM metal-binding repeat homology <LIM2>  
F:444-494/Domain: LIM metal-binding repeat homology <LIM3>  
F:503-553/Domain: LIM metal-binding repeat homology <LIM4>  
F:31,118/Binding site: lime phosphate (Tyr) (covalent) #status predicted

	Query Match	8.8%	Score 73	DB 2	Length 559;
	Best Local Similarity	20.7%	Pred. No. 27;		
	Matches	19; Conservative	18; Mismatches	29; Indels	26; Gaps
QY	14 QLCFSLQTTHDIILICVCYCCKOQLAREVDAPFDLCTVADGNGPYAVXDKDCKREYSKI	73			
	:::::				
Dd	336 QVTVMKGTMBEHEHCVTHCDEISKRNF-----RDGPCEKD--YHNLF	381			
QY	74 SEVRHYCYSVYGTTLEQQNKPLCDLLRCIN	105			
	:::::				
Dd	382 SPCRYC-----NGLIRKVATLD	401			

RESULT 77  
 T01171  
 G1/S transition control protein Rb1 - maize  
 N:Alternative names: retinoblastoma susceptibility protein Rb1; retinoblastoma-related prot  
 C:Species: Zea mays (maize)  
 C:Date: 12-Feb-1999 #sequence \_revision 12-Feb-1999 #text\_change 09-Jul-2004  
 C:Accession: T01171; S72272  
 R:Arch. R.A.; Duffee, T.; Miller, A.B.; Taranto, P.; Hanley-Bowdoin, L.; Zambryski, P.C.;  
 Mol. Cell. Biol. 17, 5077-5086, 1997  
 A:Title: RRB1 and RRB2 encode maize retinoblastoma-related proteins that interact with a  
 A:Reference number: Z09601; MUID:9741586; PMID:9271385  
 A:Accession: T01171  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-866 <ACH>  
 A:Cross-references: UNIPROT:022344; UNIPARC:UPI00000043DEF; EMBL:AF007793; NID:G2352794; F  
 R:Xie, Q.; Sanz-Burgos, A.P.; Hannon, G.J.; Gutierrez, C.  
 EMOB J. 15, 4900-4908, 1996  
 A:Title: Plant cells contain a novel member of the retinoblastoma family of growth regula  
 A:Reference number: S72272; MUID:97045098; PMID:8890163  
 A:Accession: S72272  
 A:Molecule type: mRNA  
 A:Residues: 184-866 <XIE>  
 A:Cross-references: UNIPARC:UPI0000002EEEB; EMBL:X89823; NID:G1617473; PIDN:CA67422.1; P  
 C:Genetics:  
 A:Gene: RRB1; Rb1  
 C:Function:  
 A:Description: cell cycle control; probably controls G1/S phase transition in plants  
 C:Superfamily: retinoblastoma-associated protein  
 C:Keywords: cell cycle control

Matches 34; Conservative 22; Mismatches 49; Indels 41; Gaps 7;  
Qy 4 DPGRPRKLPOLCTELQTHIDILLECVCYCKQ-----LLRREYV-----DAFRLDLCIV 54  
Db 526 DDNADPSPKPSKCSBSRATVVERNLQTPPKQSHWSTSLAKCHPLQSTPASC--- 582  
Qy 55 RDGNPVAVXDKLCKL-----FYSKISE-----YRHYC-----YSVYGTTLSEQ- 91  
Db 583 ---NPVGNEKCAVDVTHIIFFSKILKLAIRIRNLCEKRVQCEQTERVYVNFKQLLEQOT 639  
Qy 92 ---YKPLCDLLIRLCINXQKPLCPBE 114  
Db 640 TLFPRRHIDQLILCLCYGAVKVCQLE 665

RESULT 78  
G82108  
conserved hypothetical protein VC2176 [imported] - Vibrio cholerae (strain N16961 serogroup C)  
C:Species: Vibrio cholerae  
C>Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004  
C:Accession: G82108  
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardon, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, F. I.; R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.  
Nature 406, 477-483, 2000  
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.  
A:Reference number: A82035; MUID:20406633; PMID:10952301  
A:Accession: G82108  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-270 <HEI>  
A:Cross-references: UNIPROT:Q9KQ28; UNIPARC:UPI00001387DF; GB:AE004289; GB:AE003852; NID A:Experimental source: serogroup O1, strain N16961; biotype El Tor  
C:Genetics:  
A:Gene: VC2176  
A:Map position: 1  
Query Match 8.7%; Score 72; DB 2; Length 270;  
Best Local Similarity 27.5%; Pred. No. 16;  
Matches 22; Conservative 13; Mismatches 29; Indels 16; Gaps 3;  
Qy 34 KQQLLRREYVDPAPR--DLCTVARDGNPYAVXDKLCKFY-----KISYRHYCYSVYG 85  
Db 188 KSALLREERYTLARCTDLALTFVDPDDYIRDRGFYQQLQCHQIAISDYQF----- 241  
Qy 86 TTLEQYVXKPLCDLLIRLCIN 105  
Db 242 --IEHCPNDPAEELKTOVN 259

RESULT 79  
T21820  
hypothetical protein F35H8.3 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T21820  
R:Berks, M.  
submitted to the EMBL Data Library, August 1994  
A:Reference number: Z19475  
A:Accession: T21820  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-422 <WIL>  
A:Cross-references: UNIPROT:Q20082; UNIPARC:UPI000007866E; EMBL:Z36752; PIDN:CAA85325.1;  
A:Experimental source: clone F35H8  
C:Genetics:  
A:Gene: CESP:F35H8.3  
A:Map position: 2  
A:Introns: 24/1; 52/2; 98/1; 191/3; 274/3; 368/2  
Query Match 8.7%; Score 72; DB 2; Length 422;  
Best Local Similarity 23.6%; Pred. No. 25;  
Matches 29; Conservative 13; Mismatches 43; Indels 38; Gaps 7;

Qy 27 ILLECVCYKQQLLRREYVDFAPRLDCTVYRDGNPYAVXDKLCKFYKISYRHYCYSVYGT 86  
Db 170 LYRCLNCKTYFNGKNEVQ---RHIGVHGADARPRCNCGRFANKTSMTH----- 218  
Qy 87 TLEQYVXKPL--CDLLIRLCINXQKPLCP-----EEKQRLDKQRFHNI RGRWTRGMS 138  
Db 219 LKDHSLKLPMSCD-----YCPRIFSKLESXTRH---HKHGFTR---STCOT 259  
Qy 139 CCR 141  
Db 260 CWR 262

RESULT 80  
H86477  
protein F1504.19 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C>Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C:Accession: H86477  
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federapfel, N.A.; Kaul, S.; White, O.; Alonso, Chiu, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Ansen, N.F.; Hughes, B.; Huizart, L.  
Nature 408, 816-820, 2000  
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maltli, R.; Marzall, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salberg, S.L.; Schwartz, J.R.; Shinn, P.; Southerick, A.M.; Sun, H.; Tallon, I. ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: A86141; MUID:21016719; PMID:11130712  
A:Accession: H86477  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-565 <STO>  
A:Cross-references: UNIPROT:Q9LQ66; UNIPARC:UPI00000A7592; GB:AE005172; NID:9878343; PII A:Genetics:  
A:Gene: F1504.19  
A:Map position: 1  
Query Match 8.6%; Score 71.5; DB 2; Length 565;  
Best Local Similarity 33.9%; Pred. No. 37;  
Matches 20; Conservative 6; Mismatches 26; Indels 7; Gaps 3;  
Qy 83 VYGTLEQYVXKPLCDLLIRLCINXQKPLCPBEKQRLDKQRFHNI-RGRWTRGMSCC 140  
Db 217 VYSGVLEBSSTSVYCAL---CID---DYCWEKRIILPCGHKHYAVICIDSLGCRSFC 269

RESULT 81  
T11850  
C:Species: Synechococcus sp. (PCC 7942)  
A:Variety: PCC 7942  
C>Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004  
C:Accession: T11850  
R:Bird, A.J.; Turner-Cavet, J.S.; Lakey, J.H.; Robinson, N.J.  
J. Biol. Chem. 273, 21246-21252, 1998  
A:Title: A carboxyl-terminal Cys2/His2-type zinc-finger motif in DNA primase influences D:  
A:Reference number: Z17359; MUID:98362004; PMID:9694883  
A:Accession: T11850  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-616 <BR>  
A:Cross-references: UNIPROT:P74893; UNIPARC:UPI00001321F0; EMBL:X94247  
C:Genetics:  
A:Gene: dnaG  
A:Function:  
A:Description: interacts with DNA to synthesize the primer RNA that initiates DNA replic  
C:Superfamily: DNA primase  
C:Keywords: DNA replication, nucleotidyltransferase  
Query Match 8.6%; Score 71.5; DB 2; Length 616;

Best Local Similarity 22.3%; Pred. No. 40;  
Matches 31; Conservative 27; Mismatches 46; Indels 35; Gaps 8;

Qy 7 ERPRKLPQLCTEL--QTTHIDILCEVCYKQQLLRREYVFAFRDLCTVYKDGNPVAVXD 64  
D 2 DTRRLHETIAAVERADIYDISE-----QVVLKKGKQFV--GLCPFHDDKSPSTVS 54  
Qy 65 KCLKFSKISBYRHYCS--VYGTTL-----EQYNNKPLCDLL-----IRCIYQKP 109  
D 55 PAQKPY-----YCFSCGAGNPRIKFLMELKQSFSEVVLDAKRYQVPRFLVEVQO- 105  
Qy 110 LCPKPKRHLDKKQRFNFI 128  
D 106 --HQLQRQLSRRLRYEV 122

# RESULT 82

A23689  
limulus clotting enzyme (EC 3.4.21.86) precursor - horseshoe crab (Tachyples tridentatus)

C/Species: Tachyples tridentatus  
C/Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C/Accession: A23689

R/Mita, T.; Hashimoto, R.; Miyata, T.; Nishimura, H.; Toh, Y.; Iwanaga, S.  
J. Biol. Chem. 265, 22426-22433, 1990

A/Title: Proclotting enzyme from horseshoe crab hemocytes. cDNA cloning, disulfide locat  
A/Reference number: A23689; MUID:91093088; PMID:2266134

A/Accession: A23689

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-375 <MUT>

A/Cross-references: UNIPROT:P21902; UNIPARC:UPI00001313DC; GB:M58366; NID:g161657; PIDN:

C/Superfamily: serine proteinase esterase; trypsin homology

C/Keywords: hydrolase; serine proteinase

P/1-21/Domain: signal sequence #status predicted <SIG>

F/128-370/Domain: trypsin homology <TRY>

F/172,228,326/Active site: His, Asp, Ser #status predicted

Query Match 8.6%; Score 71; DB 1; Length 375;

Best Local Similarity 23.7%; Pred. No. 28;

Matches 46; Conservative 19; Mismatches 69; Indels 60; Gaps 9;

Qy 5 PQRRRLPQLCTELQTHIDII-----LQVYKQQLR-----RE 41  
D 107 PKQPLPPLPVCGIHNHTTRIRIGGRAPIGAMPWMAVYIKQGISVOCGALVTNRH 166  
Qy 42 VYDFAPRDLCTVYKDG-----NRYAVXDKLKYKISSEYRHYCYSYVG 85  
D 167 VITASH---CVVNSAGTDWMPADYFSVRLGSHNLYSTDDSNPIDPAVTSVKGHEHYLA 223  
Qy 86 TTLEQQYNNKPLCDLLIRCIYQK-----KPLC--PEEKQRLDKKQRFNIRGRWTCRCM 137  
D 224 TYLN-----DIAITLNDVTFTDRIRICLPYRLKRYDDLAMKRPFTTG-W-GTTA 273  
Qy 138 SCRRSRTRETOI 151  
D 274 FNGBSSAVLRVQL 287

# RESULT 83

T40217

hypothetical protein SPBC31P10.14c - fission yeast (Schizosaccharomyces pombe)

C/Species: Schizosaccharomyces pombe

C/Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004

C/Accession: T40217

R/Mood, V.; Rajandream, M.A.; Barrell, B.G.; Pohl, T.

submitted to the EMBL Data Library, August 1997

A/Reference number: Z21913

A/Accession: T40217

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-1630 <MOO>

A/Cross-references: UNIPROT:P87315; UNIPARC:UPI000006956C; EMBL:297204; PIDN:CA10090.1;  
A/Experimental source: strain 972h-; cosmid c31P10

C/Genetics:  
A/Gene: SPBC31P10.14c  
A/Map position: 2

Query Match 8.6%; Score 71; DB 2; Length 1630;  
Best Local Similarity 22.8%; Pred. No. 1,1e+02;  
Matches 39; Conservative 24; Mismatches 46; Indels 62; Gaps 10;

Qy 2 FQDPRKRL-----DQLCTELQTHIDILCEVCYKQQLLRREYV 43  
D 486 FVESMLRPRLEPPFLQCGCKGFKKKFTTICRISTLHELV-----KASIQTEVF 539  
Qy 44 DPAFRDLCTVYRQGNPFAVADKCLKFS-----KISEYHYCYSVYGTTLQOYNNKPLC 97  
D 540 NIS-QSLFELFLDYFLA-----LKSSNDQKDDNSEI-----PTESLEYK- 581  
Qy 98 DLIRCIYQK-----KPLCPKPKRHLDKKQRF--HNIRGRWTCRCMS 138  
D 582 ---LRCLRWKSLTEQVVELQPSCKSSQRLIIRNSARMLRLRLTG-CSS 628

# RESULT 84

D87749  
protein unc-73b (imported) - Caenorhabditis elegans

C/Species: Caenorhabditis elegans  
C/Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004  
C/Accession: D87749

R/anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A/Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog.

A/Reference number: A75000; MUID:99069613; PMID:9851916

A/Note: see webistes genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C\_eleg

A/Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and

A/Accession: D87749

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-1638 <STO>

A/Cross-references: UNIPROT:O61528; UNIPARC:UPI000002A21C; GB:chr\_I; PIDN:NACT1109.1; PI

A/Note: F55C7.7b

A/Genetics:

A/Map position: 1

Query Match 8.6%; Score 71; DB 2; Length 1638;

Best Local Similarity 24.2%; Pred. No. 1.2e+02;

Matches 40; Conservative 25; Mismatches 52; Indels 48; Gaps 11;

Qy 34 KQQLR-----REVYD---FAFRDLCTVYKDG---AVXDKLKYF---- 70  
D 872 KQELRAFRDAVQHKLEPYDAFVIRFRELMEKNRLANRDEVYHNEALQAKYCRLANLCE 931  
Qy 71 --SKISEYRHYCYSVYGT-----LEQYNNKPLCDLLIRCIYQK-----QKPLCPKPK 116  
D 932 DRNKLKSAHGCKYTYTAVLPILNQLSESYHSYTVDWKAGCSTSDADRAAVADLLS 991  
Qy 117 RHLDKQRF-----HNIRG-----RWTGRMSSCRRSRTRETOI 151  
D 992 KHMVYKRFEGKGYALRNQDFLLRYIRR--STVQSERKKEHETKI 1035

# RESULT 85

T42739

guanine nucleotide exchange factor unc-73a - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 09-Jul-2004

C/Accession: T42739; T42740; T34430; T34426

R/Steven, R.; Kubisek, T.J.; Zheng, H.; Kulikarni, S.; Mancillas, J.; Ruiz Morales, A.;

Cell 92, 785-795, 1998

A/Title: UNC-73 activates the Rac GTPase and is required for cell and growth cone migrati

A/Reference number: Z22256; MUID:9818103; PMID:9529254

A/Accession: T42739

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A:Residues: 1-2488 <STE>  
A:Cross-references: UNIPROT:O61528; UNIPARC:UPI00000611F8; EMBL:AF048834; NID:G2944395;  
A:Accession: T342740  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-1634,'ON',1637,'E' <ST2>  
A:Cross-references: UNIPARC:UPI000002A21C; EMBL:AF048835; NID:G2944397; PIDN:AACT12932.1;  
R:Du, Z.; Le, T.  
submitted to the EMBL Data Library, November 1996  
A:Description: The sequence of C. elegans coamid F55C7.  
A:Reference number: 221524  
A:Accession: T34427  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-2488 <DU2>  
A:Cross-references: UNIPARC:UPI00000611F8; EMBL:U80436; PIDN:AACT1108.1; GSPDB:GN00019;  
A:Experimental source: strain Bristol N2; clone F55C7  
A:Accession: T34430  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-1634,'ON',1637,'E' <DU2>  
A:Cross-references: UNIPARC:UPI000002A21C; EMBL:U80436; PIDN:AACT1109.1; GSPDB:GN00019;  
A:Experimental source: strain Bristol N2; clone F55C7  
A:Accession: T34426  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 'MWIKCFT',1568,'LRK',1572-2488 <DU3>  
A:Cross-references: UNIPARC:UPI000002A21D; EMBL:U80436; PIDN:AACT1110.1; GSPDB:GN00019;  
A:Experimental source: strain Bristol N2; clone F55C7  
C:Genetics:  
A:Gene: unc-73; F55C7.7a; unc-73; F55C7.7b; CESP:F55C7.7c  
A:Map position: 1  
A:Insertions: 7/3; 64/2; 95/3; 230/3; 265/2; 335/3; 360/3; 488/3; 569/1; 695/1; 1028/2; 106  
19/3; 2262/2; 2331/1; 2351/3; 2396/1; 2431/1  
Query Match 8.6%; Score 71; DB 2; Length 2488;  
Best Local Similarity 24.2%; Pred. No. 1.7e+02;  
Matches 40; Conservative 25; Mismatches 52; Indels 48; Gaps 11;  
34 KOQLLR-----REYVD---FAFRDLC---IVYDDGNPY---AXXDCCLKY---- 70  
Db 872 KOEELRAFRADVAOHKLKEPYDAFVIRFRELLENRLANDEVVYHNEALQAKYCRIMNICE 931  
Qy 71 --SKISEYRHVCYSVYGT-----LEQYNNKP-LCDLLIRCIKX----QKPLCPBEKQ 116  
Db 932 DRNKLKSAHGCYKTYERAVLPIINQLESEYHSPVTVTCWAGCTSSIDADAAYVADLLS 991  
Qy 117 RHLDKQRF-----HNIRG-----RWGRCMSCCRSSRTRETOL 151  
Db 992 KHM DYKERFSGKCTYALRN GDFLRLYIRR-STVNSERKRHETKI 1035  
RESULT 86  
C97723  
aspartate-LRNA liase (EC 6.1.1.12) - Rickettsia conorii (strain Malish 7)  
C:Species: Rickettsia conorii  
C:Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 03-Jun-2002  
C:Accession: C97723  
R:Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Ro  
Science 293, 2093-2098, 2001  
A:Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.  
A:Reference number: A97700; MUID:21442074; PMID:11557893  
A:Accession: C97723  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-615 <KUR>  
A:Cross-references: UNIPARC:UPI00001648B8; GB:AE006914; PIDN:AAL02725.1; PID:G15619236;  
C:Genetics:  
A:Gene: asps  
C:Superfamily: lysine-trna ligase  
C:Keywords: ligase  
Query Match 8.5%; Score 70.5; DB 2; Length 615;

Best Local Similarity 27.3%; Pred. No. 50;  
Matches 39; Conservative 13; Mismatches 50; Indels 41; Gaps 8;  
Qy 16 CTEIQTTHIDILIECVCKQQLRREYVDFAFRLL-----CIVYDDGNPYAXXDCCLK 68  
Db 22 CNELO--ISDVEYEVKLSGWHRRRDHGNLFFDLRDHYGTQIVFTDQNFQMEDASRL 79  
Qy 69 FYSKISEYRHVCYSVYGTTL---EQYNNKP-----CDLLIRCIKXQK 108  
Db 80 RYBSV-----IVRGTVARS EDTLNNTLPCHVEVLAVFESVESAADLPVIVNTEK 132  
Qy 109 PLCPBE---KQRLHD-KKQRFHN 127  
Db 133 D-APEESRLKRFDFLRREKLN 154  
RESULT 87  
C86496  
hypotheical protein Cpi0041 [imported] - Chlamydia pneumoniae (strain J138)  
C:Species: Chlamydia pneumoniae  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C:Accession: C86496  
R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ioi  
Nucleic Acids Res. 28, 2311-2314, 2000  
A:Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.  
A:Reference number: A86491; MUID:20330349; PMID:10871162  
A:Accession: C86496  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-449 <STO>  
A:Cross-references: UNIPROT:Q9JS25; UNIPARC:UPI000002F9A; GB:BA000008; NID:G8978416; PII  
A:Experimental source: strain J138  
C:Genetics:  
A:Gene: Cpi0041  
Query Match 8.4%; Score 70; DB 2; Length 449;  
Best Local Similarity 27.6%; Pred. No. 42;  
Matches 27; Conservative 13; Mismatches 40; Indels 18; Gaps 6;  
Qy 40 REYVDFAFRDICTIYR-----DGNPYAVXDKCLKFYSEYRHVCYSVYGTLEQYNNK 94  
Db 210 REVVDPRFRITTCNIRKIAMTFDRHVSVAKTA---FEKAGALETC--VY-ESMRSEYRE 263  
Qy 95 PLCDLLIRCIKXQKPLCPBEKORHLDKQRFHNIRGRW 132  
Db 264 AFCE-----YEKAKLIGDEKSAVAE--QRQDIKRW 294  
RESULT 88  
D72127  
hypotheical protein - Chlamydia pneumoniae (strain CWL029)  
C:Species: Chlamydia pneumoniae  
C:Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004  
C:Accession: D72127  
R:Kaiman, S.; Mitchell, W.; Marathe, R.; Lamme, C.; Fan, J.; Olinger, L.; Grimwood, J.;  
Nature Genet. 21, 385-389, 1999  
A:Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.  
A:Reference number: A72000; MUID:99206606; PMID:10192388  
A:Accession: D72127  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-449 <ARN>  
A:Cross-references: UNIPROT:Q9Z9E0; UNIPARC:UPI00000C11BC; GB:AE001589; GB:AE001363; NID  
A:Experimental source: strain CWL029  
C:Genetics:  
A:Gene: Cpn0041  
Query Match 8.4%; Score 70; DB 2; Length 449;  
Best Local Similarity 27.6%; Pred. No. 42;  
Matches 27; Conservative 13; Mismatches 40; Indels 18; Gaps 6;  
Qy 40 REYVDFAFRDICTIYR-----DGNPYAVXDKCLKFYSEYRHVCYSVYGTLEQYNNK 94

Db 210 REVVDREPARTTCNRIKIAMTFEDRHVSVAKTA---PEKAFGALFTC--VY-ESMRESEYRE 263

Qy 95 PLCDLIRICINXOKPLCEPEKORHLDKORFNIRGM 132

Db 264 AFCE-----YEKALIDGDEKSAHAE--QRFOIDIKRM 294

## RESULT 89

hypotheical protein CP0733 (imported) - Chlamydia pneumoniae (strain AR39)

C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae

C:Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 09-Jul-2004

C:Accession: AB1544

R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; Deboy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000

A:Title: Genome sequences of Chlamydia trachomatis Mopn and Chlamydia pneumoniae AR39.

A:Reference number: AB1500; PMID:10684935

A:Accession: AB1544

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-449 <REA>

A:Cross-references: UNIPROT:Q9US25; UNIPARC:UPI00000D2P9A; GB:AE002232; GB:AE002161; NID

C:Genetics:

A:Gene: CP0733

Query Match

Best Local Similarity 8.4%; Score 70; DB 2; Length 449;

Matches 27; Conservative 13; Mismatches 40; Indels 18; Gaps 6;

Qy 40 REVVDREPARTTCNRIKIAMTFEDRHVSVAKTA---PEKAFGALFTC--VY-ESMRESEYRE 263

Db 210 REVVDREPARTTCNRIKIAMTFEDRHVSVAKTA---PEKAFGALFTC--VY-ESMRESEYRE 263

Qy 95 PLCDLIRICINXOKPLCEPEKORHLDKORFNIRGM 132

Db 264 AFCE-----YEKALIDGDEKSAHAE--QRFOIDIKRM 294

## RESULT 90

hypotheical protein K118.1c - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 05-Oct-2004

C:Accession: T23616

R:Wild, A.

submitted to the EMBL Data Library, March 1996

A:Reference number: Z19771

A:Accession: T23616

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-708 <WIL>

A:Cross-references: UNIPROT:O62305; UNIPARC:UPI000017A3A1; EMBL:Z70279; PIDN:CAA94244.1;

C:Genetics:

A:Gene: CESP:K118.1c

A:Map position: 4

A:Introns: 8/2; 78/2; 100/2; 124/3; 186/1; 217/3; 258/3; 286/3; 401/2; 501/1; 536/1; 574

Query Match

Best Local Similarity 8.4%; Score 70; DB 2; Length 708;

Matches 23; Conservative 23; Mismatches 36; Indels 24; Gaps 5;

Qy 9 PRKLPOLCTELQTIHDIIECVYCKQQLRREYVDFAFRDLG-----IVYEDG----- 57

Db 347 PQKPRMC-----VHPPTTHPYSPKSSKKKLFITLLFEVCHTSRSHLLDNTKNI 400

Qy 58 -NPAAVADCKLKFYSKISEYRHVCYSGVGTLEQYKPLVDLLIR 102

Db 401 YHPY---HC---FTNKMSYERAA PSSHSGSTTKKINAIADLVIR 440

## RESULT 91

conserved hypotheical protein TC0424 (imported) - Chlamydia muridarum (strain Nigg)

C:Species: Chlamydia muridarum, Chlamydia trachomatis Mopn

C:Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 09-Jul-2004

C:Accession: B81704

R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; Deboy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000

A:Title: Genome sequences of Chlamydia trachomatis Mopn and Chlamydia pneumoniae AR39.

A:Reference number: AB1500; PMID:10684935

A:Accession: B81704

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1436 <TET>

A:Cross-references: UNIPROT:Q9PKP1; UNIPARC:UPI0000057904; GB:AE002309; GB:AE002160; NID

A:Experimental source: strain Nigg (Mopn)

C:Genetics:

A:Gene: TC0424

Query Match

Best Local Similarity 8.4%; Score 70; DB 2; Length 1436;

Matches 40; Conservative 21; Mismatches 50; Indels 72; Gaps 9;

Qy 6 QERPKLPOLCTELQTIHDIIECVYCKQQLRREYVDFAFRDLGTVYRDG-NPY----- 60

Db 358 KDRIRSLAQ-----QKTLTALRLKLYC-----ETED-AMERICI-EDGISPIYODQ 402

Qy 61 -AVXDRCLK-----KPLCDLIRICINXOKPLCEPEKOR-HDKKORFNTI 128

Db 403 VRIYQKCLREBELDKTDEBLKPCDSLKIQSVCLFATSVSYLLEGRMGVSEKSIK 462

Qy 75 EYRHVCYSGVGTLEQYKPLCDLIRICINXOKPLCEPEKOR-HDKKORFNTI 128

Db 463 EIEETVRELGSITLQGLSGGITPLIDNVHKAIRGALSNELRSIOIQAHPERRFRL 522

Qy 129 RGR 131

Db 523 QAK 525

## RESULT 92

hypotheical protein C15H9.3 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004

C:Accession: T15519

R:Bentley, D.

submitted to the EMBL Data Library, April 1996

A:Description: The sequence of C. elegans cosmid C15H9.

A:Reference number: Z18364

A:Accession: T15519

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-314 <BEN>

A:Cross-references: UNIPROT:Q18029; UNIPARC:UPI000007A22F; EMBL:U56965; NID:g1945492; PII

A:Experimental source: strain Bristol N2; clone C15H9

C:Genetics:

A:Gene: CESP:C15H9.3

A:Map position: X

A:Introns: 76/1; 177/3; 210/3; 266/2

Query Match

Best Local Similarity 8.4%; Score 69.5; DB 2; Length 314;

Matches 26; Conservative 11; Mismatches 31; Indels 31; Gaps 4;

Qy 9 PRKLPOLCTELQTIHDIIECVYCKQQLRREYVDFAFRDLGTVYRDG-----P 59

Db 233 PRKTSRYSTELKLSINIIIVSMFLVOTLI-----YNICTLYEDNNLCFLFLIAP 283

Qy 60 YAAVADCKLKFYSKISEYRHVCYSGVGTLEQYKPLVDLLIR 102

Db 284 IFRGSKCL-----AYWVSGSALRNALVNLILIC 310

RESULT 93  
B84474  
hypothetical protein At2g06010 (imported) - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
C:Accession: B84474  
R:Lin, X.; Kaul, S.; Rounseley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Mofeit, K.S.; Cronin, L.A.; Shen, M.; Vankken, S.E.; Unayam, L.; Tallon, L.;  
euser, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
Nature 402, 761-768, 1999  
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A:Reference number: A84420; MUID:20083487; PMID:10617197  
A:Accession: B84474  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-298 <STD>  
A:Cross-references: UNIPROT:Q8VY85; UNIPARC:UPI000017A73D; GB:AE002093; NID:g4388730; PI  
C:Genetics:  
A:Gene: At2g06010  
A:Map position: 2

Query Match 8.3%; Score 69; DB 2; Length 298;  
Best Local Similarity 30.9%; Pred. No. 35;  
Matches 29; Conservative 7; Mismatches 28; Indels 30; Gaps 6;  
Qy 86 TTLEQYKPKCDLLIRCIKXKPKCEK-----QRHDKK---QRF----- 125  
Db 109 STNNQVNEPTNDYHAKLV--LKPICPERKWKFIYEPHGEVRLSKIPVTRFLNIQVG 166  
Qy 126 --HNIRGR--WTGRCSGCCRS---SRTRETQL 151  
Db 167 VGHNFQMAIGMKWKLTSLGSDGVSRIRNKTTL 200

RESULT 94  
T33884  
hypothetical protein H14E04.5 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 31-Dec-2004  
C:Accession: T33884  
R:Becker, M.; Wamaley, P.; Twyman, B.; Beck, C.; Bradshaw, H.  
submitted to the EMBL Data Library, February 1999  
A:Description: The sequence of C. elegans cosmid H14E04.  
A:Reference number: Z21431  
A:Accession: T33884  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-327 <BEC>  
A:Cross-references: UNIPROT:Q9TYP2; UNIPARC:UPI000007A0C9; EMBL:AF125448; PIDD:AAD12812.  
A:Experimental source: strain Bristol N2; clone H14E04  
C:Genetics:  
A:Gene: CESP:H14E04.5  
A:Map position: 4  
A:Initrons: 11/2; 47/1; 84/2; 125/1; 167/2; 181/1; 215/1; 275/3  
C:Superfamily: cyclin, C/H/G types

Query Match 8.3%; Score 69; DB 2; Length 327;  
Best Local Similarity 23.7%; Pred. No. 38;  
Matches 28; Conservative 15; Mismatches 35; Indels 40; Gaps 6;  
Qy 31 VYCKQQLRRVYDFAPRDLCTIVYDGNPYAVXDCLRFYSKISEYRYCVSV----- 83  
Db 76 IYFKRFYIRQ-----SFRDKC-----PFLVASTALFLACKVER--HTTISVSSFLKNT 121  
Qy 84 -----YGTLEQYKPK-----LCDLLIRCI---NXQKPLCEBKORHLDKK 122  
Db 122 AIVLPKRGVTFETSTKGVVYDSEFIVLEHLDCLVHHASRWMCPPPPRRIFDK 179

RESULT 95  
A71928

cag island protein - Helicobacter pylori (strain J99)  
C:Species: Helicobacter pylori  
A:Variety: strain J99  
C:Date: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change 09-Jul-2004  
C:Accession: A71928  
R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;  
Ives, C.; Gibson, R.; Medberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;  
Nature 397, 176-180, 1999  
A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric path  
A:Reference number: A71800; MUID:99120557; PMID:9923682  
A:Accession: A71928  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1819 <ARN>  
A:Cross-references: UNIPROT:Q9ZLV0; UNIPARC:UPI00000D3637; GB:AE001481; GB:AE001439; NID  
A:Experimental source: strain J99  
C:Genetics:  
A:Gene: orf13/14

Query Match 8.3%; Score 69; DB 2; Length 1819;  
Best Local Similarity 23.2%; Pred. No. 2e+02;  
Matches 33; Conservative 13; Mismatches 48; Indels 48; Gaps 5;  
Qy 8 RPRKLPLCTELQTTIHDIIECYCKQQLRREVDPAFRDLCTIVYDGNPYAVXDCL 67  
Db 1252 RNEKEKOECEKLTLPARKFLE---KQ---RQCKKAIKD-CLKRADPDRAAIMKCL 1302  
Qy 68 KFYs-----KISEYRYHCVSVYGTLEQYKPKCDLLIRCI 104  
Db 1303 DGLSDEKLYLQAREKAVLDCLTKARTDBEKKCONLSDLIQETQNK----- 1353  
Qy 105 NXQKPLCEBKORHLDKKORFH 126  
Db 1354 -----AQNKQQLSTERLH 1368

RESULT 96  
S56101  
outer dense fiber protein - bovine  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 10-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 09-Jul-2004  
C:Accession: S56101  
R:Kim, Y.; Adham, I.W.; Haack, T.; Kremling, H.; Engel, W.  
Biol. Chem. Hoppe-Seyler 376, 431-435, 1995  
A:Title: Molecular cloning and characterization of the bovine and porcine outer dense fil  
A:Reference number: S56100; MUID:96062278; PMID:7576240  
A:Accession: S56101  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-262 <KIM>  
A:Cross-references: UNIPROT:Q29438; UNIPARC:UPI0000130BD1; GB:X69514; NID:g1165005; PIDD

Query Match 8.3%; Score 68.5; DB 2; Length 262;  
Best Local Similarity 26.7%; Pred. No. 34;  
Matches 32; Conservative 14; Mismatches 37; Indels 37; Gaps 7;  
Qy 40 REYVDFAPRDLCTIVYDGNPYAVXD-----KCLRFYSKISEYRYHCVSVYGTLEQYK 94  
Db 26 RCIDELSARCLCDLYM--HPYCCDLHPYCL-----CYS-----KGRSVC 65  
Qy 95 PLCDLLIRCIKXKPKCEBKORHL-----DKQRFHNTIGRWTCRM--SCCRSS 143  
Db 66 GLCDLYPCCLCDVLYCLRSLRLERKAIKRAIEDERELAKLR-RFTNRILASSCCSSN 124

RESULT 97  
GQHTU1  
tumor necrosis factor receptor 1 precursor (validated) - human  
N:Alternate names: p55 tumor necrosis factor receptor; TNF receptor type 1  
N:Contains: tumor necrosis factor alpha inhibitor; tumor necrosis factor binding protein  
C:Species: Homo sapiens (man)  
C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 09-Jul-2004  
C:Accession: A38208; A34899; A34900; A36555; A36555; A38281; S12057; J10758; A60231; A38

R:Fuchs, P.; Strehl, S.; Dworzak, M.; Himmler, A.; Ambros, P.F.  
 Genomics 13, 219-224, 1992  
 A:Title: Structure of the human TNF receptor 1 (p60) gene (TNFRP1) and localization to ch  
 A:Reference number: A38208; MUID:92250049; PMID:1315717  
 A:Accession: A38208  
 A:Molecule type: DNA  
 A:Residues: 1-455 <FUC>  
 A:Cross-references: UNIPARC:UPI000002CE11; GB:M75864; GB:M75865; GB:M75866; GB:M75867  
 R:Loetscher, H.; Pan, Y.C.E.; Lahm, H.W.; Gentz, R.; Brockhaus, M.; Tachibana, H.; Lesslauer  
 Cell 61, 351-359, 1990  
 A:Title: Molecular cloning and expression of the human 55 kd tumor necrosis factor recep  
 A:Reference number: A34899; MUID:90235284; PMID:2158862  
 A:Accession: A34899  
 A:Molecule type: mRNA  
 A:Residues: 1-455 <LOE>  
 A:Cross-references: UNIPARC:UPI000002CE11; GB:M58286; GB:M33480; NID:G339753; PIDN:AAA36  
 A:Experimental source: placenta  
 R:Schall, T.J.; Lewis, M.; Koller, K.J.; Lee, A.; Rice, G.C.; Wong, G.H.W.; Gatanaga, T.  
 Cell 61, 361-370, 1990  
 A:Title: Molecular cloning and expression of a receptor for human tumor necrosis factor.  
 A:Reference number: A34900; MUID:90235285; PMID:2158863  
 A:Accession: A34900  
 A:Molecule type: mRNA  
 A:Residues: 1-455 <SCH>  
 A:Cross-references: UNIPARC:UPI000002CE11; GB:M33294; NID:G339744; PIDN:AAA03210.1; PID  
 R:Himmeler, A.; Maurer-Fogy, I.; Krenke, M.; Scheutich, P.; Flitzmaier, K.; Lant, M.;  
 DNA Cell Biol. 9, 705-715, 1990  
 A:Title: Molecular cloning and expression of human and rat tumor necrosis factor recept  
 A:Reference number: A36555; MUID:91090841; PMID:1702293  
 A:Accession: A36555  
 A:Molecule type: mRNA  
 A:Residues: 1-455 <HIM>  
 A:Cross-references: UNIPARC:UPI000002CE11; GB:M63121; NID:G339755; PIDN:AAA36754.1; PID  
 A:Accession: C36555  
 A:Molecule type: protein  
 A:Residues: 30-38;41-53, 'X',55-79, 'XX',82-94, 'NK', 'X',100-104;107-128;162-167, 'X',169-2  
 A:Cross-references: UNIPARC:UPI000002D399; UNIPARC:UPI000002D836; UNIPARC:UPI00001736DE;  
 A:Note: the purified protein, called tumor necrosis factor binding protein, is a soluble  
 R:Gray, P.W.; Barrett, K.; Chantry, D.; Turner, M.; Feldmann, M.  
 Proc. Natl. Acad. Sci. U.S.A. 87, 7380-7384, 1990  
 A:Title: Cloning of human tumor necrosis factor (TNF) receptor cDNA and expression of re  
 A:Reference number: A38281; MUID:9101509; PMID:2170974  
 A:Accession: A38281  
 A:Molecule type: mRNA  
 A:Residues: 1-455 <GRA>  
 A:Cross-references: UNIPARC:UPI000002CE11; GB:M37764  
 A:Note: the authors translated the codon TGG for residue 371 as Thr, AAG for residue 372  
 R:Nophar, Y.; Kemper, O.; Brakubusch, C.; Engelmann, H.; Zwang, R.; Aderka, D.; Holtmann  
 EMBO J. 9, 3269-3278, 1990  
 A:Title: Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA for the TNF  
 le form of the receptor.  
 A:Reference number: S12057; MUID:91006021; PMID:1638610  
 A:Accession: S12057  
 A:Molecule type: mRNA  
 A:Residues: 1-455 <NOP>  
 A:Cross-references: UNIPARC:UPI000002CE11; EMBL:X55313; NID:G37223; PIDN:CAA39021.1; PID  
 A:Note: parts of soluble TNF binding protein 1, including its amino and carboxyl ends, w  
 R:Kemper, O.; Wallach, D.  
 Gene 134, 209-216, 1993  
 A:Title: Cloning and partial characterization of the promoter for the human p55 tumor ne  
 A:Reference number: J70758; MUID:94085779; PMID:8262379  
 A:Accession: J70758  
 A:Molecule type: DNA  
 A:Residues: 1-13 <KEM>  
 A:Cross-references: UNIPARC:UPI0000155CFB  
 R:Secklinger, P.; Vey, B.; Turcatti, G.; Wingfield, P.; Dayer, J.M.  
 Eur. J. Immunol. 20, 1167-1174, 1990  
 A:Title: Tumor necrosis factor inhibitor: purification, NH-2-terminal amino acid sequenc  
 A:Reference number: A60231; MUID:90292116; PMID:2113477  
 A:Accession: A60231  
 A:Molecule type: protein  
 A:Residues: 41-43, 'X',45-53, 'X',55-57 <SEC>

A:Cross-references: UNIPARC:UPI0000072FDB  
 R:Gatanaga, T.; Huang, C.; Kohr, W.; Capuccini, F.; Lucchi III, J.A.; Jeffes, E.W.B.; Ler  
 Proc. Natl. Acad. Sci. U.S.A. 87, 8761-8784, 1990  
 A:Title: Purification and characterization of an inhibitor (soluble tumor necrosis facto  
 clients.  
 A:Reference number: A38258; MUID:91062364; PMID:2174164  
 A:Accession: A38258  
 A:Molecule type: protein  
 A:Residues: 41-60 <GAT>  
 A:Cross-references: UNIPARC:UPI00001736E1  
 A:Experimental source: cancer patient serum  
 R:Olsson, I.; Lantz, M.; Nilsson, E.; Peetre, C.; Thyseell, H.; Grubb, A.; Adolf, G.  
 Eur. J. Haematol. 42, 270-275, 1989  
 A:Title: Isolation and characterization of a tumor necrosis factor binding protein from  
 A:Reference number: A60594; MUID:89171156; PMID:2924890  
 A:Accession: A60594  
 A:Molecule type: protein  
 A:Residues: 41-43, 'X',45-53, 'V',55-57, 'XK',60 <OLS>  
 A:Cross-references: UNIPARC:UPI00001736E2  
 A:Experimental source: renal failure patient urine  
 R:Engelmann, H.; Novick, D.; Wallach, D.  
 J. Biol. Chem. 265, 1531-1536, 1990  
 A:Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence f  
 A:Reference number: A35010; MUID:90110215; PMID:2153136  
 A:Accession: A35010  
 A:Molecule type: protein  
 A:Residues: 41-45 <ENG>  
 A:Cross-references: UNIPARC:UPI00001736E3  
 A:Experimental source: normal urine  
 R:Kajihara, J.; Asada, A.; Kirihara, S.; Kato, K.  
 Biosci. Biotechnol. Biochem. 58, 2266-2268, 1994  
 A:Title: Amino acid sequence of natural tumor necrosis factor alpha inhibitor purified f  
 A:Reference number: J02404; MUID:95128033; PMID:7765720  
 A:Accession: J02404  
 A:Molecule type: protein  
 A:Residues: 41-53, 'X',55-144, 'X',146-150, 'X',152-186, 'X',188-201 <KAJ>  
 A:Cross-references: UNIPARC:UPI00001736E4  
 A:Experimental source: urine  
 C:Comment: This protein is one of two known receptors for both TNF-alpha (cachectin) and  
 C:Genetics:  
 A:Gene: GDB:TNFR1  
 A:Cross-references: GDB:125913; OMIM:191190  
 A:Map position: 12p13.2-12p13.2  
 A:Initons: 13/3; 65/1; 108/1; 158/1; 184/2; 209/1; 247/1; 256/3; 353/1  
 C:Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homolo  
 C:Keywords: duplication; glycoprotein; receptor; transmembrane protein  
 F:1-21/Domain: signal sequence #status predicted <SIG>  
 F:22-455/Product: tumor necrosis factor receptor 1 #status predicted <MAT>  
 F:30-211/Domain: extracellular #status predicted <EXT>  
 F:41-201/Product: TNF binding protein 1 (tumor necrosis factor alpha inhibitor) #status  
 F:44-82/Domain: NGF receptor repeat homology <NG1>  
 F:84-167/Domain: NGF receptor repeat homology <NG2>  
 F:167-167/Domain: NGF receptor repeat homology <NG3>  
 F:168-196/Domain: NGF receptor repeat homology <NG4>  
 F:212-234/Domain: transmembrane #status predicted <MEM>  
 F:235-455/Domain: intracellular #status predicted <INT>  
 F:54,145,151/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 8.3%; Score 68.5; DB 1; Length 455;  
 Best Local Similarity 25.0%; Pred. No. 58;  
 Matches 31; Conservative 18; Mismatches 46; Indels 29; Gaps 7;

QY	28	LECYCKQQLRREVDPAFRDLCIVRDGNPAVAVXKCLKFKFSKSEYRHYKCVYGT	87
DB	100	LSGSKCRKEMGOVEI-----SSCTVDRD-----TVGCKR-----NQHRY-----WSEN	139
QY	88	LEQGVNPLDLDILRCINXQKPLCEPEKORHLDDKQEFHNIIRGRWTRGSCSCGSRTR	147
DB	140	LPQCFN---CSL---CLNGTVHLSCKQKQNTVCTCAAGFLR---ENECVSCSKCKSL	190
QY	148	ETQD 151	
DB	191	CTKL 194	



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## OM protein - protein search, using sw model

Run on: May 27, 2006, 05:00:16 ; Search time 232.867 Seconds  
(without alignments)  
599.815 Million cell updates/sec

Title: US-10-530-253-13ED  
Perfect score: 830  
Sequence: 1 MFQDPERRRKLPLQCTELQ.....WTGRCMSCRRSSRTRETLQ 151

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : UniProt 7.2:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	826	99.5	151	2	Q77JCT_HPV16
2	826	99.5	151	2	Q89852_9PAP1
3	826	99.5	151	2	Q9WH13_HPV16
4	824	99.3	151	2	Q9WMP5_HPV16
5	823	99.2	151	2	Q77816_HPV16
6	823	99.2	151	2	Q89755_9PAP1
7	823	99.2	151	2	Q8BB20_HPV16
8	823	99.2	158	1	VE6_HPV16
9	823	99.2	158	2	Q547J2_HPV16
10	823	99.2	161	2	Q919C6_HPV16
11	821	98.9	151	2	Q8BB19_HPV16
12	821	98.9	158	2	Q4VRN5_HPV16
13	820	98.8	158	2	Q8ORP7_HPV16
14	820	98.8	158	2	Q8QRD8_HPV16
15	819	98.7	151	2	Q772J5_HPV16
16	819	98.7	151	2	Q89640_9PAP1
17	819	98.7	151	2	Q89648_HPV16
18	819	98.7	151	2	Q9W931_HPV16
19	819	98.7	158	2	Q2PJN9_HPV16
20	819	98.7	158	2	Q8QHT0_HPV16
21	818	98.6	151	2	Q80963_9PAP1
22	818	98.6	158	2	Q8QHP5_HPV16
23	817	98.4	151	2	Q8BS64_9PAP1
24	817	98.4	151	2	Q9W8C3_HPV16
25	817	98.4	151	2	Q919P4_HPV16
26	816	98.3	158	2	Q8QRP9_HPV16
27	816	98.3	158	2	Q8QRE0_HPV16
28	816	98.3	158	2	Q9QDH9_HPV16
29	815	98.2	151	2	Q89887_9PAP1
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32	814	98.1	158	2	Q9QDH3_HPV16	Q9QDH3 human papil
33	814	98.1	151	2	Q919B1_HPV16	Q919B1 human papil
34	813	98.0	158	2	Q8QRE1_HPV16	Q8QRE1 human papil
35	812	97.8	151	2	Q12335_HPV16	Q12335 human papil
36	811	97.7	151	2	Q9WMP4_HPV16	Q9WMP4 human papil
37	810	97.6	151	2	Q12336_HPV16	Q12336 human papil
38	809	97.5	158	2	Q9QDH7_HPV16	Q9QDH7 human papil
39	808	97.3	151	2	Q8BB21_HPV16	Q8BB21 human papil
40	808	97.3	151	2	Q9WMP2_HPV16	Q9WMP2 human papil
41	808	97.3	151	2	Q919A9_HPV16	Q919A9 human papil
42	806	97.1	151	2	Q76TS0_9PAP1	Q76TS0 human papil
43	806	97.1	151	2	Q80966_HPV16	Q80966 human papil
44	806	97.1	158	2	Q8JWU8_HPV16	Q8JWU8 human papil
45	804	96.9	151	2	Q77816_HPV16	Q77816 human papil
46	804	96.9	151	2	Q89708_9PAP1	Q89708 human papil
47	804	96.9	151	2	Q9WMP3_HPV16	Q9WMP3 human papil
48	804	96.9	158	2	Q8QHN0_HPV16	Q8QHN0 human papil
49	803	96.7	158	2	Q9QDH5_HPV16	Q9QDH5 human papil
50	781	94.1	143	2	Q919C4_HPV16	Q919C4 human papil
51	774	93.3	143	2	Q919B6_HPV16	Q919B6 human papil
52	754	90.8	138	2	Q919D2_HPV16	Q919D2 human papil
53	712	85.8	130	2	Q919C0_HPV16	Q919C0 human papil
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55	707	85.2	130	2	Q919B8_HPV16	Q919B8 human papil
56	707	85.2	130	2	Q919C8_HPV16	Q919C8 human papil
57	704	84.8	130	2	Q919B4_HPV16	Q919B4 human papil
58	702	84.6	130	2	Q919D0_HPV16	Q919D0 human papil
59	580	69.9	149	2	Q4TU99_HPV16	Q4TU99 human papil
60	580	69.9	149	2	Q84298_9PAP1	Q84298 human papil
61	578	69.6	149	1	VE6_HPV16	VE6_HPV16 human papil
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63	560	67.5	103	2	Q4TU64_HPV16	Q4TU64 human papil
64	532	64.1	99	2	Q919B2_HPV16	Q919B2 human papil
65	525	63.3	149	1	Q4TU61_HPV16	Q4TU61 human papil
66	523	63.0	149	1	VE6_HPV16	VE6_HPV16 human papil
67	523	63.0	149	2	Q4TU65_HPV16	Q4TU65 human papil
68	520	62.7	149	1	VE6_HPV16	VE6_HPV16 human papil
69	503	60.6	149	2	Q8QSE7_HPV16	Q8QSE7 human papil
70	502	60.5	149	2	Q919G6_HPV16	Q919G6 human papil
71	498	60.0	149	2	Q90723_HPV16	Q90723 human papil
72	497	59.9	149	2	Q4TU68_HPV16	Q4TU68 human papil
73	497	59.9	149	2	Q919G5_HPV16	Q919G5 human papil
74	496	59.8	149	1	VE6_HPV16	VE6_HPV16 human papil
75	496	59.8	149	2	Q547M1_HPV16	Q547M1 human papil
76	496	59.8	149	2	Q8QHO3_HPV16	Q8QHO3 human papil
77	495	59.6	91	2	Q80887_9PAP1	Q80887 human papil
78	492	59.3	148	2	Q4TU66_HPV16	Q4TU66 human papil
79	487	58.7	148	1	VE6_HPV16	VE6_HPV16 human papil
80	487	58.7	148	2	Q4TU64_HPV16	Q4TU64 human papil
81	487	58.7	148	2	Q4TU67_HPV16	Q4TU67 human papil
82	484	58.3	148	1	VE6_HPV16	VE6_HPV16 human papil
83	483	58.3	148	2	Q82005_HPV16	Q82005 human papil
84	481	58.0	90	2	Q80883_9PAP1	Q80883 human papil
85	481	58.0	90	2	Q80885_9PAP1	Q80885 human papil
86	476	57.3	90	2	Q80884_9PAP1	Q80884 human papil
87	468.5	56.4	158	1	VE6_HPV16	VE6_HPV16 human papil
88	468.5	56.4	158	1	VE6_HPV16	VE6_HPV16 human papil
89	468.5	56.4	158	2	Q2VJD5_HPV16	Q2VJD5 human papil
90	460	55.4	151	1	VE6_HPV16	VE6_HPV16 human papil
91	459.5	55.4	158	1	VE6_HPV16	VE6_HPV16 human papil
92	457	55.1	84	2	Q80882_9PAP1	Q80882 human papil
93	455.5	54.9	158	1	VE6_HPV16	VE6_HPV16 human papil
94	455.5	54.9	158	2	Q765Z7_HPV16	Q765Z7 human papil
95	451.5	54.4	158	1	VE6_HPV16	VE6_HPV16 human papil
96	451.5	54.4	158	2	Q7KYK8_HPV16	Q7KYK8 human papil
97	451.5	54.4	152	2	Q9UIZ9_9PAP1	Q9UIZ9 human papil
98	449.5	54.2	158	1	VE6_HPV16	VE6_HPV16 human papil
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100	449.5	54.1	151	2	Q994A0_HPV16	Q994A0 human papil

## ALIGNMENTS

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ID 073C7\_HPV16 PRELIMINARY; PRT; 151 AA.  
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DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.  
DT 05-JUL-2004, sequence version 1.  
DT 07-FEB-2006, entry version 12.  
DE Early transforming protein 16 variant (Transforming protein E6).  
OS Human papillomavirus type 16.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Alphapapillomavirus.  
NCBI\_Taxid=333760;  
RN NCBI\_Taxid=333760;  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Xinjiang;  
RA Ma Z., Qian D., Ma J., Lin R., Ming W., Zhong Z., Zhang Q., Zhang F.;  
RT "Cloning and Sequencing of HPV16 E6 gene from Cervical Carcinoma  
Biopsies in Xinjiang."  
RL Sheng Wu Hua Xue Yu Sheng Wu Wu Li Jin Zhan 0:0-0(2001).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=20112892; PubMed=10644829;  
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,  
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;  
RT "Analysis of human papillomavirus type 16 E6 variants in relation to  
p53 codon 72 polymorphism genotypes in cervical carcinogenesis."  
RL J. Gen. Virol. 81:317-325(2000).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=2224222; PubMed=12355268; DOI=10.1007/s00239-002-2344-Y;  
RA DeFillipis V.R., Ayala F.J., Villarreal L.P.;  
RT "Evidence of diversifying selection in human papillomavirus type 16 E6  
but not E7 oncogenes."  
RL J. Mol. Evol. 55:491-499(2002).  
RN [4]  
RP NUCLEOTIDE SEQUENCE.  
RA Cruz M.R., Cerqueira D.M., Camara G.N.L., Silva E.O., Carvalho L.G.S.,  
RA Martins C.R.F.;  
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP NUCLEOTIDE SEQUENCE.  
RA Cruz M.R., Martins C.R.F.;  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
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DR EMBL; AJ388057; CAB45106.1; -; Genomic DNA.  
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DR EMBL; AY089951; AAM11875.1; -; Genomic DNA.  
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DR GO; GO:0042025; C:host cell nucleus; IEA.  
DR InterPro; IPR001334; E6.  
DR Pfam; PF00518; E6; 1.  
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Best Local Similarity 98.7%; Pred. No. 2,4e-73;  
Matches 149; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
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AC 089852;  
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.  
DT 01-NOV-1996, sequence version 1.  
DT 07-FEB-2006, entry version 25.  
DE Early transforming protein E6.  
OS Human papillomavirus.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC unclassified Papillomaviridae.  
NCBI\_Taxid=10566;  
RN NCBI\_Taxid=10566;  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=96079021; PubMed=7494284;  
RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,  
RA Jenison S.A.;  
RT "Human papillomavirus type 16 variant lineages in United States  
populations characterized by nucleotide sequence analysis of the E6,  
L2, and L1 coding segments."  
RL J. Virol. 69:7743-7753(1995).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RA Farmer A.D.;  
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.  
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CC EMBL; U34134; AAA91681.1; -; Genomic DNA.  
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DR EMBL; U34133; AAA91680.1; -; Genomic DNA.  
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DR GO; GO:0003677; F:DNA binding; IEA.  
DR InterPro; IPR001334; E6.  
DR Pfam; PF00518; E6; 1.  
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DT 01-NOV-1999, sequence version 1.  
DT 07-FEB-2006, entry version 19.  
DE E6.  
OS Human papillomavirus type 16.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Alphapapillomavirus.  
NCBI\_Taxid=333760;  
RN NCBI\_Taxid=333760;  
RP NUCLEOTIDE SEQUENCE.

RA MEDLINE=99434235; PubMed=10502513; DOI=10.1006/viro.1999.9868;  
RA Flores E.R., Allen-Hoffmann B.L., Lee D., Sattler C.A., Lambert P.F.;  
RT "establishment of the human papillomavirus type 16 (HPV-16) life cycle  
in an immortalized human foreskin keratinocyte cell line.";  
RL Virology 262:344-354(1999).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=E-C109G;  
RX MEDLINE=22182962; PubMed=12195358; DOI=10.1086/342048;  
RA Chan P.K.S., Lam C.W., Cheng T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,  
RA Cheng J.L.K., Xu L.Y., Cheng A.F.;  
RT "human papillomavirus type 16 intracyclic variant infection and risk  
for cervical neoplasia in southern China.";  
RL J. Infect. Dis. 186:696-700(2002).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=QY16936E;  
RX PubMed=15890941; DOI=10.1128/JVI.79.11.7014-7023.2005;  
RA Chen Z., Terai M., Fu L., Herrero R., Desalle R., Burk R.D.;  
RT "diversifying selection in human papillomavirus type 16 lineages based  
on complete genome analyses.";  
RL J. Virol. 79:7014-7023(2005).  
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DR EMBL; AF125673; AAD33252.1; -; Genomic DNA.  
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DR EMBL; AY86580; AAV91652.1; -; Genomic DNA.  
DR GO; GO:0042025; C:host cell nucleus; IEA.  
DR GO; GO:0003677; F:DNA binding; IEA.  
DR InterPro; IPR001334; B6.  
DR Pfam; PF00518; B6; 1.  
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QY 121 KKORFNIRGRWGRGCMSCCRSSRTRETOL 151  
DB 128 KKORFNIRGRWGRGCMSCCRSSRTRETOL 158  
  
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DT 01-NOV-1999, integrated into UniProtKB/TrEMBL.  
DT 01-NOV-1999, sequence version 1.  
DT 07-FEB-2006, entry version 18.  
DE B6 protein.  
OS Human papillomavirus type 16.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Alphapapillomavirus.  
OC NCBI\_Taxid=333760;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=20112892; PubMed=10644829;  
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,  
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;  
RT "Analysis of human papillomavirus type 16 B6 variants in relation to  
p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";  
RL J. Gen. Virol. 81:317-325(2000).  
RN [2]

RP NUCLEOTIDE SEQUENCE.  
RA Duin M.;  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
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DR EMBL; AJ242581; CAB45381.1; -; Genomic DNA.  
DR GO; GO:0042025; C:host cell nucleus; IEA.  
DR GO; GO:0003677; F:DNA binding; IEA.  
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DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.  
DT 05-JUL-2004, sequence version 1.  
DT 07-FEB-2006, entry version 11.  
DE B6 protein.  
OS Human papillomavirus type 16.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Alphapapillomavirus.  
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RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,  
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;  
RT "Analysis of human papillomavirus type 16 B6 variants in relation to  
p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";  
RL J. Gen. Virol. 81:317-325(2000).  
RN [2]  
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DR GO; GO:0003677; F:DNA binding; IEA.  
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RESULT 6
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DT      01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT      01-NOV-1996, sequence version 1.
DT      07-FEB-2006, entry version 24.
DE      Early transforming protein E6.
OS      Human papillomavirus.
OC      Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC      unclassified Papillomaviridae.
OX      NCBI_TaxID=10566;
RN      [1]
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RX      MEDLINE=96079021; PubMed=7494284;
RA      Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
RA      Jensen S.A.;
RT      "Human papillomavirus type 16 variant lineages in United States
RT      populations characterized by nucleotide sequence analysis of the E6,
RT      L2, and L1 coding segments.";
RL      J. Virol. 69:7743-7753(1995).
RN      [2]
RP      NUCLEOTIDE SEQUENCE.
RA      Farmer A.D.;
RL      Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
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DR      EMBL: U34126; AAA91673.1; -; Genomic DNA.
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DR      GO: GO:0003677; F:DNA binding; IEA.
DR      InterPro: IPR001334; E6.
DR      Pfam: PF00518; E6; 1.
SQ      SEQUENCE 151 AA; 18334 MW; F8F82A2FCEBA6C02 CRC64;

Query Match      99.2%; Score 823; DB 2; Length 151;
Best Local Similarity 98.0%; Pred. No. 4.7e-73;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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OC      Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC      Alphapapillomavirus.
OX      NCBI_TaxID=333760;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RX      MEDLINE=2224222; PubMed=12355268; DOI=10.1007/s00239-002-2344-Y;
RA      Defillipis V.R., Ayala F.J., Villarreal L.P.;
RT      "Evidence of diversifying selection in human papillomavirus type 16 E6
RT      but not E7 oncogenes.";
RL      J. Mol. Evol. 55:491-499(2002).
CC      -----
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NonDerivs License
CC      -----
DR      EMBL: AY089953; AAM1879.1; -; Genomic DNA.
DR      GO: GO:0042025; C:host cell nucleus; IEA.
DR      GO: GO:0003677; F:DNA binding; IEA.
DR      InterPro: IPR001334; E6.
DR      Pfam: PF00518; E6; 1.
SQ      SEQUENCE 151 AA; 18319 MW; 7C8D23EFCFAF8C17 CRC64;

Query Match      99.2%; Score 823; DB 2; Length 151;
Best Local Similarity 98.0%; Pred. No. 4.7e-73;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Qy      1 MFODPQRPRLPOLCTELQTTIHDIILECYCKQQLRREVDFAFRDLCIVYRDGNY 60
      |||
Db      1 MFODPQRPRLPOLCTELQTTIHDIILECYCKQQLRREVDFAFRDLCIVYRDGNY 60
      |||

RESULT 8
ID      V66_HPV16 STANDARD; PRT; 158 AA.
AC      P03126; Q71B17;
DT      21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
DT      21-JUL-1986, sequence version 1.
DT      07-MAR-2006, entry version 45.
DE      Protein E6.
GN      Name=E6;
OS      Human papillomavirus type 16.
OC      Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC      Alphapapillomavirus.
OX      NCBI_TaxID=333760;
RN      [1]
RP      NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX      MEDLINE=85246220; PubMed=2950099;
RA      Seedorf K., Krammer G., Durst M., Suhai S., Roweckamp W.G.;
RT      "Human papillomavirus type 16 DNA sequence.";
RL      Virology 145:181-185(1985).
RN      [2]
RP      NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC      STRAIN=Isolate European German 131;
RA      Terafi M., Fu L., Ma Z., Burk R.D.;
RT      "Cloning and sequencing of non-European human papillomavirus (HPV)
RT      variant complete genomes from cervicovaginal cells by an overlapping
RT      PCR method.";
RL      Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
RN      [3]
RP      NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 31-50.
RX      MEDLINE=90218027; PubMed=2157796;
RA      Schneider-Maunoury S., Pehau-Arnaudet G., Breitburd F., Orth G.;
RT      "Expression of the human papillomavirus type 16 genome in SK-V cells,
RT      a line derived from a vulvar intraepithelial neoplasia.";
RL      J. Gen. Virol. 71:809-817(1990).
RN      [4]

```

RP INTERACTION WITH HUMAN EBV1, AND INHIBITION OF E6-MEDIATED  
RP TRANSFORMATION.  
RX MEDLINE=22188366; PubMed=12200142; DOI=10.1016/S0006-291X(02)02041-7;  
RA Du M., Fan X., Hong E., Chen J.J.;  
RT "Interaction of oncogenic Papillomavirus E6 proteins with E6ublin-1";  
RL Biochem. Biophys. Res. Commun. 296:962-969(2002).  
CC -1- FUNCTION: Transcriptional transactivator. Binds double stranded  
CC DNA. Has transforming activity. Inactivates, with E6-AP ubiquitin-  
CC protein ligase, the human TP53/p53 tumor suppressor protein by  
CC targeting it to degradation. Binds and targets human MDM2/MDM2  
CC protein to degradation. Those two functions presumably contribute  
CC to transforming activity (By similarity). Interaction with human  
CC EBV1 protein also seems to be linked to cell transformation.  
CC -1- SUBUNIT: Forms a complex with E6-AP ubiquitin-protein ligase which  
CC interacts with human P53. Binds to human EBV1 and MDM2 (By  
CC similarity).  
CC -1- SUBCELLULAR LOCATION: Nuclear matrix-associated.  
CC -1- MISCELLANEOUS: HPV16, in comparison to HPV types 6 and 11, is more  
CC often associated with malignant genital cancers in humans.  
CC -1- SIMILARITY: Belongs to the papillomaviruses E6 protein family.  
CC -----  
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
CC Distributed under the Creative Commons Attribution-NonDerivs License  
CC -----  
DR EMBL: K02718; AAA4693.1; -; Genomic DNA.  
DR EMBL: AF536179; AA010712.1; -; Genomic DNA.  
DR EMBL: D00735; BAA00632.1; -; Genomic DNA.  
DR PIR: A03682; W6WLS.  
DR PDB: 2FK4; NMR; A=87-158.  
DR InterPro: IPR001334; E6.  
DR Pfam: PF00518; E6; 1.  
DR 3D-structure: Activator; DNA-binding; Early protein; Metal-binding;  
DR Nuclear protein; Oncogene; Transcription; Transcription regulation;  
DR Zinc; Zinc-finger.  
KM CHAIN 1 158 Protein E6.  
FT FTID=PRO\_000013336.  
FT ZN\_FING 37 73 Potential.  
FT ZN\_FING 110 146 Potential.  
FT MOTIF 155 158 PDZ-binding (By similarity).  
FT CONFLICT 17 17 R -> G (in Ref. 2).  
FT CONFLICT 90 90 L -> V (in Ref. 2).  
SQ SEQUENCE 158 AA; 19187 MW; 01FEF5ADCDFD37EB CRC64;  
Query Match 99.2%; Score 823; DB 1; Length 158;  
Best Local Similarity 98.0%; Pred. No. 4.9e-73;  
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 MFODPQRPRLPOLCTELQTTIHDIILECYCKQQLLRREVDFAFRDLCTVYRDGNY 60  
DB 8 MFODPQRPRLPOLCTELQTTIHDIILECYCKQQLLRREVDFAFRDLCTVYRDGNY 67  
QY 61 AVXDCKLFYSKISEYHYCYSVYGTLEQYNNKPLCDLLIRCIINXOKPLCPBEKORHLD 120  
DB 68 AVCDCKLFYSKISEYHYCYSVYGTLEQYNNKPLCDLLIRCIINXOKPLCPBEKORHLD 127  
QY 121 KKQRFNIRGRWTCRSCSSSRTRETOL 151  
DB 128 KKQRFNIRGRWTCRSCSSSRTRETOL 158  
RESULT 9  
ID Q54732\_HPV16 PRELIMINARY; PRT; 158 AA.  
AC Q54732;  
DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.  
DT 24-MAY-2005, sequence version 1.  
DT 07-FEB-2006, entry version 5.  
DE Transforming protein E6.  
GN Name=E6;  
OS Human papillomavirus type 16.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Alphapapillomavirus.  
NCBI\_TaxID=333760;

RN [1]  
RE NUCLEOTIDE SEQUENCE.  
RC STRAIN=E-P, E-G241T, E-G187T, and E-G538T;  
RX MEDLINE=22182962; PubMed=12195358; DOI=10.1086/342048;  
RA Chan P.K.S., Lam C.W., Cheng T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,  
RA Chang J.L.K., Xu L.Y., Cheng A.F.;  
RT "Human papillomavirus type 16 intertypic variant infection and risk  
RT for cervical neoplasia in southern China.";  
RL J. Infect. Dis. 186:696-700(2002).  
RN [2]  
RN NUCLEOTIDE SEQUENCE.  
RP STRAIN=QV17722E, and QV15521E;  
RX PubMed=15890941; DOI=10.1128/JVI.79.11.7014-7023.2005;  
RA Chen Z., Terai M., Fu L., Herrero R., Desalle R., Burk R.D.;  
RT "Diversifying selection in human papillomavirus type 16 lineages based  
RT on complete genome analyses.";  
RL J. Virol. 79:7014-7023(2005).  
RN [3]  
RN NUCLEOTIDE SEQUENCE.  
RC STRAIN=Beb-102;  
RA Cruz M.R., Cergueta D.M., Camara G.N.L., Silva E.O., Carvalho L.G.S.,  
RA Martins C.R.F.;  
RT "Human papillomavirus type 16 variants in Central Brazil.";  
RL Submitted (APR-2002) to the EMBL/Genbank/DBJ databases.  
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CC -----  
DR EMBL: AF486311; AAL96616.1; -; Genomic DNA.  
DR EMBL: AY686584; AAV91684.1; -; Genomic DNA.  
DR EMBL: AF486310; AAL96615.1; -; Genomic DNA.  
DR EMBL: AF486312; AAL96617.1; -; Genomic DNA.  
DR EMBL: AF486313; AAL96618.1; -; Genomic DNA.  
DR EMBL: AF486317; AAL96622.1; -; Genomic DNA.  
DR EMBL: AF486320; AAL96625.1; -; Genomic DNA.  
DR EMBL: AF486321; AAL96626.1; -; Genomic DNA.  
DR EMBL: AF486321; AAL96626.1; -; Genomic DNA.  
DR EMBL: AY098919; AAM29167.1; -; Genomic DNA.  
DR EMBL: AY686581; AAV91660.1; -; Genomic DNA.  
DR GO: 0042025; C:host cell nucleus; IEA.  
DR GO: 0003677; F:DNA binding; IEA.  
SQ SEQUENCE 158 AA; 19187 MW; 01FEF5ADCDFD37EB CRC64;  
Query Match 99.2%; Score 823; DB 2; Length 158;  
Best Local Similarity 98.0%; Pred. No. 4.9e-73;  
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 MFODPQRPRLPOLCTELQTTIHDIILECYCKQQLLRREVDFAFRDLCTVYRDGNY 60  
DB 8 MFODPQRPRLPOLCTELQTTIHDIILECYCKQQLLRREVDFAFRDLCTVYRDGNY 67  
QY 61 AVXDCKLFYSKISEYHYCYSVYGTLEQYNNKPLCDLLIRCIINXOKPLCPBEKORHLD 120  
DB 68 AVCDCKLFYSKISEYHYCYSVYGTLEQYNNKPLCDLLIRCIINXOKPLCPBEKORHLD 127  
QY 121 KKQRFNIRGRWTCRSCSSSRTRETOL 151  
DB 128 KKQRFNIRGRWTCRSCSSSRTRETOL 158  
RESULT 10  
ID Q919C6\_HPV16 PRELIMINARY; PRT; 161 AA.  
AC Q919C6;  
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.  
DT 01-DEC-2001, sequence version 1.  
DT 07-FEB-2006, entry version 16.  
DE E6 protein (fragment).  
OS Human papillomavirus type 16.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Alphapapillomavirus.  
NCBI\_TaxID=333760;  
RN [1]  
RN NUCLEOTIDE SEQUENCE.

```

RX MEDLINE=21846229; PubMed=11857370; DOI=10.1002/jfc.10103;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RL cervical cancer isolates from Australia and New Caledonia.";
CC -----
CC Int. J. Cancer 97:868-874(2002).
CC -----
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CC -----
DR EMBL: AF404697; AAL01351.1; -: Genomic DNA.
DR GO: GO:0042025; C:host cell nucleus; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
DR NON TER 1 1
FT SEQUENCE 161 AA; 19628 MW; 15D32F0F12E00460 CRC64;

Query Match 99.2%; Score 823; DB 2; Length 161;
Best Local Similarity 98.0%; Pred. No. 5e-73;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFQDPOERPRKLPOLCTELQTTIHDIILECYCKQQLRREYDFAFRDLCIVYRDGPNY 60
DB 11 MFQDPOERPRKLPOLCTELQTTIHDIILECYCKQQLRREYDFAFRDLCIVYRDGPNY 70
QY 61 AVCDKCLKFYSKISEYRHYCYSVYGTTLLEQYKNKPLCDLLIRCIHQKPLCPBEKQRLHD 120
DB 71 AVCDKCLKFYSKISEYRHYCYSVYGTTLLEQYKNKPLCDLLIRCIHQKPLCPBEKQRLHD 130

QY 121 KKQRFHNIRGRWTRGCMSCCRSSRTRETOL 151
DB 131 KKQRFHNIRGRWTRGCMSCCRSSRTRETOL 161

RESULT 11
Q8BB19 HPV16 PRELIMINARY; PRT; 151 AA.
AC Q8BB19;
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003, sequence version 1.
DT 07-FEB-2006, entry version 13.
DE Early transforming protein E6.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22242222; PubMed=12355268; DOI=10.1007/s00239-002-2344-Y;
RA Deillipis V.R., Ayala F.J., Villarreal L.P.;
RT "Evidence of diversifying selection in human papillomavirus type 16 E6
RL but not E7 oncogenes.";
CC -----
CC J. Mol. Evol. 55:491-499(2002).
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CC -----
DR EMBL: AY089955; AAM11883.1; -: Genomic DNA.
DR GO: GO:0042025; C:host cell nucleus; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
DR SEQUENCE 151 AA; 18319 MW; 6F9D2A2FD5AF08F7 CRC64;

Query Match 98.9%; Score 821; DB 2; Length 151;
Best Local Similarity 98.0%; Pred. No. 7.4e-73;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFQDPOERPRKLPOLCTELQTTIHDIILECYCKQQLRREYDFAFRDLCIVYRDGPNY 60
DB 1 MFQDPOERPRKLPOLCTELQTTIHDIILECYCKQQLRREYDFAFRDLCIVYRDGPNY 60
QY 61 AVXDCLKFYSKISEYRHYCYSVYGTTLLEQYKNKPLCDLLIRCIHQKPLCPBEKQRLHD 120
DB 61 AVXDCLKFYSKISEYRHYCYSVYGTTLLEQYKNKPLCDLLIRCIHQKPLCPBEKQRLHD 120

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DB 61 AVCDKCLKFYSKISEYRHYCYSVYGTTLLEQYKNKPLCDLLIRCIHQKPLCPBEKQRLHD 120
QY 121 KKQRFHNIRGRWTRGCMSCCRSSRTRETOL 151
DB 121 KKQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

RESULT 12
Q4VRN5 HPV16 PRELIMINARY; PRT; 158 AA.
AC Q4VRN5;
DT 05-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE E6.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=QV18158E;
RX PubMed=15890941; DOI=10.1128/JVI.79.11.7014-7023.2005;
RA Chen Z., Terai M., Fu L., Herrero R., Desalle R., Burk R.D.;
RT "Diversifying selection in human papillomavirus type 16 lineages based
RL on complete genome analyses.";
CC -----
CC J. Virol. 79:7014-7023(2005).
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CC -----
DR EMBL: AY686583; AAV91676.1; -: Genomic DNA.
DR GO: GO:0042025; C:host cell nucleus; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
DR SEQUENCE 158 AA; 19172 MW; 91ECF5ADD4CED31E CRC64;

Query Match 98.9%; Score 821; DB 2; Length 158;
Best Local Similarity 98.0%; Pred. No. 7.8e-73;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFQDPOERPRKLPOLCTELQTTIHDIILECYCKQQLRREYDFAFRDLCIVYRDGPNY 60
DB 8 MFQDPOERPRKLPOLCTELQTTIHDIILECYCKQQLRREYDFAFRDLCIVYRDGPNY 67
QY 61 AVXDCLKFYSKISEYRHYCYSVYGTTLLEQYKNKPLCDLLIRCIHQKPLCPBEKQRLHD 120
DB 68 AVCDKCLKFYSKISEYRHYCYSVYGTTLLEQYKNKPLCDLLIRCIHQKPLCPBEKQRLHD 127

QY 121 KKQRFHNIRGRWTRGCMSCCRSSRTRETOL 151
DB 128 KKQRFHNIRGRWTRGCMSCCRSSRTRETOL 158

RESULT 13
Q8ORD7 HPV16 PRELIMINARY; PRT; 158 AA.
AC Q8ORD7;
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2002, sequence version 1.
DT 07-FEB-2006, entry version 13.
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=E-C442T;
RX MEDLINE=22182962; PubMed=12195358; DOI=10.1086/342048;
RA Chan P.K.S., Lam C.W., Cheng T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RT "Human papillomavirus type 16 intracyclic variant infection and risk

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RT for cervical neoplasia in southern China."
RL J. Infect. Dis. 186:696-700(2002).
CC -----
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CC -----
DR EMBL: AF486318; AAL96623.1; -; Genomic DNA.
DR GO: GO:0042025; C:host cell nucleus; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
SQ SEQUENCE 158 AA; 19173 MW; 14BFB5ADCDB3640 CRC64;

Query Match 98.8%; Score 820; DB 2; Length 158;
Best Local Similarity 97.4%; Pred. No. 9.8e-73;
Matches 147; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFODPOBPRKLPOLCTELQTTIHDIIECYCKQQLLRREVDPAFRDLCTIVRDGNY 60
DB 8 MFODPOBPRKLPOLCTELQTTIHDIIECYCKQQLLRREVDPAFRDLCTIVRDGNY 67
QY 61 AVXDKCLKFYSKISEYRHVCYSVGTTLBQYNNKPLCDLLIRCTINXOKPLCPBEKORHLD 120
DB 68 AVCDKCLKFYSKISEYRHVCYSVGTTLBQYNNKPLCDLLIRCTINXOKPLCPBEKORHLD 127
QY 121 KKORFNHNRGRWTRGCMSCCRSSSTRRETOL 151
DB 128 KKORFNHNRGRWTRGCMSCCRSSSTRRETOL 158

RESULT 14
OBORD8_HPV16 PRELIMINARY; PRT; 158 AA.
ID OBORD8_HPV16
AC OBORD8;
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2002, sequence version 1.
DT 07-FEB-2006, entry version 13.
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OC NCBI_TaxId=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=E-6449T; PubMed=12195358; DOI=10.1086/342048;
RX MEDLINE=22182962; PubMed=12195358; DOI=10.1086/342048;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
RT "Human papillomavirus type 16 intracypic variant infection and risk
RT for cervical neoplasia in southern China.";
RL J. Infect. Dis. 186:696-700(2002).
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CC -----
DR EMBL: AF486316; AAL96621.1; -; Genomic DNA.
DR GO: GO:0042025; C:host cell nucleus; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
SQ SEQUENCE 158 AA; 19188 MW; 01PEFSBD21AF7EB CRC64;

Query Match 98.8%; Score 820; DB 2; Length 158;
Best Local Similarity 97.4%; Pred. No. 9.8e-73;
Matches 147; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFODPOBPRKLPOLCTELQTTIHDIIECYCKQQLLRREVDPAFRDLCTIVRDGNY 60
DB 8 MFODPOBPRKLPOLCTELQTTIHDIIECYCKQQLLRREVDPAFRDLCTIVRDGNY 67
QY 61 AVXDKCLKFYSKISEYRHVCYSVGTTLBQYNNKPLCDLLIRCTINXOKPLCPBEKORHLD 120
DB 68 AVCDKCLKFYSKISEYRHVCYSVGTTLBQYNNKPLCDLLIRCTINXOKPLCPBEKORHLD 127

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QY 121 KKORFNHNRGRWTRGCMSCCRSSSTRRETOL 151
DB 128 KKORFNHNRGRWTRGCMSCCRSSSTRRETOL 158

RESULT 15
077ZJ5_HPV16 PRELIMINARY; PRT; 151 AA.
ID 077ZJ5_HPV16
AC 077ZJ5;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OC NCBI_TaxId=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=97437474; PubMed=9292007;
RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Giraldo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus
RT type 16 in penile carcinomas from Ugandan patients.";
RL J. Gen. Virol. 78:2199-2208(1997).
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CC -----
DR EMBL: AF003018; AAB70736.1; -; Genomic DNA.
DR EMBL: AF003018; AAB70735.1; -; Genomic DNA.
DR GO: GO:0042025; C:host cell nucleus; IEA.
DR GO: GO:0003677; F:DNA binding; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18221 MW; 60CD2A34DAF48CB7 CRC64;

Query Match 98.7%; Score 819; DB 2; Length 151;
Best Local Similarity 98.0%; Pred. No. 1.2e-72;
Matches 148; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MFODPOBPRKLPOLCTELQTTIHDIIECYCKQQLLRREVDPAFRDLCTIVRDGNY 60
DB 1 MFODPOBPRKLPOLCTELQTTIHDIIECYCKQQLLRREVDPAFRDLCTIVRDGNY 60
QY 61 AVXDKCLKFYSKISEYRHVCYSVGTTLBQYNNKPLCDLLIRCTINXOKPLCPBEKORHLD 120
DB 61 AVCDKCLKFYSKISEYRHVCYSVGTTLBQYNNKPLCDLLIRCTINXOKPLCPBEKORHLD 120
QY 121 KKORFNHNRGRWTRGCMSCCRSSSTRRETOL 151
DB 121 KKORFNHNRGRWTRGCMSCCRSSSTRRETOL 151

RESULT 16
Q89640_9PAPI PRELIMINARY; PRT; 151 AA.
ID Q89640_9PAPI
AC Q89640;
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 22.
DE Early transforming protein E6.
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC unclassified Papillomaviridae.
OC NCBI_TaxId=10566;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96079021; PubMed=7494284;
RA Yanada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
RA Jensen S.A.;
RT "Human papillomavirus type 16 variant lineages in United States

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RT populations characterized by nucleotide sequence analysis of the E6,  
RT 12, and 13 coding segments." ;  
RL J. Virol. 69:7743-7753(1995).  
RN [2]  
RA NUCLEOTIDE SEQUENCE.  
RP Farmer A.D.;  
RL Submitted (Aug-1995) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RA Ponglikitmongkol M.; Vaeteewootacharn K.;  
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
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DR EMBL; U34129; AAA91676.1; -; Genomic DNA.  
DR EMBL; AF469198; AA015693.1; -; Genomic DNA.  
DR EMBL; U34115; AAA91662.1; -; Genomic DNA.  
DR EMBL; U34120; AAA91667.1; -; Genomic DNA.  
DR EMBL; U34124; AAA91671.1; -; Genomic DNA.  
DR GO; GO:0042025; C:host cell nucleus; IEA.  
DR GO; GO:0003677; F:DNA binding; IEA.  
DR InterPro; IPR001334; E6.  
DR Pfam; PF00518; E6; 1.  
SQ SEQUENCE 151 AA; 18348 MW; FE3F2A2FCF0A6CB2 CRC64;  
  
Query Match 98.7%; Score 819; DB 2; Length 151;  
Best Local Similarity 97.4%; Pred. No. 1.2e-72;  
Matches 147; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 MFODPQERPRKLPOLCTELQTTIHDIILECYCKQQLLRREYDFAFDLCIVYRDGNY 60  
DB 1 MFODPQERPRKLPOLCTELQTTIHDIILECYCKQQLLRREYDFAFDLCIVYRDGNY 60  
  
QY 61 AVXDKCLKFYSKISEYHHYCYSVYGTTLLEQYKNPCLDLLIRCTNKKPLCPPEKQKRLD 120  
DB 61 AVCDKCLKFYSKISEYHHYCYSLVGTTLLEQYKNPCLDLLIRCTNCKPLCPPEKQKRLD 120  
  
QY 121 KKQRFHNIRGWRGCMSCCRSSRTRETOL 151  
DB 121 KKQRFHNIRGWRGCMSCCRSSRTRETOL 151  
  
RESULT 17  
ID Q89648.9PAPI PRELIMINARY; PRT; 151 AA.  
AC Q89648; O12653; O12928; O12929;  
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.  
DT 07-FEB-2006, entry version 21.  
DE Early transforming protein E6.  
OS Human papillomavirus.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC unclassified Papillomaviridae.  
OX NCBI\_TaxID=10566;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=96079021; PubMed=7494284;  
RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,  
RA Jensen S.A.;  
RT "Human papillomavirus type 16 variant lineages in United States  
RT populations characterized by nucleotide sequence analysis of the E6,  
RT 12, and 13 coding segments." ;  
RL J. Virol. 69:7743-7753(1995).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RA Farmer A.D.;  
RL Submitted (Aug-1995) to the EMBL/GenBank/DBJ databases.  
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EMBL; U34110; AAA91657.1; -; Genomic DNA.

DR EMBL; U34109; AAA91656.1; -; Genomic DNA.  
DR EMBL; U34113; AAA91660.1; -; Genomic DNA.  
DR EMBL; U34135; AAA91682.1; -; Genomic DNA.  
DR GO; GO:0042025; C:host cell nucleus; IEA.  
DR GO; GO:0003677; F:DNA binding; IEA.  
DR InterPro; IPR001334; E6.  
DR Pfam; PF00518; E6; 1.  
SQ SEQUENCE 151 AA; 18221 MW; 60CD2A34DAF48CB7 CRC64;  
  
Query Match 98.7%; Score 819; DB 2; Length 151;  
Best Local Similarity 98.0%; Pred. No. 1.2e-72;  
Matches 148; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 MFODPQERPRKLPOLCTELQTTIHDIILECYCKQQLLRREYDFAFDLCIVYRDGNY 60  
DB 1 MFODPQERPRKLPOLCTELQTTIHDIILECYCKQQLLRREYDFAFDLCIVYRDGNY 60  
  
QY 61 AVXDKCLKFYSKISEYHHYCYSVYGTTLLEQYKNPCLDLLIRCTNKKPLCPPEKQKRLD 120  
DB 61 AVCDKCLKFYSKISEYHHYCYSVYGTTLLEQYKNPCLDLLIRCTNCKPLCPPEKQKRLD 120  
  
QY 121 KKQRFHNIRGWRGCMSCCRSSRTRETOL 151  
DB 121 KKQRFHNIRGWRGCMSCCRSSRTRETOL 151  
  
RESULT 18  
ID Q9W931.HPV16 PRELIMINARY; PRT; 151 AA.  
AC Q9W931;  
DT 01-NOV-1999, integrated into UniProtKB/TrEMBL.  
DT 01-NOV-1999, sequence version 1.  
DT 07-FEB-2006, entry version 16.  
DE E6 protein.  
OS Human papillomavirus type 16.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Alphapapillomavirus.  
OX NCBI\_TaxID=333760;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=20112892; PubMed=10644829;  
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorthorst F.,  
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;  
RT "Analysis of human papillomavirus type 16 E6 variants in relation to  
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis." ;  
RL J. Gen. Virol. 81:317-325(2000).  
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DR EMBL; AJ388059; CAB45110.1; -; Genomic DNA.  
DR EMBL; AJ388058; CAB45108.1; -; Genomic DNA.  
DR GO; GO:0042025; C:host cell nucleus; IEA.  
DR GO; GO:0003677; F:DNA binding; IEA.  
DR InterPro; IPR001334; E6.  
DR Pfam; PF00518; E6; 1.  
SQ SEQUENCE 151 AA; 18306 MW; 6FB3D9E0F24A5300 CRC64;  
  
Query Match 98.7%; Score 819; DB 2; Length 151;  
Best Local Similarity 97.4%; Pred. No. 1.2e-72;  
Matches 147; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 MFODPQERPRKLPOLCTELQTTIHDIILECYCKQQLLRREYDFAFDLCIVYRDGNY 60  
DB 1 MFODPQERPRKLPOLCTELQTTIHDIILECYCKQQLLRREYDFAFDLCIVYRDGNY 60  
  
QY 61 AVXDKCLKFYSKISEYHHYCYSVYGTTLLEQYKNPCLDLLIRCTNKKPLCPPEKQKRLD 120  
DB 61 AVCDKCLKFYSKISEYHHYCYSLVGTTLLEQYKNPCLDLLIRCTNCKPLCPPEKQKRLD 120  
  
QY 121 KKQRFHNIRGWRGCMSCCRSSRTRETOL 151  
DB 121 KKQRFHNIRGWRGCMSCCRSSRTRETOL 151

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RESULT 19
Q2PUN9 HPV16 PRELIMINARY; PRT; 158 AA.
ID Q2PUN9 HPV16 PRELIMINARY; PRT; 158 AA.
AC Q2PUN9;
DT 24-JAN-2006, integrated into UniProtKB/TrEMBL.
DT 24-JAN-2006, sequence version 1.
DT 07-FEB-2006, entry version 2.
DE E6 protein.
GN Name=E6;
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_Taxid=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Mischak H., Soliman H., Meskhat Z., Bamdad T.;
RT "Cloning and sequence analysis of human papillomavirus type 16 E6.";
RL Submitted (DEC-2005) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; DQ333982; ABC48950.1; -; Genomic DNA.
SQ SEQUENCE 158 AA; 19074 MW; 9EBCF5BDB95075E CRC64;

Query Match 98.7%; Score 819; DB 2; Length 158;
Best Local Similarity 98.0%; Pred. No. 1.2e-72;
Matches 148; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MFQDPQRPRLPOLCTELQTTIHDIIECYCCKQQLLRREYDFAFRDLCTVYRDGPNY 60
DB 8 MFQDPQRPRLPOLCTELQTTIHDIIECYCCKQQLLRREYDFAFRDLCTVYRDGPNY 67
QY 61 AVXDKCKLFYSKISEYRHYCYVYGTLEQYKPKCDLLIRCNXKPKLCPPEEKORHLD 120
DB 68 AVCDKCKLFYSKISEYRHYCYVYGTLEQYKPKCDLLIRCNXKPKLCPPEEKORHLD 127
QY 121 KKQRFNHRGWRGRCMSCSSSRTRETOL 151
DB 128 KKQRFNHRGWRGRCMSCSSSRTRETOL 158

RESULT 20
Q8OHT0 HPV16 PRELIMINARY; PRT; 158 AA.
ID Q8OHT0 HPV16 PRELIMINARY; PRT; 158 AA.
AC Q8OHT0;
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2002, sequence version 1.
DT 07-FEB-2006, entry version 15.
DE Putative transforming protein E6.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_Taxid=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA STEAIN=As-P, and As-A178;
RC MEDLINE=22182962; PubMed=12195358; DOI=10.1086/342048;
RX Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
RT "Human papillomavirus type 16 intracyclic variant infection and risk
for cervical neoplasia in southern China.";
RL J. Infect. Dis. 186:696-700(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Terai M., Fu L., Ma Z., Burk R.D.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
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DR EMBL; AF486299; AAL96604.1; -; Genomic DNA.
DR EMBL; AF486300; AAL96605.1; -; Genomic DNA.
DR EMBL; AF486301; AAL96606.1; -; Genomic DNA.
DR EMBL; AF486302; AAL96607.1; -; Genomic DNA.
DR EMBL; AF486306; AAL96611.1; -; Genomic DNA.
DR EMBL; AF486308; AAL96613.1; -; Genomic DNA.
DR EMBL; AF534061; AAO10403.1; -; Genomic DNA.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR01334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 158 AA; 19201 MW; 004E5ADCE6B375B CRC64;

Query Match 98.7%; Score 819; DB 2; Length 158;
Best Local Similarity 97.4%; Pred. No. 1.2e-72;
Matches 147; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFQDPQRPRLPOLCTELQTTIHDIIECYCCKQQLLRREYDFAFRDLCTVYRDGPNY 60
DB 8 MFQDPQRPRLPOLCTELQTTIHDIIECYCCKQQLLRREYDFAFRDLCTVYRDGPNY 67
QY 61 AVXDKCKLFYSKISEYRHYCYVYGTLEQYKPKCDLLIRCNXKPKLCPPEEKORHLD 120
DB 68 AVCDKCKLFYSKISEYRHYCYVYGTLEQYKPKCDLLIRCNXKPKLCPPEEKORHLD 127
QY 121 KKQRFNHRGWRGRCMSCSSSRTRETOL 151
DB 128 KKQRFNHRGWRGRCMSCSSSRTRETOL 158

RESULT 21
Q80963 9PAPI PRELIMINARY; PRT; 151 AA.
ID Q80963 9PAPI PRELIMINARY; PRT; 151 AA.
AC Q80963;
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 22.
DE Early transforming protein E6.
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC unclassified Papillomaviridae.
OX NCBI_Taxid=10566;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96079021; PubMed=7494284;
RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
RA Jensen S.A.;
RT "Human papillomavirus type 16 variant lineages in United States
RT populations characterized by nucleotide sequence analysis of the E6,
RT L2, and L1 coding segments.";
RL J. Virol. 69:7743-7753(1995).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Farmer A.D.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; U34122; AAA91669.1; -; Genomic DNA.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR01334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18291 MW; 97C7028D5169382D CRC64;

Query Match 98.6%; Score 818; DB 2; Length 151;
Best Local Similarity 97.4%; Pred. No. 1.5e-72;
Matches 147; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFQDPQRPRLPOLCTELQTTIHDIIECYCCKQQLLRREYDFAFRDLCTVYRDGPNY 60
DB 1 MFQDPQRPRLPOLCTELQTTIHDIIECYCCKQQLLRREYDFAFRDLCTVYRDGPNY 60

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Qy 61 AVXDKCLKFYSKISEYRHVCYSVYGTTLLEQOYKPKCDLLIRICINXOKPLCPBEKORHLD 120
Db 61 AVCDKCLKFYSKISEYRHVCYSVYGTTLLEQOYKPKCDLLIRICINXOKPLCPBEKORHLD 120
Qy 121 KKORFHNIRGRWTCRSCCSSRTRRETOL 151
Db 121 KKORFHNIRGRWTCRSCCSSRTRRETOL 151

RESULT 22
Q80HP5 HPV16 PRELIMINARY; PRT; 158 AA.
AC Q80HP5;
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2002, sequence version 1.
DT 07-FEB-2006, entry version 13.
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxId=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=E-6276T, and E-6276G442T;
RX MEDLINE=22182962; PubMed=12195358; DOI=10.1086/342048;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
RA "Human papillomavirus type 16 intracytic variant infection and risk
RT for cervical neoplasia in southern China.";
RL J. Infect. Dis. 186:696-700(2002).
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CC
DR EMBL; AF486315; AAL96620.1; -; Genomic DNA.
DR EMBL; AF486315; AAL96620.1; -; Genomic DNA.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 158 AA; 19160 MW; AFD01553FCTFAF7 CRC64;

Query Match 98.4%; Score 818; DB 2; Length 158;
Best Local Similarity 97.4%; Pred. No. 1.5e-72;
Matches 147; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MFODPQERPRKLPQLCTELQTTIHDIIECVYCKQQLRREYDFAFRDLCIVYRDGNPY 60
Db 8 MFODPQERPRKLPQLCTELQTTIHDIIECVYCKQQLRREYDFAFRDLCIVYRDGNPY 67
Qy 61 AVXDKCLKFYSKISEYRHVCYSVYGTTLLEQOYKPKCDLLIRICINXOKPLCPBEKORHLD 120
Db 61 AVCDKCLKFYSKISEYRHVCYSVYGTTLLEQOYKPKCDLLIRICINXOKPLCPBEKORHLD 127
Qy 121 KKORFHNIRGRWTCRSCCSSRTRRETOL 151
Db 121 KKORFHNIRGRWTCRSCCSSRTRRETOL 158

RESULT 23
Q80HP5 HPV16 PRELIMINARY; PRT; 151 AA.
AC Q80HP5;
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003, sequence version 1.
DT 07-FEB-2006, entry version 13.
DE E6 protein.
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC unclassified Papillomaviridae.
OX NCBI_TaxId=10566;
RN [1]
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RP NUCLEOTIDE SEQUENCE.
RA Ponglikitmongkol M., Vaeewooteacharn K.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
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CC
DR EMBL; AF548023; AAO16239.1; -; Genomic DNA.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18348 MW; FE3F2D5FCD7A69B2 CRC64;

Query Match 98.4%; Score 817; DB 2; Length 151;
Best Local Similarity 96.7%; Pred. No. 1.8e-72;
Matches 146; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MFODPQERPRKLPQLCTELQTTIHDIIECVYCKQQLRREYDFAFRDLCIVYRDGNPY 60
Db 1 MFODPQERPRKLPQLCTELQTTIHDIIECVYCKQQLRREYDFAFRDLCIVYRDGNPY 60
Qy 61 AVXDKCLKFYSKISEYRHVCYSVYGTTLLEQOYKPKCDLLIRICINXOKPLCPBEKORHLD 120
Db 61 AVCDKCLKFYSKISEYRHVCYSVYGTTLLEQOYKPKCDLLIRICINXOKPLCPBEKORHLD 120
Qy 121 KKORFHNIRGRWTCRSCCSSRTRRETOL 151
Db 121 KKORFHNIRGRWTCRSCCSSRTRRETOL 151

RESULT 24
Q80HP5 HPV16 PRELIMINARY; PRT; 151 AA.
AC Q80HP5;
DT 01-NOV-1999, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1999, sequence version 1.
DT 07-FEB-2006, entry version 18.
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxId=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=20112892; PubMed=10644829;
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RA "Analysis of human papillomavirus type 16 E6 variants in relation to
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
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CC
DR EMBL; AJ388064; CAB45120.1; -; Genomic DNA.
DR EMBL; AJ388062; CAB45116.1; -; Genomic DNA.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18360 MW; FF9A2A3ADBBA7902 CRC64;

Query Match 98.4%; Score 817; DB 2; Length 151;
Best Local Similarity 97.4%; Pred. No. 1.8e-72;
Matches 147; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MFODPQERPRKLPQLCTELQTTIHDIIECVYCKQQLRREYDFAFRDLCIVYRDGNPY 60
Db 1 MFODPQERPRKLPQLCTELQTTIHDIIECVYCKQQLRREYDFAFRDLCIVYRDGNPY 60
Qy 61 AVXDKCLKFYSKISEYRHVCYSVYGTTLLEQOYKPKCDLLIRICINXOKPLCPBEKORHLD 120
Db 61 AVCDKCLKFYSKISEYRHVCYSVYGTTLLEQOYKPKCDLLIRICINXOKPLCPBEKORHLD 120
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Db      61 AVCDKCLKFYSKISEYHYCYVGTLEQYNNKPLCDLIRNCINCKPLCPBEKORHLD 120
Qy      121 KQRFHNIRGWTGRCMSCCSSSRTRETOL 151
Db      121 KQRFHNIRGWTGRCMSCCSSSRTRETOL 151

RESULT 25
Q919D4 HPV16 PRELIMINARY; PRT; 161 AA.
ID Q919D4 HPV16 PRELIMINARY; PRT; 161 AA.
AC Q919D4;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE E6 protein (fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=333760;
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=21846229; PubMed=11857370; DOI=10.1002/1jc.10103;
RA Watts K.J., Thompson C.H., Coesart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
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DR EMBL; AF404693; AL01343.1; -, Genomic DNA.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
DR NOD TER
SQ SEQUENCE 161 AA; 19624 MW; 10C72CDB14200460 CRC64;

Query Match      98.4%; Score 817; DB 2; Length 161;
Best Local Similarity 97.4%; Pred. No. 2e-72;
Matches 147; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy      1 MFQDPQERPRKLPOLCTELQTTIHDIIECYCKQQLRREVDFAFRDLCIVYRDGPNY 60
Db      11 MFQDPQERPRKLPOLCTELQTTIHDIIECYCKQQLRREVDFAFRDLCIVYRDGPNY 70
Qy      61 AVXDKCLKFYSKISEYHYCYVGTLEQYNNKPLCDLIRNCINCKPLCPBEKORHLD 120
Db      71 AVCDKCLKFYSKISEYHYCYVGTLEQYNNKPLCDLIRNCINCKPLCPBEKORHLD 130
Qy      121 KQRFHNIRGWTGRCMSCCSSSRTRETOL 151
Db      131 KQRFHNIRGWTGRCMSCCSSSRTRETOL 161

RESULT 26
Q08QD9 HPV16 PRELIMINARY; PRT; 158 AA.
ID Q08QD9 HPV16 PRELIMINARY; PRT; 158 AA.
AC Q08QD9;
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2002, sequence version 1.
DT 07-FEB-2006, entry version 14.
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=333760;
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=As-A267;
RX MEDLINE=22182962; PubMed=12195358; DOI=10.1086/342048;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
```

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RT      "Human papillomavirus type 16 intratypic variant infection and risk
RT for cervical neoplasia in southern China.";
RL J. Infect. Dis. 186:696-700(2002).
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-----
DR EMBL; AF486309; AL96614.1; -, Genomic DNA.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 158 AA; 19173 MW; 161AD3EFAA4D636B CRC64;

Query Match      98.3%; Score 816; DB 2; Length 158;
Best Local Similarity 96.7%; Pred. No. 2.4e-72;
Matches 146; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy      1 MFQDPQERPRKLPOLCTELQTTIHDIIECYCKQQLRREVDFAFRDLCIVYRDGPNY 60
Db      8 MFQDPQERPRKLPOLCTELQTTIHDIIECYCKQQLRREVDFAFRDLCIVYRDGPNY 67
Qy      61 AVXDKCLKFYSKISEYHYCYVGTLEQYNNKPLCDLIRNCINCKPLCPBEKORHLD 120
Db      68 AVCDKCLKFYSKISEYHYCYVGTLEQYNNKPLCDLIRNCINCKPLCPBEKORHLD 127
Qy      121 KQRFHNIRGWTGRCMSCCSSSRTRETOL 151
Db      128 KQRFHNIRGWTGRCMSCCSSSRTRETOL 158

RESULT 27
Q08QEO HPV16 PRELIMINARY; PRT; 158 AA.
ID Q08QEO HPV16 PRELIMINARY; PRT; 158 AA.
AC Q08QEO;
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2002, sequence version 1.
DT 07-FEB-2006, entry version 14.
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=333760;
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=As-G137;
RX MEDLINE=22182962; PubMed=12195358; DOI=10.1086/342048;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
RT "Human papillomavirus type 16 intratypic variant infection and risk
RT for cervical neoplasia in southern China.";
RL J. Infect. Dis. 186:696-700(2002).
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DR EMBL; AF486307; AL96612.1; -, Genomic DNA.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 158 AA; 19187 MW; 005E2FCE1B617C55B CRC64;

Query Match      98.3%; Score 816; DB 2; Length 158;
Best Local Similarity 96.7%; Pred. No. 2.4e-72;
Matches 146; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy      1 MFQDPQERPRKLPOLCTELQTTIHDIIECYCKQQLRREVDFAFRDLCIVYRDGPNY 60
Db      8 MFQDPQERPRKLPOLCTELQTTIHDIIECYCKQQLRREVDFAFRDLCIVYRDGPNY 67
Qy      61 AVXDKCLKFYSKISEYHYCYVGTLEQYNNKPLCDLIRNCINCKPLCPBEKORHLD 120
Db      61 AVXDKCLKFYSKISEYHYCYVGTLEQYNNKPLCDLIRNCINCKPLCPBEKORHLD 120
```

```
Db 68 AVCDKCLKFYSKISEYRHVYCSLVGTTLLEQYKPLCDLLIRNCINCQKPLCPREEKORHLD 127
Qy 121 KKORFHNIRGRWTCGCMSCCRSSRRRETOL 151
Db 128 KKORFHNIRGRWTCGCMSCCRSSRRRETOL 158

RESULT 28
Q0QDH9 HPV16 PRELIMINARY; PRT; 158 AA.
AC Q0QDH9;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DE 07-FEB-2006, entry version 17.
DE E6 protein.
OS Human Papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
RA Submitted (SSP-1999) to the EMBL/Genbank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=22182962; PubMed=12195358; DOI=10.1086/342048;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.U.K., Xu L.Y., Cheng A.F.;
RT "Human papillomavirus type 16 intratypic variant infection and risk
RT for cervical neoplasia in southern China.";
RL J. Infect. Dis. 186:696-700(2002).
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DR EMBL; AF187866; AAF13392.1; -; Genomic DNA.
DR EMBL; AF486304; AAL96609.1; -; Genomic DNA.
DR EMBL; AF486305; AAL96610.1; -; Genomic DNA.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 158 AA; 19187 MW; 155BFA5DCE6B36F0 CRC64;

Query Match 98.3%; Score 816; DB 2; Length 158;
Best Local Similarity 96.7%; Pred. No. 2.4e-72;
Matches 146; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MFQDPOEPRKLPOLCTELQTTIHDIIECYCKQQLRREYVDFARFDLCIVYRDGNPY 60
Db 8 MFQDPOEPRKLPOLCTELQTTIHDIIECYCKQQLRREYVDFARFDLCIVYRDGNPY 67
Qy 61 AVXDKCLKFYSKISEYRHVYCSLVGTTLLEQYKPLCDLLIRNCINCQKPLCPREEKORHLD 120
Db 68 AVCDKCLKFYSKISEYRHVYCSLVGTTLLEQYKPLCDLLIRNCINCQKPLCPREEKORHLD 127
Qy 121 KKORFHNIRGRWTCGCMSCCRSSRRRETOL 151
Db 128 KKORFHNIRGRWTCGCMSCCRSSRRRETOL 158

RESULT 29
Q08887 9PAPI PRELIMINARY; PRT; 151 AA.
AC Q08887;
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DE 07-FEB-2006, entry version 22.
DE Early transforming protein E6.
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Unclassified Papillomaviridae.
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OX NCBI_TaxID=10566;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96079021; PubMed=7494284;
RA Yamada T., Wheeler C.W., Halpern A.L., Stewart A.C., Hildesheim A.,
RA Jenison S.A.;
RT "Human papillomavirus type 16 variant lineages in United States
RT populations characterized by nucleotide sequence analysis of the E6,
RT L2, and L1 coding segments.";
RL J. Virol. 69:7743-7753(1995).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Farmer A.D.;
RA Submitted (AUG-1995) to the EMBL/Genbank/DBJ databases.
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DR EMBL; U34108; AAA91655.1; -; Genomic DNA.
DR EMBL; U34107; AAA91654.1; -; Genomic DNA.
DR EMBL; U34112; AAA91659.1; -; Genomic DNA.
DR EMBL; U34116; AAA91663.1; -; Genomic DNA.
DR EMBL; U34119; AAA91666.1; -; Genomic DNA.
DR EMBL; U34132; AAA91679.1; -; Genomic DNA.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18355 MW; 4695A0D5F34F9908 CRC64;

Query Match 98.2%; Score 815; DB 2; Length 151;
Best Local Similarity 97.4%; Pred. No. 2.9e-72;
Matches 147; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MFQDPOEPRKLPOLCTELQTTIHDIIECYCKQQLRREYVDFARFDLCIVYRDGNPY 60
Db 1 MFQDPOEPRKLPOLCTELQTTIHDIIECYCKQQLRREYVDFARFDLCIVYRDGNPY 60
Qy 61 AVXDKCLKFYSKISEYRHVYCSLVGTTLLEQYKPLCDLLIRNCINCQKPLCPREEKORHLD 120
Db 61 AVCDKCLKFYSKISEYRHVYCSLVGTTLLEQYKPLCDLLIRNCINCQKPLCPREEKORHLD 120
Qy 121 KKORFHNIRGRWTCGCMSCCRSSRRRETOL 151
Db 121 KKORFHNIRGRWTCGCMSCCRSSRRRETOL 151

RESULT 30
Q080RDS HPV16 PRELIMINARY; PRT; 158 AA.
AC Q080RDS;
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2002, sequence version 1.
DE 07-FEB-2006, entry version 14.
DE Transforming protein E6.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NA1;
RC MEDLINE=22182962; PubMed=12195358; DOI=10.1086/342048;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.U.K., Xu L.Y., Cheng A.F.;
RT "Human papillomavirus type 16 intratypic variant infection and risk
RT for cervical neoplasia in southern China.";
RL J. Infect. Dis. 186:696-700(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=QV15351AA, and QV15321AA;
RC PubMed=15890941; DOI=10.1128/JVI.79.11.7014-7023.2005;
RX Chen Z., Teraï M., Fu L., Herrero R., Desalle R., Burk R.D.;
```

"Diversifying selection in human papillomavirus type 16 lineages based on complete genome analyses." J. Virol. 79:7014-7023 (2005).

RT on complete genome analyses."  
RL J. Virol. 79:7014-7023 (2005).  
RN  
RA NUCLEOTIDE SEQUENCE.  
RP Teraai M., Burk R.D.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
RN  
RN NUCLEOTIDE SEQUENCE.  
RA Cruz M.R., Cerveira D.M., Camara G.N.L., Silva E.O., Carvalho L.G.S.,  
RP Martins C.R.F.;  
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
RN  
RN NUCLEOTIDE SEQUENCE.  
RA Cruz M.R., Cerveira D.M., Camara G.N.L., Silva E.O., Carvalho L.G.S.,  
RP Martins C.R.F.;  
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
RN  
RN NUCLEOTIDE SEQUENCE.  
RA Cruz M.R., Martins C.R.F.;  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
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DR EMBL: AF486325; AAL96630.1; -; Genomic DNA.  
DR EMBL: AY686582; AAV91668.1; -; Genomic DNA.  
DR EMBL: AF402678; AAO85408.1; -; Genomic DNA.  
DR EMBL: AY098923; AAM29171.1; -; Genomic DNA.  
DR EMBL: AY112662; AAM51853.1; -; Genomic DNA.  
DR EMBL: AY686579; AAV91664.1; -; Genomic DNA.  
DR GO: GO:0042025; C:host cell nucleus; IEA.  
DR GO: GO:0003677; F:DNA binding; IEA.  
DR InterPro: IPR001334; B6.  
DR Pfam: PF00518; B6; 1.  
DR SEQUENCE 158 AA; 19208 MW; B8E47F57F22EC2E1 CRC64;

Query Match 98.1%; Score 815; DB 2; Length 158;  
Best Local Similarity 97.4%; Pred. No. 3e-72;  
Matches 147; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MFODPOERPRKLTQLCTELQTTIHDIILCEVCYCKQQLLRREYVDFAFRDLCTIVYRDGPNPY 60  
DB 8 MFODPOERPRKLTQLCTELQTTIHDIILCEVCYCKQQLLRREYVDFAFRDLCTIVYRDGPNPY 67

QY 61 AVXDKLKFYSKISEYRHVCYSYVGTTLBOQYNNKPLCDLLIRCNQKPLCPBEKQRHLD 120  
DB 68 AVCDKCLKFYSKISEYRHVCYSYVGTTLBOQYNNKPLCDLLIRCNQKPLCPBEKQRHLD 127

QY 121 KKQRFNIRGRMTGRCMSCCRSSRTRETOL 151  
DB 128 KKQRFNIRGRMTGRCMSCCRSSRTRETOL 158

RESULT 31  
Q080D6\_HPV16 PRELIMINARY; PRT; 158 AA.  
ID Q080D6\_HPV16  
AC Q080D6;  
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.  
DT 01-JUN-2002, sequence version 1.  
DT 07-FEB-2006, entry version 13.  
DE B6 protein.  
OS Human papillomavirus type 16.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Alphapapillomavirus.  
OX NCBI\_Taxid=333760;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=B-7360T;  
RX MEDLINE=2182962; PubMed=12195358; DOI=10.1086/342048;  
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,  
RA Cheung J.L.K., Xu L.Y., Cheng A.F.;  
RT "Human papillomavirus type 16 intracyclic variant infection and risk

for cervical neoplasia in southern China." J. Infect. Dis. 186:686-700 (2002).

RT J. Infect. Dis. 186:686-700 (2002).  
RL  
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DR EMBL: AF486319; AAL96624.1; -; Genomic DNA.  
DR GO: GO:0042025; C:host cell nucleus; IEA.  
DR GO: GO:0003677; F:DNA binding; IEA.  
DR InterPro: IPR001334; B6.  
DR Pfam: PF00518; B6; 1.  
DR SEQUENCE 158 AA; 19246 MW; 01FEF70F45F137EB CRC64;

Query Match 98.1%; Score 814; DB 2; Length 158;  
Best Local Similarity 97.4%; Pred. No. 3.8e-72;  
Matches 147; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MFODPOERPRKLTQLCTELQTTIHDIILCEVCYCKQQLLRREYVDFAFRDLCTIVYRDGPNPY 60  
DB 8 MFODPOERPRKLTQLCTELQTTIHDIILCEVCYCKQQLLRREYVDFAFRDLCTIVYRDGPNPY 67

QY 61 AVXDKLKFYSKISEYRHVCYSYVGTTLBOQYNNKPLCDLLIRCNQKPLCPBEKQRHLD 120  
DB 68 AVCDKCLKFYSKISEYRHVCYSYVGTTLBOQYNNKPLCDLLIRCNQKPLCPBEKQRHLD 127

QY 121 KKQRFNIRGRMTGRCMSCCRSSRTRETOL 151  
DB 128 KKQRFNIRGRMTGRCMSCCRSSRTRETOL 158

RESULT 32  
Q090D3\_HPV16 PRELIMINARY; PRT; 158 AA.  
ID Q090D3\_HPV16  
AC Q090D3;  
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.  
DT 01-MAY-2000, sequence version 1.  
DT 07-FEB-2006, entry version 17.  
DE B6 protein.  
OS Human papillomavirus type 16.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Alphapapillomavirus.  
OX NCBI\_Taxid=333760;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;  
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
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DR EMBL: AF187869; AAF13398.1; -; Genomic DNA.  
DR GO: GO:0042025; C:host cell nucleus; IEA.  
DR GO: GO:0003677; F:DNA binding; IEA.  
DR InterPro: IPR001334; B6.  
DR Pfam: PF00518; B6; 1.  
DR SEQUENCE 158 AA; 19210 MW; 004EF5ADD6FA8E5B CRC64;

Query Match 98.1%; Score 814; DB 2; Length 158;  
Best Local Similarity 96.7%; Pred. No. 3.8e-72;  
Matches 146; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MFODPOERPRKLTQLCTELQTTIHDIILCEVCYCKQQLLRREYVDFAFRDLCTIVYRDGPNPY 60  
DB 8 MFODPOERPRKLTQLCTELQTTIHDIILCEVCYCKQQLLRREYVDFAFRDLCTIVYRDGPNPY 67

QY 61 AVXDKLKFYSKISEYRHVCYSYVGTTLBOQYNNKPLCDLLIRCNQKPLCPBEKQRHLD 120  
DB 68 AVCDKCLKFYSKISEYRHVCYSYVGTTLBOQYNNKPLCDLLIRCNQKPLCPBEKQRHLD 127

QY 121 KKQRFNIRGRMTGRCMSCCRSSRTRETOL 151  
DB 128 KKQRFNIRGRMTGRCMSCCRSSRTRETOL 158

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RESULT 33
ID Q919B1_HPV16 PRELIMINARY; PRT; 161 AA.
AC Q919B1;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DE 07-FEB-2006, entry version 16.
DE E6 protein (fragment) type 16.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21846229; PubMed=11857370; DOI=10.1002/jc.10103;
RA Watts K.J., Thompson C.H., Cossett Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
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CC -----
DR EMBL; AF404705; AL013366.1; -; Genomic DNA.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 161 AA; 19616 MW; E4722F0F134104DC CRC64;

Query Match 98.1%; Score 814; DB 2; Length 161;
Best Local Similarity 96.7%; Pred. No. 3.9e-72;
Matches 146; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFQDPQERPRKLPQLCTELQTTIHDIILCEVCYKQQLRREYVDFAFRDLCTIYRDGPNY 60
DB 11 MFQDPQERPRKLPQLCTELQTTIHDIILCEVCYKQQLRREYVDFAFRDLCTIYRDGPNY 70
QY 61 AYVXDKLKFYSKISEYRHVCYSYVGTTLLEQYNNKPLCDLLIRICNNKQKPLCPBEKQRLD 120
DB 71 AYVXDKLKFYSKISEYRHVCYSYVGTTLLEQYNNKPLCDLLIRICNNKQKPLCPBEKQRLD 130
QY 121 KKORFHNIRGRMTGRCMSCCRSSRTTRRETOL 151
DB 131 KKORFHNIRGRMTGRCMSCCRSSRTTRRETOL 161

RESULT 34
ID Q8QRE1_HPV16 PRELIMINARY; PRT; 158 AA.
AC Q8QRE1;
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2002, sequence version 1.
DE 07-FEB-2006, entry version 14.
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=AS-C131;
RC MEDLINE=22182962; PubMed=12195358; DOI=10.1086/342048;
RA Chan P.K.-S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
RT "Human papillomavirus type 16 intracyclic variant infection and risk
RT for cervical neoplasia in southern China.";
RL J. Infect. Dis. 186:696-700(2002).
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CC -----
DR EMBL; AF486303; AA196608.1; -; Genomic DNA.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 158 AA; 19146 MW; CB6EF5A91548727C CRC64;

Query Match 98.0%; Score 813; DB 2; Length 158;
Best Local Similarity 96.7%; Pred. No. 4.8e-72;
Matches 146; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MFQDPQERPRKLPQLCTELQTTIHDIILCEVCYKQQLRREYVDFAFRDLCTIYRDGPNY 60
DB 8 MFQDPQERPRKLPQLCTELQTTIHDIILCEVCYKQQLRREYVDFAFRDLCTIYRDGPNY 67
QY 61 AYVXDKLKFYSKISEYRHVCYSYVGTTLLEQYNNKPLCDLLIRICNNKQKPLCPBEKQRLD 120
DB 68 AYVXDKLKFYSKISEYRHVCYSYVGTTLLEQYNNKPLCDLLIRICNNKQKPLCPBEKQRLD 127
QY 121 KKORFHNIRGRMTGRCMSCCRSSRTTRRETOL 151
DB 128 KKORFHNIRGRMTGRCMSCCRSSRTTRRETOL 158

RESULT 35
ID Q12335_HPV16 PRELIMINARY; PRT; 151 AA.
AC Q12335;
DT 01-JUL-1997, integrated into UniProtKB/TrEMBL.
DT 01-JUL-1997, sequence version 1.
DE 07-FEB-2006, entry version 23.
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=97437474; PubMed=9292007;
RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Giraldo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus
RT type 16 in penile carcinomas from Ugandan patients.";
RL J. Gen. Virol. 78:2199-2208(1997).
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CC -----
DR EMBL; AF003015; AA870732.1; -; Genomic DNA.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18238 MW; BEF32A8B01CC88B CRC64;

Query Match 97.8%; Score 812; DB 2; Length 151;
Best Local Similarity 96.7%; Pred. No. 5.7e-72;
Matches 146; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MFQDPQERPRKLPQLCTELQTTIHDIILCEVCYKQQLRREYVDFAFRDLCTIYRDGPNY 60
DB 1 MFQDPQERPRKLPQLCTELQTTIHDIILCEVCYKQQLRREYVDFAFRDLCTIYRDGPNY 60
QY 61 AYVXDKLKFYSKISEYRHVCYSYVGTTLLEQYNNKPLCDLLIRICNNKQKPLCPBEKQRLD 120
DB 61 AYVXDKLKFYSKISEYRHVCYSYVGTTLLEQYNNKPLCDLLIRICNNKQKPLCPBEKQRLD 120
QY 121 KKORFHNIRGRMTGRCMSCCRSSRTTRRETOL 151
DB 121 KKORFHNIRGRMTGRCMSCCRSSRTTRRETOL 151

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RESULT 36
Q9WMP4_HPV16 PRELIMINARY; PRT; 151 AA.
AC Q9WMP4;
DT 01-NOV-1999, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1999, sequence version 1.
DT 07-FEB-2006, entry version 18.
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_Taxid=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=2011892; PubMed=10644829;
RA van Duijn M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
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CC -----
DR EMBL: AJ388060; CAB45112.1; -; Genomic DNA.
DR GO: GO:0042025; C:host cell nucleus; IEA.
DR GO: GO:0003677; F:DNA binding; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18387 MW; E2244784BBA6C02 CRC64;

Query Match 97.7%; Score 811; DB 2; Length 151;
Best Local Similarity 97.4%; Pred. No. 7.2e-72;
Matches 147; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MFODPQRPRLPOLCTELQTTIHDIILBCYCKQQLLRREVDFAFRDLCTVYRDGNY 60
DB 1 MFODPQRPRLPOLCTELQTTIHDIILBCYCKQQLLRREVDFAFRDLCTVYRDGNY 60
QY 61 AVXDCKLKFYSKISEYHHCYSYVGTLEQYNNKPLCDLIRINCINXQKPLCPBEKQRHLD 120
DB 61 AVCDKCLKFYSKISEYHHCYSYVGTLEQYNNKPLCDLIRINCINXQKPLCPBEKQRHLD 120
QY 121 KKQRFNIRGRWTRGCMSCCRSSRTRETOL 151
DB 121 KKQRFNIRGRWTRGCMSCCRSSRTRETOL 151
QY 121 KKQRFNIRGRWTRGCMSCCRSSRTRETOL 151
DB 121 KKQRFNIRGRWTRGCMSCCRSSRTRETOL 151

RESULT 37
O12336_HPV16 PRELIMINARY; PRT; 151 AA.
AC O12336;
DT 01-JUL-1997, integrated into UniProtKB/TrEMBL.
DT 01-JUL-1997, sequence version 1.
DT 07-FEB-2006, entry version 23.
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_Taxid=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=97437474; PubMed=9292007;
RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Giraldo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus
RT type 16 in penile carcinomas from Ugandan patients.";
RL J. Gen. Virol. 78:2199-2208(1997).
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CC -----
DR EMBL: AF003016; AAB70733.1; -; Genomic DNA.

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DR GO: GO:0042025; C:host cell nucleus; IEA.
DR GO: GO:0003677; F:DNA binding; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18206 MW; 51C12A8B149C6DBA CRC64;

Query Match 97.6%; Score 810; DB 2; Length 151;
Best Local Similarity 96.0%; Pred. No. 9e-72;
Matches 145; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MFODPQRPRLPOLCTELQTTIHDIILBCYCKQQLLRREVDFAFRDLCTVYRDGNY 60
DB 1 MFODPQRPRLPOLCTELQTTIHDIILBCYCKQQLLRREVDFAFRDLCTVYRDGNY 60
QY 61 AVXDCKLKFYSKISEYHHCYSYVGTLEQYNNKPLCDLIRINCINXQKPLCPBEKQRHLD 120
DB 61 AVCDKCLKFYSKISEYHHCYSYVGTLEQYNNKPLCDLIRINCINXQKPLCPBEKQRHLD 120
QY 121 KKQRFNIRGRWTRGCMSCCRSSRTRETOL 151
DB 121 KKQRFNIRGRWTRGCMSCCRSSRTRETOL 151
QY 121 KKQRFNIRGRWTRGCMSCCRSSRTRETOL 151
DB 121 KKQRFNIRGRWTRGCMSCCRSSRTRETOL 151

RESULT 38
Q9QDH7_HPV16 PRELIMINARY; PRT; 158 AA.
AC Q9QDH7;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 07-FEB-2006, entry version 17.
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_Taxid=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
RL Submitted (Sep-1999) to the EMBL/Genbank/DBJ databases.
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CC -----
DR EMBL: AF187867; AAP13394.1; -; Genomic DNA.
DR GO: GO:0042025; C:host cell nucleus; IEA.
DR GO: GO:0003677; F:DNA binding; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
SQ SEQUENCE 158 AA; 19215 MW; FCSBF2B06576864B CRC64;

Query Match 97.5%; Score 809; DB 2; Length 158;
Best Local Similarity 96.0%; Pred. No. 1.2e-71;
Matches 145; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 MFODPQRPRLPOLCTELQTTIHDIILBCYCKQQLLRREVDFAFRDLCTVYRDGNY 60
DB 8 MFODPQRPRLPOLCTELQTTIHDIILBCYCKQQLLRREVDFAFRDLCTVYRDGNY 67
QY 61 AVXDCKLKFYSKISEYHHCYSYVGTLEQYNNKPLCDLIRINCINXQKPLCPBEKQRHLD 120
DB 68 AVCDKCLKFYSKISEYHHCYSYVGTLEQYNNKPLCDLIRINCINXQKPLCPBEKQRHLD 127
QY 121 KKQRFNIRGRWTRGCMSCCRSSRTRETOL 151
DB 128 KKQRFNIRGRWTRGCMSCCRSSRTRETOL 158
QY 121 KKQRFNIRGRWTRGCMSCCRSSRTRETOL 151
DB 121 KKQRFNIRGRWTRGCMSCCRSSRTRETOL 151

RESULT 39
Q8BB21_HPV16 PRELIMINARY; PRT; 151 AA.
AC Q8BB21;
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003, sequence version 1.

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DT 07-FEB-2006, entry version 13.
DE Early transforming protein E6.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=2242222; PubMed=12355268; DOI=10.1007/s00239-002-2344-Y;
RA Derlijpils V.R., Ayala F.J., Villarreal L.P.;
RT "Evidence of diversifying selection in human papillomavirus type 16 E6
but not E7 oncogenes."
RL J. Mol. Evol. 55:491-499(2002).
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CC -----
CC EMBL; AY089952; AAM1877.1; -; Genomic DNA.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18398 MW; 4695B485FC1F8208 CRC64;

Query Match 97.3%; Score 808; DB 2; Length 151;
Best Local Similarity 96.7%; Pred. No. 1.4e-71;
Matches 146; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MFQDPQERPRKLPQCTELQTTIHDIIECYCKQQLRREVDFAFRDLCIVRDGPNY 60
DB 1 MFQDPQERPRKLPQCTELQTTIHDIIECYCKQQLRREVDFAFRDLCIVRDGPNY 60
QY 61 AVXDKCLKFYSKISEYHYCYSVYGTLEQYNNKPLCDLLIRICINXOKPLCPPEEKQRHLD 120
DB 61 AVXDKCLKFYSKISEYHYCYSVYGTLEQYNNKPLCDLLIRICINXOKPLCPPEEKQRHLD 120
QY 121 KKQRFHNIRGRWTCRSCSSRTRETOL 151
DB 121 KKQRFHNIRGRWTCRSCSSRTRETOL 151

RESULT 40
Q9NMP2_HPV16 PRELIMINARY; PRT; 151 AA.
ID Q9NMP2_HPV16 PRELIMINARY; PRT; 151 AA.
AC Q9NMP2;
DT 01-NOV-1999, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 18.
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=2011892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to
p53 codon 72 polymorphism genotypes in cervical carcinogenesis."
RL J. Gen. Virol. 81:317-325(2000).
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CC -----
CC EMBL; AJ388067; CAB45126.1; -; Genomic DNA.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18306 MW; 5E71B4EF44993C34 CRC64;

Query Match 97.3%; Score 808; DB 2; Length 151;

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Best Local Similarity 96.0%; Pred. No. 1.4e-71;
Matches 145; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 MFQDPQERPRKLPQCTELQTTIHDIIECYCKQQLRREVDFAFRDLCIVRDGPNY 60
DB 1 MFQDPQERPRKLPQCTELQTTIHDIIECYCKQQLRREVDFAFRDLCIVRDGPNY 60
QY 61 AVXDKCLKFYSKISEYHYCYSVYGTLEQYNNKPLCDLLIRICINXOKPLCPPEEKQRHLD 120
DB 61 AVXDKCLKFYSKISEYHYCYSVYGTLEQYNNKPLCDLLIRICINXOKPLCPPEEKQRHLD 120
QY 121 KKQRFHNIRGRWTCRSCSSRTRETOL 151
DB 121 KKQRFHNIRGRWTCRSCSSRTRETOL 151

RESULT 41
Q919A9_HPV16 PRELIMINARY; PRT; 161 AA.
ID Q919A9_HPV16 PRELIMINARY; PRT; 161 AA.
AC Q919A9;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE E6 protein (fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21846229; PubMed=11857370; DOI=10.1002/jic.10103;
RA Watts K.J., Thompson C.H., Coscart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
cervical cancer isolates from Australia and New Caledonia."
RL Int. J. Cancer 97:868-874(2002).
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CC -----
CC EMBL; AF04706; AAL01368.1; -; Genomic DNA.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
FT NON TER
SQ SEQUENCE 161 AA; 19692 MW; ACC9B1A52045EA6A CRC64;

Query Match 97.3%; Score 808; DB 2; Length 161;
Best Local Similarity 96.7%; Pred. No. 1.5e-71;
Matches 146; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MFQDPQERPRKLPQCTELQTTIHDIIECYCKQQLRREVDFAFRDLCIVRDGPNY 60
DB 1 MFQDPQERPRKLPQCTELQTTIHDIIECYCKQQLRREVDFAFRDLCIVRDGPNY 70
QY 61 AVXDKCLKFYSKISEYHYCYSVYGTLEQYNNKPLCDLLIRICINXOKPLCPPEEKQRHLD 120
DB 71 AVXDKCLKFYSKISEYHYCYSVYGTLEQYNNKPLCDLLIRICINXOKPLCPPEEKQRHLD 130
QY 121 KKQRFHNIRGRWTCRSCSSRTRETOL 151
DB 131 KKQRFHNIRGRWTCRSCSSRTRETOL 161

RESULT 42
Q76TS0_9PAPI PRELIMINARY; PRT; 151 AA.
ID Q76TS0_9PAPI PRELIMINARY; PRT; 151 AA.
AC Q76TS0;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE Early transforming protein E6.
OS Human papillomavirus.

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OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC unclassified Papillomaviridae.  
OX NCBI\_TaxID=10566;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=96079021; PubMed=7494284;  
RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,  
RJ Jensen S.A.  
RT "Human papillomavirus type 16 variant lineages in United States  
RT populations characterized by nucleotide sequence analysis of the E6,  
RT L2, and L1 coding segments.";  
RL J. Virol. 69:7743-7753(1995).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RA Farmer A.D.;  
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.  
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-----  
DR EMBL; U34114; AAA91661.1; -; Genomic DNA.  
DR EMBL; U34125; AAA91672.1; -; Genomic DNA.  
DR EMBL; U34130; AAA91677.1; -; Genomic DNA.  
DR EMBL; U34131; AAA91678.1; -; Genomic DNA.  
DR GO; GO:0042025; C:host cell nucleus; IEA.  
DR GO; GO:0003677; F:DNA binding; IEA.  
DR InterPro; IPR01334; B6.  
DR Pfam; PF00518; B6; 1.  
SQ SEQUENCE 151 AA; 18292 MW; 35012A9E01993C35 CRC64;  
  
Query Match 97.1%; Score 806; DB 2; Length 151;  
Best Local Similarity 96.0%; Pred. No. 2.2e-71;  
Matches 145; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
  
QY 1 MFQDPQERPRKLPOLCTELQTTIHDIIECYCCKQQLRREVDYFARFDLCIVRDGPNY 60  
DB 1 MFQDPQERPRKLPOLCTELQTTIHDIIECYCCKQQLRREVDYFARFDLCIVRDGPNY 60  
  
QY 61 AVNKKLKFYSKISEYHYHCYSVGTLEQYNNKPLCDLIRCNXKPLCPBEKORHLD 120  
DB 61 AVNKKLKFYSKISEYHYHCYSVGTLEQYNNKPLCDLIRCNXKPLCPBEKORHLD 120  
  
QY 121 KQRFNHRGWRGRCMCCSSRTRRETQL 151  
DB 121 KQRFNHRGWRGRCMCCSSRTRRETQL 151  
  
RESULT 43  
080966 HPV16 PRELIMINARY; PRT; 151 AA.  
AC Q80966; O12650; O12651; O12652; O12925; O12926; O12927; Q80962;  
AC Q80964; Q80965;  
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.  
DT 01-NOV-1996, sequence version 1.  
DT 07-FEB-2006, entry version 26.  
DE E6 protein.  
OS Human papillomavirus type 16.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Alphapapillomavirus.  
OX NCBI\_TaxID=333760;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=97437474; PubMed=9292007;  
RA Tomecello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,  
RA Beth-Giraldo E., Giraldo G.;  
RT "Sequence variations and viral genomic state of human papillomavirus  
RT type 16 in penile carcinomas from Ugandan patients.";  
RL J. Gen. Virol. 78:2199-2208(1997).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RA Terafi M., Ma Z., Burk R.D.;  
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.

RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=20112892; PubMed=10644829;  
RA Van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,  
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;  
RT "Analysis of human papillomavirus type 16 E6 variants in relation to  
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";  
RL J. Gen. Virol. 81:317-325(2000)  
RN [1]  
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DR EMBL; AF003014; AAB70731.1; -; Genomic DNA.  
DR EMBL; AF003017; AAB70734.1; -; Genomic DNA.  
DR EMBL; AF472508; AAO15697.1; -; Genomic DNA.  
DR EMBL; AF388068; CAB45128.1; -; Genomic DNA.  
DR EMBL; AF003013; AAB70730.1; -; Genomic DNA.  
DR GO; GO:0042025; C:host cell nucleus; IEA.  
DR GO; GO:0003677; F:DNA binding; IEA.  
DR InterPro; IPR01334; B6.  
DR Pfam; PF00518; B6; 1.  
SQ SEQUENCE 151 AA; 18292 MW; 35012A9E01993C35 CRC64;  
  
Query Match 97.1%; Score 806; DB 2; Length 151;  
Best Local Similarity 96.0%; Pred. No. 2.2e-71;  
Matches 145; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
  
QY 1 MFQDPQERPRKLPOLCTELQTTIHDIIECYCCKQQLRREVDYFARFDLCIVRDGPNY 60  
DB 1 MFQDPQERPRKLPOLCTELQTTIHDIIECYCCKQQLRREVDYFARFDLCIVRDGPNY 60  
  
QY 61 AVNKKLKFYSKISEYHYHCYSVGTLEQYNNKPLCDLIRCNXKPLCPBEKORHLD 120  
DB 61 AVNKKLKFYSKISEYHYHCYSVGTLEQYNNKPLCDLIRCNXKPLCPBEKORHLD 120  
  
QY 121 KQRFNHRGWRGRCMCCSSRTRRETQL 151  
DB 121 KQRFNHRGWRGRCMCCSSRTRRETQL 151  
  
RESULT 44  
08JMU8 HPV16 PRELIMINARY; PRT; 158 AA.  
AC 08JMU8;  
DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.  
DT 01-OCT-2002, sequence version 1.  
DT 07-FEB-2006, entry version 12.  
DE Transforming protein E6.  
OS Human papillomavirus type 16.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Alphapapillomavirus.  
OX NCBI\_TaxID=333760;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Cruz M.R., Cerveira D.M., Camara G.N.L., Silva E.O., Carvalho L.G.S.,  
RA Martins C.R.P.;  
RT Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RA Terafi M., Fu L., Ma Z., Burk R.D.;  
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.  
RN [3]  
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DR EMBL; AY098922; AAM29170.1; -; Genomic DNA.  
DR EMBL; AF536180; AAO10720.1; -; Genomic DNA.  
DR GO; GO:0042025; C:host cell nucleus; IEA.  
DR GO; GO:0003677; F:DNA binding; IEA.  
DR InterPro; IPR01334; B6.  
DR Pfam; PF00518; B6; 1.  
SQ SEQUENCE 158 AA; 19145 MW; CB70F51C00F867DC CRC64;  
  
Query Match 97.1%; Score 806; DB 2; Length 158;

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Best Local Similarity 96.0%; Pred. No. 2.4e-71;
Matches 145; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MFQDPQERPRKLPOLCTELQTTIHDIIECYCKQQLRREVDPAFADLCIVRDGPNY 60
DB 8 MFQDPQERPRKLPOLCTELQTTIHDIIECYCKQQLRREVDPAFADLCIVRDGPNY 67
QY 61 AVXDKCLKFYKISSEYRHYCYVYGTTLLEQYKNPCLDLLIRCTINXQKPLCPBEKQRLHD 120
DB 68 AVXDKCLKFYKISSEYRHYCYVYGTTLLEQYKNPCLDLLIRCTINXQKPLCPBEKQRLHD 127
QY 121 KKQRFHNIRGRWTRCSCSSSRTRETOL 151
DB 128 KKQRFHNIRGRWTRCSCSSSRTRETOL 158

RESULT 45
Q77E16 HPV16 PRELIMINARY; PRT; 151 AA.
ID 077E16 HPV16
AC 077E16
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DE E6 oncoprotein (E6 protein).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=333760;
RN NM
RP NUCLEOTIDE SEQUENCE.
RA Ponglikitmongkol M., Vaeteewootacharn K.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
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CC -----
DB EMBL; AF469197; AA015691.1; -: Genomic DNA.
DB EMBL; AJ388063; CAB45118.1; -: Genomic DNA.
DB GO; GO:0042025; C:host cell nucleus; IEA.
DB GO; GO:0003677; F:DNA binding; IEA.
DB InterPro; IPR001334; E6.
DB Pfam; PF00518; E6; 1.
DR SEQUENCE 151 AA; 18304 MW; 0F312A8BDBA6CF1F CRC64;

Query Match 96.9%; Score 804; DB 2; Length 151;
Best Local Similarity 96.0%; Pred. No. 3.5e-71;
Matches 145; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MFQDPQERPRKLPOLCTELQTTIHDIIECYCKQQLRREVDPAFADLCIVRDGPNY 60
DB 1 MFQDPQERPRKLPOLCTELQTTIHDIIECYCKQQLRREVDPAFADLCIVRDGPNY 60
QY 61 AVXDKCLKFYKISSEYRHYCYVYGTTLLEQYKNPCLDLLIRCTINXQKPLCPBEKQRLHD 120
DB 61 AVXDKCLKFYKISSEYRHYCYVYGTTLLEQYKNPCLDLLIRCTINXQKPLCPBEKQRLHD 120
QY 121 KKQRFHNIRGRWTRCSCSSSRTRETOL 151
DB 121 KKQRFHNIRGRWTRCSCSSSRTRETOL 151

RESULT 46
Q89708 9PAPI PRELIMINARY; PRT; 151 AA.
ID 089708 9PAPI
AC Q89708;
```

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DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 24.
DE Early transforming protein E6.
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC unclassified Papillomaviridae.
OX NCBI_TaxID=10566;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96079021; PubMed=7494284;
RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
RA Jenison S.A.;
RT "Human papillomavirus type 16 variant lineages in United States
RT populations characterized by nucleotide sequence analysis of the E6,
RT E2, and L1 coding segments.";
RL J. Virol. 69:7743-7753(1995).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Farmer A.D.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
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CC -----
DB EMBL; U34128; AAA91675.1; -: Genomic DNA.
DB EMBL; U34117; AAA91664.1; -: Genomic DNA.
DB EMBL; U34118; AAA91665.1; -: Genomic DNA.
DB GO; GO:0042025; C:host cell nucleus; IEA.
DB GO; GO:0003677; F:DNA binding; IEA.
DB InterPro; IPR001334; E6.
DB Pfam; PF00518; E6; 1.
DR SEQUENCE 151 AA; 18304 MW; 0F312A8BDBA6CF1F CRC64;

Query Match 96.9%; Score 804; DB 2; Length 151;
Best Local Similarity 96.0%; Pred. No. 3.5e-71;
Matches 145; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MFQDPQERPRKLPOLCTELQTTIHDIIECYCKQQLRREVDPAFADLCIVRDGPNY 60
DB 1 MFQDPQERPRKLPOLCTELQTTIHDIIECYCKQQLRREVDPAFADLCIVRDGPNY 60
QY 61 AVXDKCLKFYKISSEYRHYCYVYGTTLLEQYKNPCLDLLIRCTINXQKPLCPBEKQRLHD 120
DB 61 AVXDKCLKFYKISSEYRHYCYVYGTTLLEQYKNPCLDLLIRCTINXQKPLCPBEKQRLHD 120
QY 121 KKQRFHNIRGRWTRCSCSSSRTRETOL 151
DB 121 KKQRFHNIRGRWTRCSCSSSRTRETOL 151

RESULT 47
Q9MMP3 HPV16 PRELIMINARY; PRT; 151 AA.
ID 09MMP3 HPV16
AC 09MMP3;
DT 01-NOV-1999, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1999, sequence version 1.
DT 07-FEB-2006, entry version 19.
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
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CC EMBL; AJ388065; CAB45122.1; -; Genomic DNA.  
DR GO; GO:0042025; C:host cell nucleus; IEA.  
DR GO; GO:0003677; F:DNA binding; IEA.  
DR InterPro; IPR001334; E6.  
DR Pfam; PF00518; E6; 1.  
SQ SEQUENCE 151 AA; 18412 MW; E794A494FD0E8209 CRC64;  
  
Query Match 96.9%; Score 804; DB 2; Length 151;  
Best Local Similarity 96.0%; Pred. No. 3.5e-71;  
Matches 145; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
  
Qy 1 MFODPOERPRKLPOLCTELQTTIHDIILCEVCYCKQQLLRREVDFAFRDLCIVYRDGNPY 60  
Db 1 MFODPOERPRKLPOLCTELQTTIHDIILCEVCYCKQQLLRREVDFAFRDLCIVYRDGNPY 60  
Qy 61 AVXDCKLKFYSKISEYHYCYSVYGTLEQOYNKPLCDLIRCTINXOKPLCPBEKORHLD 120  
Db 61 AVCEKCLKFYSKISEYHYCYSVYGTLEQOYNKPLCDLIRCTINXOKPLCPBEKORHLD 120  
Qy 121 KKORFHNIRGRWTRGCMSCCRSSRTRETOL 151  
Db 121 KKORFHNIRGRWTRGCMSCCRSSRTRETOL 151  
  
RESULT 48  
Q08QNO HPV16 PRELIMINARY; PRT; 158 AA.  
ID O8QNO HPV16  
AC O8QNO;  
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.  
DT 01-JUN-2002, sequence version 1.  
DT 07-FEB-2006, entry version 13.  
DE Transforming protein E6.  
OS Human papillomavirus type 16.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Alphapapillomavirus.  
OX NCBI\_TaxID=333760;  
RN NUCLEOTIDE SEQUENCE.  
RP STRAIN=E-350G, and Af2-a;  
RC MEDLINE=22182962; PubMed=12195358; DOI=10.1086/342048;  
RX Chan P.K.S., Lam C.W., Cheng T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,  
RA Cheung J.L.K., Xu L.Y., Cheng A.F.;  
RT "Human papillomavirus type 16 intracyclic variant infection and risk  
for cervical neoplasia in southern China.";  
RT Infect. Dis. 186:696-700(2002).  
RL NUCLEOTIDE SEQUENCE.  
RP Teral M., Ma Z., Burk R.D.;  
RA Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RA Cruz M.R., Gerqueire D.M., Camara G.N.L., Silva E.O., Carvalho L.G.S.,  
RA Martins C.R.F.;  
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
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CC EMBL; AF486314; AAU96619.1; -; Genomic DNA.  
DR EMBL; AF472509; AAO15705.1; -; Genomic DNA.  
DR EMBL; AF486314; AAU96629.1; -; Genomic DNA.  
DR EMBL; AY098918; AAM29166.1; -; Genomic DNA.  
DR GO; GO:0042025; C:host cell nucleus; IEA.  
DR GO; GO:0003677; F:DNA binding; IEA.  
DR InterPro; IPR001334; E6.  
DR Pfam; PF00518; E6; 1.  
SQ SEQUENCE 158 AA; 19157 MW; F140F509DAC794F6 CRC64;  
  
Query Match 96.9%; Score 804; DB 2; Length 158;  
Best Local Similarity 96.0%; Pred. No. 3.7e-71;  
Matches 145; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MFODPOERPRKLPOLCTELQTTIHDIILCEVCYCKQQLLRREVDFAFRDLCIVYRDGNPY 60  
Db 8 MFODPOERPRKLPOLCTELQTTIHDIILCEVCYCKQQLLRREVDFAFRDLCIVYRDGNPY 67  
Qy 61 AVXDCKLKFYSKISEYHYCYSVYGTLEQOYNKPLCDLIRCTINXOKPLCPBEKORHLD 120  
Db 68 AVCDCKLKFYSKISEYHYCYSLYGTLEQOYNKPLCDLIRCTINXOKPLCPBEKORHLD 127  
Qy 121 KKORFHNIRGRWTRGCMSCCRSSRTRETOL 151  
Db 128 KKORFHNIRGRWTRGCMSCCRSSRTRETOL 158  
  
Query Match 96.7%; Score 803; DB 2; Length 158;  
Best Local Similarity 96.0%; Pred. No. 4.7e-71;  
Matches 145; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
  
Qy 1 MFODPOERPRKLPOLCTELQTTIHDIILCEVCYCKQQLLRREVDFAFRDLCIVYRDGNPY 60  
Db 8 MFODPOERPRKLPOLCTELQTTIHDIILCEVCYCKQQLLRREVDFAFRDLCIVYRDGNPY 67  
Qy 61 AVXDCKLKFYSKISEYHYCYSVYGTLEQOYNKPLCDLIRCTINXOKPLCPBEKORHLD 120  
Db 68 AVCDCKLKFYSKISEYHYCYSLYGTLEQOYNKPLCDLIRCTINXOKPLCPBEKORHLD 127  
Qy 121 KKORFHNIRGRWTRGCMSCCRSSRTRETOL 151  
Db 128 KKORFHNIRGRWTRGCMSCCRSSRTRETOL 158  
  
RESULT 50  
Q019C4 HPV16 PRELIMINARY; PRT; 143 AA.  
ID Q019C4 HPV16  
AC Q019C4;  
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.  
DT 01-DEC-2001, sequence version 1.  
DT 07-FEB-2006, entry version 16.  
DE E6 protein (Fragment).  
OS Human papillomavirus type 16.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Alphapapillomavirus.  
OX NCBI\_TaxID=333760;  
RN NUCLEOTIDE SEQUENCE.  
RP MEDLINE=21846229; PubMed=11857370; DOI=10.1002/13c.10103;  
RX

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RA  Watsc K.J., Thompson C.H., Coesart Y.E., Rose B.R.;
RT  "Sequence variation and physical state of human papillomavirus type 16
RL  Int. J. Cancer 97:868-874(2002).
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CC  -----
DR  EMBL; AF404698; AAL01353.1; -; Genomic DNA.
DR  GO; GO:0042025; C:host cell nucleus; IEA.
DR  GO; GO:0003677; F:DNA binding; IEA.
DR  InterPro; IPR001334; E6.
DR  Pfam; PF00518; E6; 1.
FT  NON TER
SQ  SEQUENCE 143 AA; 17274 MW; 5FB0F7E1EC6DBA82 CRC64;

Query Match 94.1%; Score 781; DB 2; Length 143;
Best Local Similarity 97.9%; Pred. No. 6.2e-69;
Matches 140; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 9 PRKLPOLCTELQTTIHDIILCEVCYCKQQLLRREYVDFAFRDLCTIYRDGNPYAVXDKCLK 68
Db 1 PRKLPOLCTELQTTIHDIILCEVCYCKQQLLRREYVDFAFRDLCTIYRDGNPYAVXDKCLK 60
Qy 69 FYSKISEYRHVCYSYVGTTLLEQYNNKPLCDLLIRICINXQKPLCPBEKQRLDKQRFHNI 128
Db 61 FYSKISEYRHVCYSYVGTTLLEQYNNKPLCDLLIRICINXQKPLCPBEKQRLDKQRFHNI 120
Qy 129 RGRWTCRCMSSCRSSRTRETQL 151
Db 121 RGRWTCRCMSSCRSSRTRETQL 143

RESULT 51
Q019B6 HPV16 PRELIMINARY; PRT; 143 AA.
AC Q019B6;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DE 07-FEB-2006, entry version 16.
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA MEDLINE=21846229; PubMed=11857370; DOI=10.1002/ijc.10103;
RA Watsc K.J., Thompson C.H., Coesart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RL Int. J. Cancer 97:868-874(2002).
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CC -----
DR EMBL; AF404702; AAL01361.1; -; Genomic DNA.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
FT NON TER
SQ SEQUENCE 143 AA; 17272 MW; 071F14EE3E6BE2AC CRC64;

Query Match 93.3%; Score 774; DB 2; Length 143;
Best Local Similarity 97.2%; Pred. No. 3e-66;
Matches 139; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 9 PRKLPOLCTELQTTIHDIILCEVCYCKQQLLRREYVDFAFRDLCTIYRDGNPYAVXDKCLK 68
Db 1 PRKLPOLCTELQTTIHDIILCEVCYCKQQLLRREYVDFAFRDLCTIYRDGNPYAVXDKCLK 60
Qy 69 FYSKISEYRHVCYSYVGTTLLEQYNNKPLCDLLIRICINXQKPLCPBEKQRLDKQRFHNI 128

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Db 61 FYSKISEYRHVCYSYVGTTLLEQYNNKPLCDLLIRICINXQKPLCPBEKQRLDKQRFHNI 120
Qy 129 RGRWTCRCMSSCRSSRTRETQL 151
Db 121 RGRWTCRCMSSCRSSRTRETQL 143

RESULT 52
Q019D2 HPV16 PRELIMINARY; PRT; 138 AA.
ID Q019D2 HPV16 PRELIMINARY; PRT; 138 AA.
AC Q019D2;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DE 07-FEB-2006, entry version 16.
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA MEDLINE=21846229; PubMed=11857370; DOI=10.1002/ijc.10103;
RA Watsc K.J., Thompson C.H., Coesart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RL Int. J. Cancer 97:868-874(2002).
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CC -----
DR EMBL; AF404694; AAL01345.1; -; Genomic DNA.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
FT NON TER
SQ SEQUENCE 138 AA; 16696 MW; 481E5AEA90895FC2 CRC64;

Query Match 90.8%; Score 754; DB 2; Length 138;
Best Local Similarity 98.6%; Pred. No. 2.8e-66;
Matches 136; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 14 QLCTELQTTIHDIILCEVCYCKQQLLRREYVDFAFRDLCTIYRDGNPYAVXDKCLKFYSKI 73
Db 1 QLCTELQTTIHDIILCEVCYCKQQLLRREYVDFAFRDLCTIYRDGNPYAVXDKCLKFYSKI 60
Qy 74 SEYRHVCYSYVGTTLLEQYNNKPLCDLLIRICINXQKPLCPBEKQRLDKQRFHNI RGRWT 133
Db 61 SEYRHVCYSYVGTTLLEQYNNKPLCDLLIRICINXQKPLCPBEKQRLDKQRFHNI RGRWT 120
Qy 134 GRCMSSCRSSRTRETQL 151
Db 121 GRCMSSCRSSRTRETQL 138

RESULT 53
Q019C0 HPV16 PRELIMINARY; PRT; 130 AA.
ID Q019C0 HPV16 PRELIMINARY; PRT; 130 AA.
AC Q019C0;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DE 07-FEB-2006, entry version 16.
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA MEDLINE=21846229; PubMed=11857370; DOI=10.1002/ijc.10103;
RA Watsc K.J., Thompson C.H., Coesart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16

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RT cervical cancer isolates from Australia and New Caledonia."  
RL Int. J. Cancer 97:868-874(2002).  
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CC -----  
DR EMBL: AF404700; AL01357.1; -; Genomic DNA.  
DR GO: GO:0042025; C:host cell nucleus; IEA.  
DR GO: GO:0003677; F:DNA binding; IEA.  
DR InterPro: IPR001334; E6.  
DR Pfam: PF00518; E6; 1.  
FT NON TER 1 1  
SQ SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;  
  
Query Match 85.8%; Score 712; DB 2; Length 130;  
Best Local Similarity 98.5%; Pred. No. 3.6e-62;  
Matches 128; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 22 TTHDILIECVYCKQOQLRREYVDFAFRDLCTVYRDGNFYAVXDKLKFYSKISEYRHICY 81  
DB 1 TTHDILIECVYCKQOQLRREYVDFAFRDLCTVYRDGNFYAVCDKLFYSKISEYRHICY 60  
  
QY 82 SVYGTLEQYNNKPLCDLLIRICINXQKPLCPEEKQRHLDKKQRFNINIRGRTGRCMSCCR 141  
DB 61 SVYGTLEQYNNKPLCDLLIRICINQKPLCPEEKQRHLDKKQRFNINIRGRTGRCMSCCR 120  
  
QY 142 SSRTRETOL 151  
DB 121 SSRTRETOL 130  
  
RESULT 54  
QY 0919C2\_HPV16 PRELIMINARY; PRT; 130 AA.  
ID 0919C2\_HPV16  
AC 0919C2;  
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.  
DT 01-DEC-2001, sequence version 1.  
DT 07-FEB-2006, entry version 16.  
DE E6 protein (fragment).  
OS Human Papillomavirus type 16.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Alphapapillomavirus.  
OX NCBI\_TaxID=333760;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=21846229; PubMed=11857370; DOI=10.1002/jic.10103;  
RA Watts K.U., Thompson C.H., Cossart Y.E., Rose B.R.;  
RT "Sequence variation and physical state of human papillomavirus type 16  
RT cervical cancer isolates from Australia and New Caledonia."  
RL Int. J. Cancer 97:868-874(2002).  
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CC -----  
DR EMBL: AF404699; AL01355.1; -; Genomic DNA.  
DR GO: GO:0042025; C:host cell nucleus; IEA.  
DR GO: GO:0003677; F:DNA binding; IEA.  
DR InterPro: IPR001334; E6.  
DR Pfam: PF00518; E6; 1.  
FT NON TER 1 1  
SQ SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;  
  
Query Match 85.8%; Score 712; DB 2; Length 130;  
Best Local Similarity 98.5%; Pred. No. 3.6e-62;  
Matches 128; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 22 TTHDILIECVYCKQOQLRREYVDFAFRDLCTVYRDGNFYAVXDKLKFYSKISEYRHICY 81  
DB 1 TTHDILIECVYCKQOQLRREYVDFAFRDLCTVYRDGNFYAVCDKLFYSKISEYRHICY 60  
  
QY 82 SVYGTLEQYNNKPLCDLLIRICINXQKPLCPEEKQRHLDKKQRFNINIRGRTGRCMSCCR 141  
DB 61 SVYGTLEQYNNKPLCDLLIRICINQKPLCPEEKQRHLDKKQRFNINIRGRTGRCMSCCR 120

QY 142 SSRTRETOL 151  
DB 121 SSRTRETOL 130  
  
RESULT 55  
QY 0919B8\_HPV16 PRELIMINARY; PRT; 130 AA.  
ID 0919B8\_HPV16  
AC 0919B8;  
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.  
DT 01-DEC-2001, sequence version 1.  
DT 07-FEB-2006, entry version 16.  
DE E6 protein (fragment).  
OS Human Papillomavirus type 16.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Alphapapillomavirus.  
OX NCBI\_TaxID=333760;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=21846229; PubMed=11857370; DOI=10.1002/jic.10103;  
RA Watts K.U., Thompson C.H., Cossart Y.E., Rose B.R.;  
RT "Sequence variation and physical state of human papillomavirus type 16  
RT cervical cancer isolates from Australia and New Caledonia."  
RL Int. J. Cancer 97:868-874(2002).  
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CC -----  
DR EMBL: AF404701; AL01359.1; -; Genomic DNA.  
DR GO: GO:0042025; C:host cell nucleus; IEA.  
DR GO: GO:0003677; F:DNA binding; IEA.  
DR InterPro: IPR001334; E6.  
DR Pfam: PF00518; E6; 1.  
FT NON TER 1 1  
SQ SEQUENCE 130 AA; 15775 MW; 92D3C07BF96B092F CRC64;  
  
Query Match 85.2%; Score 707; DB 2; Length 130;  
Best Local Similarity 96.4%; Pred. No. 1.1e-61;  
Matches 127; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 23 IHDHILIECVYCKQOQLRREYVDFAFRDLCTVYRDGNFYAVXDKLKFYSKISEYRHICY 82  
DB 2 IHDHILIECVYCKQOQLRREYVDFAFRDLCTVYRDGNFYAVCDKLFYSKISEYRHICY 61  
  
QY 83 VYGTLEQYNNKPLCDLLIRICINXQKPLCPEEKQRHLDKKQRFNINIRGRTGRCMSCCR 142  
DB 62 VYGTLEQYNNKPLCDLLIRICINQKPLCPEEKQRHLDKKQRFNINIRGRTGRCMSCCR 121  
  
QY 143 SSRTRETOL 151  
DB 122 SSRTRETOL 130  
  
RESULT 56  
QY 0919C8\_HPV16 PRELIMINARY; PRT; 130 AA.  
ID 0919C8\_HPV16  
AC 0919C8;  
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.  
DT 01-DEC-2001, sequence version 1.  
DT 07-FEB-2006, entry version 16.  
DE E6 protein (fragment).  
OS Human Papillomavirus type 16.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Alphapapillomavirus.  
OX NCBI\_TaxID=333760;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=21846229; PubMed=11857370; DOI=10.1002/jic.10103;  
RA Watts K.U., Thompson C.H., Cossart Y.E., Rose B.R.;  
RT "Sequence variation and physical state of human papillomavirus type 16  
RT cervical cancer isolates from Australia and New Caledonia."  
RL Int. J. Cancer 97:868-874(2002).

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CC -----
DR EMBL; AF404696; AAL01349.1; -, Genomic DNA.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
FT NON TER
SQ SEQUENCE 130 AA; 15778 MW; 2830147D378BDDC9 CRC64;

Query Match 85.2%; Score 707; DB 2; Length 130;
Best Local Similarity 97.7%; Pred. No. 1.1e-61;
Matches 127; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 22 TIHDIIECVYCKQOLLRREYVDFAFRDLCTVYRGNPYAVXDCLKPYSKISEYRHICY 81
Db 1 TIHNIILCEVCYCKQOLLRREYVDFAFRDLCTVYRGNPYAVCDKCLKPYSKISEYRHICY 60
Oy 82 SVYGTLEEQYNKPLCDLLIRNCINQKPLCEBEKORHLDKKORFHNIRGRWTGRMSCCR 141
Db 61 SVYGTLEEQYNKPLCDLLIRNCINQKPLCEBEKORHLDKKORFHNIRGRWTGRMSCCR 120
Oy 142 SSRTRRETOL 151
Db 121 SSRTRRETOL 130

RESULT 57
Oy 0919B4 HPV16 PRELIMINARY; PRT; 130 AA.
ID 0919B4 HPV16
AC 0919B4;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxId=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21846229; PubMed=11857370; DOI=10.1002/jic.10103;
RA Wacts K.J., Thompson C.H., Coesart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
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CC -----
DR EMBL; AF404703; AAL01363.1; -, Genomic DNA.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
FT NON TER
SQ SEQUENCE 130 AA; 15792 MW; B6C2147D227EEDDC CRC64;

Query Match 84.8%; Score 704; DB 2; Length 130;
Best Local Similarity 96.9%; Pred. No. 2.2e-61;
Matches 126; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 22 TIHDIIECVYCKQOLLRREYVDFAFRDLCTVYRGNPYAVXDCLKPYSKISEYRHICY 81
Db 1 TIHNIILCEVCYCKQOLLRREYVDFAFRDLCTVYRGNPYAVCDKCLKPYSKISEYRHICY 60
Oy 82 SVYGTLEEQYNKPLCDLLIRNCINQKPLCEBEKORHLDKKORFHNIRGRWTGRMSCCR 141
Db 61 SVYGTLEEQYNKPLCDLLIRNCINQKPLCEBEKORHLDKKORFHNIRGRWTGRMSCCR 120
Oy 142 SSRTRRETOL 151
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Db 121 SSRTRRETOL 130

RESULT 58
Oy 0919D0 HPV16 PRELIMINARY; PRT; 130 AA.
ID 0919D0 HPV16
AC 0919D0;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxId=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21846229; PubMed=11857370; DOI=10.1002/jic.10103;
RA Wacts K.J., Thompson C.H., Coesart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
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CC -----
DR EMBL; AF404695; AAL01347.1; -, Genomic DNA.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
FT NON TER
SQ SEQUENCE 130 AA; 15735 MW; 9EFB30EBDCA21AF3 CRC64;

Query Match 84.6%; Score 702; DB 2; Length 130;
Best Local Similarity 96.9%; Pred. No. 3.5e-61;
Matches 126; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 22 TIHDIIECVYCKQOLLRREYVDFAFRDLCTVYRGNPYAVXDCLKPYSKISEYRHICY 81
Db 1 TIHNIILCEVCYCKQOLLRREYVDFAFRDLCTVYRGNPYAVCDKCLKPYSKISEYRHICY 60
Oy 82 SVYGTLEEQYNKPLCDLLIRNCINQKPLCEBEKORHLDKKORFHNIRGRWTGRMSCCR 141
Db 61 SVYGTLEEQYNKPLCDLLIRNCINQKPLCEBEKORHLDKKORFHNIRGRWTGRMSCCR 120
Oy 142 SSRTRRETOL 151
Db 121 SSRTRRETOL 130

RESULT 59
Oy 04TUF9 HPV35 PRELIMINARY; PRT; 149 AA.
ID 04TUF9 HPV35
AC 04TUF9;
DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2005, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE E6 protein.
GN Name=E6;
OS Human papillomavirus type 35.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxId=10587;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=NM1215, NM1301, NM2760, and NM3793;
RX PubMed=16227283; DOI=10.1128/JVI.79.21.13630-13640.2005;
RA Calleja-Macias I.E., Villa L.L., Prado J.C., Kalantar M., Allan B.,
RA Williamson A.L., Chung L.P., Collins R.J., Zuna R.E., Dunn S.T.,
RA Chu T.Y., Cudde H.A., Cuschieri K., von Knebel-Deebertz M.,
RA Martins C.R., Sanchez G.I., Bosch F.X., Munoz N., Bernard H.U.;
```

"Worldwide genomic diversity of the high-risk human papillomavirus  
RT types 31, 35, 52, and 58, four close relatives of human papillomavirus  
RT type 16." J. Virol. 79:13630-13640(2005).  
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DR EMBL: DQ057309; AAY58340.1; -; Genomic DNA.  
DR EMBL: DQ057310; AAY58341.1; -; Genomic DNA.  
DR EMBL: DQ057311; AAY58342.1; -; Genomic DNA.  
DR EMBL: DQ057312; AAY58343.1; -; Genomic DNA.  
DR GO: GO:0042025; C:host cell nucleus; IEA.  
DR GO: GO:0003677; F:DNA binding; IEA.  
SQ SEQUENCE 149 AA; 18015 MW; 8354D5CFA2935026 CRC64;  
Query Match 69.9%; Score 580; DB 2; Length 149;  
Best Local Similarity 71.5%; Pred. No. 4.4e-49;  
Matches 108; Conservative 13; Mismatches 28; Indels 2; Gaps 1;  
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QY 1 MFODPQPRPKLPTCLTELQTTIHDIILECYCKQQLRREVDYDFARDLCTVYRDGPNY 60  
DB 1 MFODPQPRPKLPTCLTELQTTIHDIILECYCKQQLRREVDYDFARDLCTVYRDGPNY 60  
QY 61 AYVXDKLKFYSKISEYRHYCYVGTTLLEQYKPLCDLLIRCNXKPLCPPEKORHLD 120  
DB 61 GVCWKCKLKFYSKISEYRHYCYVGTTLLEQYKPLCDLLIRCNXKPLCPPEKORHLD 120  
QY 121 KKQRFNHRGRWTCRSCSCSSRTRETOL 151  
DB 121 EKGRFHNIGRWTCRSCSCSSRTRETOL 151  
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RESULT 60  
Q84298 9PAPI PRELIMINARY; PRT; 149 AA.  
ID O84298 9PAPI  
CD O84298 9PAPI  
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.  
DT 07-FEB-2006, entry version 26.  
DE E6 protein.  
OS Human papillomavirus.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC unclassified Papillomaviridae.  
OX NCBI\_TaxID=10566;  
RN [1]  
RA NUCLEOTIDE SEQUENCE.  
RP Fujinaga K.;  
RL Submitted (FEB-1992) to the EMBL/Genbank/DBJ databases.  
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DR EMBL: D10597; BAA01447.1; -; Genomic DNA.  
DR GO: GO:0042025; C:host cell nucleus; IEA.  
DR GO: GO:0003677; F:DNA binding; IEA.  
DR InterPro: IPR001334; E6.  
DR Pfam: PF00518; E6; 1.  
SQ SEQUENCE 149 AA; 18015 MW; 8354D5CFA2935026 CRC64;  
Query Match 69.9%; Score 580; DB 2; Length 149;  
Best Local Similarity 71.5%; Pred. No. 4.4e-49;  
Matches 108; Conservative 13; Mismatches 28; Indels 2; Gaps 1;  
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QY 1 MFODPQPRPKLPTCLTELQTTIHDIILECYCKQQLRREVDYDFARDLCTVYRDGPNY 60  
DB 1 MFODPQPRPKLPTCLTELQTTIHDIILECYCKQQLRREVDYDFARDLCTVYRDGPNY 60  
QY 61 AYVXDKLKFYSKISEYRHYCYVGTTLLEQYKPLCDLLIRCNXKPLCPPEKORHLD 120  
DB 61 GVCWKCKLKFYSKISEYRHYCYVGTTLLEQYKPLCDLLIRCNXKPLCPPEKORHLD 120  
QY 121 KKQRFNHRGRWTCRSCSCSSRTRETOL 151  
DB 121 EKGRFHNIGRWTCRSCSCSSRTRETOL 151

DB 121 EKGRFHNIGRWTCRSCSCSSRTRETOL 149  
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RESULT 61  
V66 HPV35 STANDARD; PRT; 149 AA.  
ID V66 HPV35  
AC P27228;  
DT 01-AUG-1992, integrated into UniProtKB/Swiss-Prot.  
DT 01-AUG-1992, sequence version 1.  
DT 07-FEB-2006, entry version 31.  
DE Protein E6.  
GN Name=E6;  
OS Human papillomavirus type 35.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Alphapapillomavirus.  
OX NCBI\_TaxID=10587;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
RC STRAIN=Isolate 35H;  
RX MEDLINE=94265501; PubMed=8205838;  
RA Delling H., Hofmann B.;  
RT "Primer-directed sequencing of human papillomavirus types.";  
RL Curr. Top. Microbiol. Immunol. 186:13-31(1994).  
CC -----  
CC -1- FUNCTION: Transcriptional transactivator. Binds double stranded  
CC DNA (by similarity).  
CC -1- FUNCTION: This protein may be involved in the oncogenic potential  
CC of this virus (associated with cancer of the uterine cervix).  
CC -1- SUBCELLULAR LOCATION: Nuclear matrix-associated (by similarity).  
CC -1- SIMILARITY: Belongs to the papillomaviruses E6 protein family.  
CC -----  
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DR EMBL: X74477; CA52561.1; -; Genomic DNA.  
DR EMBL: M74117; AAA4666.1; -; Genomic DNA.  
DR PIR: E40824; W6W135.  
DR InterPro: IPR001334; E6.  
DR Pfam: PF00518; E6; 1.  
DR Activator; DNA-binding; Early protein; Metal-binding; Nuclear protein;  
KW Oncogene; Transcription; Transcription regulation; Zinc; Zinc-finger.  
FT CHAIN 1 149 /FTID=PRO\_0000133355.  
FT ZN FING 30 66 Potential.  
FT ZN FING 103 139 Potential.  
SQ SEQUENCE 149 AA; 18045 MW; C605D19AF3935021 CRC64;  
Query Match 69.6%; Score 578; DB 1; Length 149;  
Best Local Similarity 71.5%; Pred. No. 6.9e-49;  
Matches 108; Conservative 13; Mismatches 28; Indels 2; Gaps 1;  
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QY 1 MFODPQPRPKLPTCLTELQTTIHDIILECYCKQQLRREVDYDFARDLCTVYRDGPNY 60  
DB 1 MFODPQPRPKLPTCLTELQTTIHDIILECYCKQQLRREVDYDFARDLCTVYRDGPNY 60  
QY 61 AYVXDKLKFYSKISEYRHYCYVGTTLLEQYKPLCDLLIRCNXKPLCPPEKORHLD 120  
DB 61 GVCWKCKLKFYSKISEYRHYCYVGTTLLEQYKPLCDLLIRCNXKPLCPPEKORHLD 120  
QY 121 KKQRFNHRGRWTCRSCSCSSRTRETOL 151  
DB 121 EKGRFHNIGRWTCRSCSCSSRTRETOL 149  
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RESULT 62  
Q4TUF4\_HPVS5

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ID O4TUFG HPV35 PRELIMINARY; PRT; 149 AA.
AC O4TUFG1
DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2005, sequence version 1.
DE E6 protein.
DE E6 protein.
GN Name=E6;
OS Human papillomavirus type 35.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=10587;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SA1505, and TW4232;
RC PubMed=16227263; DOI=10.1128/JVI.79.21.13630-13640.2005;
RA Calleja-Macias I.E., Villa L.L., Prado J.C., Kalandari M., Allan B.,
RA Williamson A.L., Chung L.P., Collins R.J., Zuna R.E., Dunn S.T.,
RA Chu T.Y., Cubie H.A., Guschleri K., von Knebel-Doeberitz M.,
RA Martins C.R., Sanchez G.I., Bosch F.X., Munoz N., Bernard H.U.;
RT "Worldwide genomic diversity of the high-risk human papillomavirus
RT types 31, 35, 52, and 58, four close relatives of human papillomavirus
RT type 16."
RL J. Virol. 79:13630-13640(2005).
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CC -----
DR EMBL; DQ057314; AY58345.1; -; Genomic DNA.
DR EMBL; DQ057313; AY58344.1; -; Genomic DNA.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
SQ SEQUENCE 149 AA; 18045 MW; C605D19AF3935021 CRC64;

Query Match 69.6%; Score 578; DB 2; Length 149;
Best Local Similarity 71.5%; Pred. No. 6.9e-49;
Matches 108; Conservative 13; Mismatches 28; Indels 2; Gaps 1;

QY 1 MFQDPQERPRKLPQCTELQTTIHDIIECYCKQQLRRREYDPAFRLCIVYRDGPNY 60
DB 1 MFQDPARPRYTLHDLCHNEVESIHEICLNCYCKQQLRRREYDPAFRLCIVYREGOPY 60
QY 61 AVXDKLKFYSKISEYRHYCYSVYGTLEQYKNRPLCDLLIRNCINXQKPLCEKXORHLD 120
DB 61 GVCKCKLKFYSKISEYRHYCYSVYGTLEQYKNRPLCDLLIRNCINXQKPLCEKXORHLD 120
QY 121 KKQRFHNRGRWTRGCMSCCRSRRRETOL 151
DB 121 EKRRFHNIGRWTRGCMSCCRSRRRETOL 149

RESULT 63
Q919D6 HPV16 PRELIMINARY; PRT; 103 AA.
ID Q919D6 HPV16
AC Q919D6;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DE E6 protein (fragment).
DE E6 protein (fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=21846229; PubMed=11857370; DOI=10.1002/jic.10103;
RA Watts K.U., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
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DR EMBL; AF404692; AAL01342.1; -; Genomic DNA.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
SQ SEQUENCE 103 AA; 12422 MW; 6F90CBAFLF25449B CRC64;

Query Match 67.5%; Score 560; DB 2; Length 103;
Best Local Similarity 96.1%; Pred. No. 2.8e-47;
Matches 99; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 49 DLCIVRDGNPYAVXDKLKFYSKISEYRHYCYSVYGTLEQYKNRPLCDLLIRNCINXQK 108
DB 1 DLCIVRDGNPYAVXDKLKFYSKISEYRHYCYSVYGTLEQYKNRPLCDLLIRNCINXQK 60
QY 109 PLCEEKXORHLDKQRFHNRGRWTRGCMSCCRSRRRETOL 151
DB 61 PLCEEKXORHLDKQRFHNRGRWTRGCMSCCRSRRRETOL 103

RESULT 64
Q919B2 HPV16 PRELIMINARY; PRT; 99 AA.
ID Q919B2 HPV16
AC Q919B2;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DE E6 protein (fragment).
DE E6 protein (fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=21846229; PubMed=11857370; DOI=10.1002/jic.10103;
RA Watts K.U., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
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CC -----
DR EMBL; AF404704; AAL01365.1; -; Genomic DNA.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
SQ SEQUENCE 99 AA; 12005 MW; C2B96025EC370E38 CRC64;

Query Match 64.1%; Score 532; DB 2; Length 99;
Best Local Similarity 97.0%; Pred. No. 1.6e-44;
Matches 96; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 25 DIIIECYCKQQLRRREYDPAFRLCIVYRDGNPYAVXDKLKFYSKISEYRHYCYSVY 84
DB 1 DIIIECYCKQQLRRREYDPAFRLCIVYRDGNPYAVXDKLKFYSKISEYRHYCYSVY 60
QY 61 GTTLEQYKNRPLCDLLIRNCINXQKPLCEEKXORHLDKQ 123
DB 61 GTTLEQYKNRPLCDLLIRNCINXQKPLCEEKXORHLDKQ 99

RESULT 65
Q4TUG1 HPV31 PRELIMINARY; PRT; 149 AA.
ID Q4TUG1 HPV31
AC Q4TUG1;
DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2005, sequence version 1.
DE E6 protein (fragment).
DE E6 protein (fragment).
OS Human papillomavirus type 35.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=10587;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SA1505, and TW4232;
RC PubMed=16227263; DOI=10.1128/JVI.79.21.13630-13640.2005;
RA Calleja-Macias I.E., Villa L.L., Prado J.C., Kalandari M., Allan B.,
RA Williamson A.L., Chung L.P., Collins R.J., Zuna R.E., Dunn S.T.,
RA Chu T.Y., Cubie H.A., Guschleri K., von Knebel-Doeberitz M.,
RA Martins C.R., Sanchez G.I., Bosch F.X., Munoz N., Bernard H.U.;
RT "Worldwide genomic diversity of the high-risk human papillomavirus
RT types 31, 35, 52, and 58, four close relatives of human papillomavirus
RT type 16."
RL J. Virol. 79:13630-13640(2005).
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DE E6 protein.  
GN Name=E6;  
OS Human papillomavirus type 31.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Alphapapillomavirus.  
OX NCBI\_Taxid=10585;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=BR1213, BR1692, and KM9917;  
RA PubMed=16227283; DOI=10.1128/JVI.79.21.13630-13640.2005;  
RA Calleja-Macias I.E., Villa L.L., Prado J.C., Kalantari M., Allan B.,  
RA Williamson A.L., Chung L.P., Collins R.J., Zuna R.E., Dunn S.T.,  
RA Chu T.Y., Cubie H.A., Cuschieri K., von Knebel-Doeberitz M.,  
RA Martins C.R., Sanchez G.I., Bosch F.X., Munoz N., Bernard H.U.;  
RT "Worldwide genomic diversity of the high-risk human papillomavirus  
RT types 31, 35, 52, and 58, four close relatives of human papillomavirus  
RT type 16.";  
RL J. Virol. 79:113630-13640(2005).  
CC -----  
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CC -----  
DR EMBL: DQ057307; AAY58338.1; -; Genomic DNA.  
DR EMBL: DQ057308; AAY58339.1; -; Genomic DNA.  
DR EMBL: DQ057305; AAY58336.1; -; Genomic DNA.  
DR GO: GO:0042025; C:host cell nucleus; IEA.  
DR GO: GO:0003677; F:DNA binding; IEA.  
SQ SEQUENCE 149 AA; 17768 MW; 61C2A96EAC2677D9 CRC64;  
  
Query Match 63.3%; Score 525; DB 2; Length 149;  
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Matches 99; Conservative 16; Mismatches 34; Indels 2; Gaps 1;  
  
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Db 1 MFKNPAPRPRLHLSALRIPYDELRLNLCYCKGQLTEFVDFATFDTLTVRRDPY 60  
QY 61 AYVXDKCLFYSKISEYHYCYVGTTLTLEQYKPLCDLIRICNKKPLCPBEKORHLD 120  
Db 61 GVCTKCLRFYSKYSEFMYRYSVGTTLKLTNKGICDLIRICITCQRLCPBEKORHLD 120  
QY 121 KKRFFHNIRGRWGRCMSCCRSSRTRETOL 151  
Db 121 KKRFFHNIRGRWGRCMSCCRSSRTRETOL 151  
QY 121 KKRFFHNIRGRWGRCMSCCRSSRTRETOL 151  
Db 121 KKRFFHNIRGRWGRCMSCCRSSRTRETOL 151  
  
RESULT 66  
VE6\_HPV31  
ID\_VE6\_HPV31 STANDARD; PRT; 149 AA.  
AC P17386;  
DT 01-AUG-1990, integrated into UniProtKB/Swiss-Prot.  
DT 01-AUG-1990, sequence version 1.  
DT 07-FEB-2006, entry version 37.  
DE Protein E6.  
GN Name=E6;  
OS Human papillomavirus type 31.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Alphapapillomavirus.  
OX NCBI\_Taxid=10585;  
RN [1]  
RP NUCLEOTIDE SEQUENCE (GENOMIC DNA).  
RA MEDLINE=89299478; PubMed=2545036;  
RA Goldsborough M.D., Disilvestre D., Temple G.F., Iorincz A.T.;  
RT "Nucleotide sequence of human papillomavirus type 31: a cervical  
RT neoplasia-associated virus.";  
RT Virology 171:306-311(1989).  
RN [2]  
RP INTERACTION WITH HUMAN PBLN1, AND INHIBITION OF E6-MEDIATED  
RP TRANSFORMATION.  
RA MEDLINE=22188366; PubMed=12200142; DOI=10.1016/S0006-291X(02)02041-7;  
RA Du M., Fan X., Hong E., Chen J.J.;  
RT "Interaction of oncogenic papillomavirus E6 proteins with fibulin-1.";  
RT Blochem. Biophys. Res. Commun. 296:962-969(2002).

RN [3]  
RP PDZ DOMAIN-BINDING MOTIF.  
RX PubMed=15507623; DOI=10.1128/JVI.78.22.12366-12377.2004;  
RA Lee C., Kaimas L.A.;  
RT "Role of the PDZ domain-binding motif of the oncoprotein E6 in the  
RT pathogenesis of human papillomavirus type 31.";  
RL J. Virol. 78:12366-12377(2004).  
CC -----  
CC FUNCTION: Transcriptional transactivator. Binds double stranded  
CC DNA. Has transforming activity. Inactivates, with E6-AP ubiquitin-  
CC protein ligase, the human TP53/p53 tumor suppressor protein by  
CC targeting it to degradation. Binds and targets human MDM2/MDM2  
CC protein to degradation. Those two functions presumably contribute  
CC to transforming activity (By similarity). Interaction with human  
CC PBLN1 protein also seems to be linked to cell transformation.  
CC -1- SUBUNIT: Forms a complex with E6-AP ubiquitin-protein ligase which  
CC interacts with human p53. Binds to human PBLN1 and MDM2 (By  
CC similarity).  
CC -1- SUBCELLULAR LOCATION: Nuclear matrix-associated (By similarity).  
CC -1- SIMILARITY: Belongs to the papillomaviruses E6 protein family.  
CC -----  
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CC -----  
DR EMBL: J04353; AAA46950.1; -; Genomic DNA.  
DR PIR: A32444; M6WL31.  
DR InterPro: IPR001334; E6.  
DR Pfam: PF00518; E6; 1.  
KW Activator; DNA-binding; Early protein; Metal-binding; Nuclear protein;  
KW Oncogene; Transcription; Transcription regulation; Zinc; Zinc-finger.  
FT CHAIN 1 149 /FRTID=PRO\_0000133351.  
FT ZN\_FING 30 66 Potential.  
FT ZN\_FING 103 139 Potential.  
FT MOTIF 146 149 PDZ-binding.  
SQ SEQUENCE 149 AA; 17714 MW; 61D2A86C362767D9 CRC64;  
  
Query Match 63.0%; Score 523; DB 1; Length 149;  
Best Local Similarity 64.9%; Pred. No. 1.9e-43;  
Matches 98; Conservative 18; Mismatches 33; Indels 2; Gaps 1;  
  
QY 1 MFODPQPRPKLPTCLTELQTTIHDIILECYCKQQLRREVDYFAFRLCIVYRDGNY 60  
Db 1 MFKNPAPRPRLHLSALRIPYDELRLNLCYCKGQLTEFVDFATFDTLTVRRDPY 60  
QY 61 AYVXDKCLFYSKISEYHYCYVGTTLTLEQYKPLCDLIRICNKKPLCPBEKORHLD 120  
Db 61 GVCTKCLRFYSKYSEFMYRYSVGTTLKLTNKGICDLIRICITCQRLCPBEKORHLD 120  
QY 121 KKRFFHNIRGRWGRCMSCCRSSRTRETOL 151  
Db 121 KKRFFHNIRGRWGRCMSCCRSSRTRETOL 151  
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Db 121 KKRFFHNIRGRWGRCMSCCRSSRTRETOL 151  
  
RESULT 67  
Q4TUG5\_HPV31  
ID Q4TUG5\_HPV31 PRELIMINARY; PRT; 149 AA.  
AC Q4TUG5;  
DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.  
DT 19-JUL-2005, sequence version 1.  
DT 07-FEB-2006, entry version 5.  
DE E6 protein.  
GN Name=E6;  
OS Human papillomavirus type 31.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Alphapapillomavirus.  
OX NCBI\_Taxid=10585;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=HK31A, HK31B, HK31C, and TL2069;  
RA PubMed=16227283; DOI=10.1128/JVI.79.21.13630-13640.2005;  
RA Calleja-Macias I.E., Villa L.L., Prado J.C., Kalantari M., Allan B.,  
RA Williamson A.L., Chung L.P., Collins R.J., Zuna R.E., Dunn S.T.,  
RA Chu T.Y., Cubie H.A., Cuschieri K., von Knebel-Doeberitz M.,

RA Martine C.R., Sanchez G.I., Bosch F.X., Munoz N., Bernard H.U.;  
RT "Worldwide genomic diversity of the high-risk human papillomavirus  
RT types 31, 35, 52, and 58, four close relatives of human papillomavirus  
RT type 16." J. Virol. 79:13630-13640(2005).  
RL J. Virol. 79:13630-13640(2005).  
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CC  
DR EMBL: DQ057303; AAY58334.1; -; Genomic DNA.  
DR EMBL: DQ057304; AAY58335.1; -; Genomic DNA.  
DR EMBL: DQ057306; AAY58337.1; -; Genomic DNA.  
DR EMBL: DQ057302; AAY58333.1; -; Genomic DNA.  
DR GO: GO:0042025; C:host cell nucleus; IEA.  
DR GO: GO:0003677; F:DNA binding; IEA.  
SQ SEQUENCE 149 AA; 17714 MW; 61D2A6C362767D9 CRC64;  
  
Query Match 63.0%; Score 523; DB 2; Length 149;  
Best Local Similarity 64.9%; Pred. No. 1.9e-43;  
Matches 96; Conservative 18; Mismatches 33; Indels 2; Gaps 1;  
  
QY 1 MFQDQERPRKLPOLCTELQTTIHDIIECYCQQLRREYVDFAFRDLCTVYRDGPNPY 60  
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DB 61 AVXDKCLKFSKISEYRHYCYSVYGTTLLEQYNNKPLCDLLIRCTNXXKPLCPCEKQRLHD 120  
61 GVCGLCLRFYSKISEYRHYCYSVYGTTLLEQYNNKPLCDLLIRCTNXXKPLCPCEKQRLHD 120  
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DB 121 KKQRFHNIRGRWTCRCMSCCRSSRTRETQL 151  
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RESULT 68  
VEE\_HPV33 STANDARD; PRT; 149 AA.  
ID VEE\_HPV33 STANDARD; PRT; 149 AA.  
AC P06427;  
DT 01-JAN-1988, integrated into UniProtKB/Swiss-Prot.  
DT 01-JAN-1988, sequence version 1.  
DT 07-FEB-2006, entry version 38.  
DE Protein E6.  
GN Name=E6;  
OS Human Papillomavirus type 33.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Alphapapillomavirus.  
OX NCBI\_TaxID=10586;  
RN NM\_001101011.1  
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
RX MEDLINE=86200464; PubMed=3009902;  
RA Cole S.T., Strebeck R.E.;  
RT "Genome organization and nucleotide sequence of human papillomavirus  
RT type 33, which is associated with cervical cancer." J.  
RL J. Virol. 58:991-995(1986).  
CC -1- FUNCTION: Transcriptional transactivator. Binds double stranded  
CC DNA (By similarity).  
CC -1- FUNCTION: This protein may be involved in the oncogenic potential  
CC of this virus (cervical neoplasia-associated virus).  
CC -1- SUBCELLULAR LOCATION: Nuclear matrix-associated (By similarity).  
CC -1- SIMILARITY: Belongs to the papillomaviruses E6 protein family.  
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CC  
DR EMBL: M12732; AAA46958.1; -; Genomic DNA.  
DR PIR: A03683; W6WL33.  
DR InterPro: IPR001334; E6.  
DR Pfam: PF00518; E6; 1.  
KM Activator; DNA-binding; Early protein; Metal-binding; Nuclear protein;  
KM Oncogene; Transcription; Transcription regulation; Zinc; Zinc-finger.  
FT CHAIN 1 149 Protein E6 /FTId=PRO\_000013353.  
FT ZN\_FING 30 66 Potential.

FT ZN\_FING 103 139 Potential.  
SQ SEQUENCE 149 AA; 17652 MW; EDD87444F9C8B1AF CRC64;  
  
Query Match 62.7%; Score 520; DB 1; Length 149;  
Best Local Similarity 63.6%; Pred. No. 3.7e-43;  
Matches 96; Conservative 19; Mismatches 34; Indels 2; Gaps 1;  
  
QY 1 MFQDQERPRKLPOLCTELQTTIHDIIECYCQQLRREYVDFAFRDLCTVYRDGPNPY 60  
DQ 1 MFQDQERPRKLPOLCTELQTTIHDIIECYCQQLRREYVDFAFRDLCTVYRDGPNPY 60  
DB 1 MFQDQERPRKLPOLCTELQTTIHDIIECYCQQLRREYVDFAFRDLCTVYRDGPNPY 60  
DB 61 AVXDKCLKFSKISEYRHYCYSVYGTTLLEQYNNKPLCDLLIRCTNXXKPLCPCEKQRLHD 120  
61 GVCGLCLRFYSKISEYRHYCYSVYGTTLLEQYNNKPLCDLLIRCTNXXKPLCPCEKQRLHD 120  
QY 121 KKQRFHNIRGRWTCRCMSCCRSSRTRETQL 151  
DB 121 KKQRFHNIRGRWTCRCMSCCRSSRTRETQL 151  
DB 121 LNKRFHNISGRWTCRCMSCCRSSRTRETQL 151  
  
RESULT 69  
Q080E7\_HPV58 PRELIMINARY; PRT; 149 AA.  
ID Q080E7\_HPV58 PRELIMINARY; PRT; 149 AA.  
AC Q080E7;  
DT 01-JUN-2002, integrated into UniProtKB/TREMBL.  
DT 01-JUN-2002, sequence version 1.  
DT 07-FEB-2006, entry version 14.  
DE E6 protein.  
OS Human papillomavirus type 58.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Alphapapillomavirus.  
OX NCBI\_TaxID=10598;  
RN NM\_001101011.1  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=E6/E7-HK-8;  
RX MEDLINE=22176796; PubMed=12189229; DOI=10.1093/jnci/94.16.1249;  
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,  
RA Cheung J.L.K., Cheng A.F.;  
RT "Association of human papillomavirus type 58 variant with the risk of  
RT cervical cancer." J.  
RL J. Natl. Cancer Inst. 94:1249-1253(2002).  
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CC  
DR EMBL: AF478157; AAL85402.1; -; Genomic DNA.  
DR GO: GO:0042025; C:host cell nucleus; IEA.  
DR GO: GO:0003677; F:DNA binding; IEA.  
DR InterPro: IPR001334; E6.  
DR Pfam: PF00518; E6; 1.  
SQ SEQUENCE 149 AA; 17793 MW; 8D06DD69ED3EDCF4 CRC64;  
  
Query Match 60.6%; Score 503; DB 2; Length 149;  
Best Local Similarity 62.3%; Pred. No. 1.7e-41;  
Matches 94; Conservative 20; Mismatches 35; Indels 2; Gaps 1;  
  
QY 1 MFQDQERPRKLPOLCTELQTTIHDIIECYCQQLRREYVDFAFRDLCTVYRDGPNPY 60  
DQ 1 MFQDQERPRKLPOLCTELQTTIHDIIECYCQQLRREYVDFAFRDLCTVYRDGPNPY 60  
DB 1 MFQDQERPRKLPOLCTELQTTIHDIIECYCQQLRREYVDFAFRDLCTVYRDGPNPY 60  
DB 61 AVXDKCLKFSKISEYRHYCYSVYGTTLLEQYNNKPLCDLLIRCTNXXKPLCPCEKQRLHD 120  
61 GVCGLCLRFYSKISEYRHYCYSVYGTTLLEQYNNKPLCDLLIRCTNXXKPLCPCEKQRLHD 120  
QY 121 KKQRFHNIRGRWTCRCMSCCRSSRTRETQL 151  
DB 121 KKQRFHNIRGRWTCRCMSCCRSSRTRETQL 151  
DB 121 LNKRFHNISGRWTCRCMSCCRSSRTRETQL 151  
  
RESULT 70  
Q91ZG6\_HPV58 PRELIMINARY; PRT; 149 AA.  
ID Q91ZG6\_HPV58 PRELIMINARY; PRT; 149 AA.  
AC Q91ZG6;  
AC Q91ZG6;

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DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2000, sequence version 1.
DT 07-FEB-2006, entry version 17.
DE E6 protein.
OS Human papillomavirus type 58.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
NCBI_TaxId=10598;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Chan P.K.S., Lam C.W., Li W.H., Chan M.Y.M., Cheung J.L.K.,
RA Cheng A.F.,
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BE/ET-HK-3, E6/E7-HK-5, and E6/E7-HK-14;
RX MEDLINE=2216796; PubMed=2189229; DOI=10.1093/jnci/94.16.1249;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.L.K., Cheng A.F.,
RT "Association of human papillomavirus type 58 variant with the risk of
RT cervical cancer."
RT J. Natl. Cancer Inst. 94:1249-1253(2002).
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CC -----
DR EMBL; AF234530; AAF60306.1; -; Genomic DNA.
DR EMBL; AF478152; AAL85397.1; -; Genomic DNA.
DR EMBL; AF478153; AAL85408.1; -; Genomic DNA.
DR EMBL; AF478154; AAL85399.1; -; Genomic DNA.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 149 AA; 17780 MW; 7CB6DCC5D31B158 CRC64;

Query Match 60.5%; Score 502; DB 2; Length 149;
Best Local Similarity 62.3%; Pred. No. 2.2e-41;
Matches 94; Conservative 20; Mismatches 35; Indels 2; Gaps 1;

QY 1 MFQDQPERPRKLTQTLCTELQTTIHDIILCEVCYKQQLRREYDFAFRDLCTIYRDGPNY 60
DB 1 MFQDAEKPRKTHDLCALETSVHEILKVCCKKTQRESEVYDFVADLRIVYRDGNPF 60
QY 61 AYXDKCLKFSKISEYHNYCYVGTTLDEQYNNKPLCDLLIRCNKXKPLCPBEKQKHLD 120
DB 61 AVCKVCLRLSKISEYHNYSLVGTLTLEQTLKCLNEILIRCIICQRPICPQEKKHVD 120
QY 121 KKORFNIRGRMTGRGCMSCCRSSRTRETLQ 151
DB 121 LMKRFNHSGRMTGRCAVCWRRP-RRRQTOV 149

RESULT 71
O90723 HPV67 PRELIMINARY; PRT; 149 AA.
AC O90723
DT 01-NOV-1998, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1998, sequence version 1.
DT 07-FEB-2006, entry version 20.
DE ORF E6.
OS Human papillomavirus type 67.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
NCBI_TaxId=37120;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99073695; PubMed=9857984; DOI=10.1023/A:1008002905588;
RA Kiri T., Matsukura T.,
RT "Nucleotide sequence and phylogenetic classification of human
RT papillomavirus type 67."
RL Virus Genes 17:117-121(1998).

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CC -----
DR EMBL; D21208; BAA28852.1; -; Genomic DNA.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 149 AA; 17833 MW; AAF28AC1BE75B197 CRC64;

Query Match 60.0%; Score 498; DB 2; Length 149;
Best Local Similarity 60.1%; Pred. No. 5.4e-41;
Matches 89; Conservative 22; Mismatches 37; Indels 0; Gaps 0;

QY 1 MFQDQPERPRKLTQTLCTELQTTIHDIILCEVCYKQQLRREYDFAFRDLCTIYRDGPNY 60
DB 1 MFQDTEKPRKTHDLCALETSVHEILKVCCKKTQRESEVYDFVADLRIVYRDGNPF 60
QY 61 AYXDKCLKFSKISEYHNYCYVGTTLDEQYNNKPLCDLLIRCNKXKPLCPBEKQKHLD 120
DB 61 GVCKQCLRLSKISEYHNYSLVGTLTLEQTLKCLNEILIRCIICQRPICPQEKKHVD 120
QY 121 KKORFNIRGRMTGRGCMSCCRSSRTRE 148
DB 121 RKKRFNHSGRMTGRGSCVCRPQRTQ 148

RESULT 72
O4TUG8 HPV58 PRELIMINARY; PRT; 149 AA.
AC O4TUG8
DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE E6 protein.
GN Name=E6;
OS Human papillomavirus type 58.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
NCBI_TaxId=10598;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ED1813;
RX PubMed=16227283; DOI=10.1126/JVI.79.21.13630-13640.2005;
RA Calleja-Macias I.E., Villa L.L., Prado J.C., Kalencari M., Allan B.,
RA Williams A.L., Chung L.P., Collins R.J., Zuna R.E., Dunn S.T.,
RA Chu T.Y., Cubie H.A., Cuschieri K., von Knebel-Deebertz M.,
RA Martins C.R., Sanchez G.I., Bosch F.X., Munoz N., Bernard H.U.;
RT "Worldwide genomic diversity of the high-risk human papillomavirus
RT types 31, 35, 52, and 58, four close relatives of human papillomavirus
RT type 16."
RT J. Virol. 79:13630-13640(2005).
CC -----
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CC -----
DR EMBL; DQ057300; AAY58331.1; -; Genomic DNA.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
SQ SEQUENCE 149 AA; 17807 MW; 8803DD6CE83EDCF4 CRC64;

Query Match 59.9%; Score 497; DB 2; Length 149;
Best Local Similarity 61.6%; Pred. No. 6.8e-41;
Matches 93; Conservative 20; Mismatches 36; Indels 2; Gaps 1;

QY 1 MFQDQPERPRKLTQTLCTELQTTIHDIILCEVCYKQQLRREYDFAFRDLCTIYRDGPNY 60
DB 1 MFQDAEKPRKTHDLCALETSVHEILKVCCKKTQRESEVYDFVADLRIVYRDGNPF 60
QY 61 AYXDKCLKFSKISEYHNYCYVGTTLDEQYNNKPLCDLLIRCNKXKPLCPBEKQKHLD 120
DB 61 AVCKVCLRLSKISEYHNYSLVGTLTLEQTLKCLNEILIRCIICQRPICPQEKKHVD 120

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Qy 121 KKORFHNIRGWRGCMSCCRSSRTRETOL 151  
 Db 121 LNKRFHNISGRWTRCAVCWMP--RRROTQV 149

## RESULT 73

091ZG5 HPV58 PRELIMINARY; PRT; 149 AA.  
 AC 091ZG5; Integrated into UniProtKB/TrEMBL.  
 DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.  
 DT 07-FEB-2006, entry version 16.  
 DE B6 protein.  
 OS Human papillomavirus type 58.  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 OC Alphapapillomavirus.  
 NCBI\_TaxID=10598;  
 RN NUCLEOTIDE SEQUENCE.  
 RC STRAIN=E6HK3.  
 RA Chan P.K.S., Lam C.W., Li W.H., Chan M.Y.M., Cheung J.L.K.,  
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
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 CC -----  
 CC EMBL; AF224531; AA060307.1; -; Genomic DNA.  
 DR GO; GO:0042025; C:host cell nucleus; IEA.  
 DR GO; GO:0003677; F:DNA binding; IEA.  
 DR InterPro; IPR001334; E6.  
 DR Pfam; PF00518; E6; 1.  
 SQ SEQUENCE 149 AA; 17863 MW; 4C6A61AD9CEC302D CRC64;

Query Match 59.9%; Score 497; DB 2; Length 149;  
 Best Local Similarity 61.6%; Pred. No. 6.8e-41;  
 Matches 93; Conservative 20; Mismatches 36; Indels 2; Gaps 1;

Qy 1 MFQDPQRPRLPOLCTELQTTIHDIILECYCKQQLRREYVDFARFDLCIVYRDGPNY 60  
 Db 1 MFQDAEKPRTHLDCQALETSVHIELKVCCKKTLQRESEYDFVADLRIVYRDGNPF 60  
 Qy 61 AVXDCKKFKYSKISEYHACYSVYGTLEQYQNKPLCDLIRCIHXKPLCPCEKORHLD 120  
 Db 61 AVCVCLRLSKISEYHNYNSLYGNTLEQTLKKLEBILIRCIICQRLCPQEKGRHVD 120  
 Qy 121 KKORFHNIRGWRGCMSCCRSSRTRETOL 151  
 Db 121 LNKRFHNISGRWTRCAVCWMP--RRROTQV 149

RESULT 74  
 VE6 HPV58 STANDARD; PRT; 149 AA.  
 AC P26555; Integrated into UniProtKB/Swiss-Prot.  
 DT 01-AUG-1992, integrated into UniProtKB/Swiss-Prot.  
 DT 01-AUG-1992, sequence version 1.  
 DT 07-FEB-2006, entry version 28.  
 DE Protein E6.  
 GN Name=E6;  
 OS Human papillomavirus type 58.  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 OC Alphapapillomavirus.  
 NCBI\_TaxID=10598;  
 RN NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
 RP MEDLINE=92024102; PubMed=1656594;  
 RA Kiril' Y., Iwamoto S., Matsukura T.;  
 RT "Human papillomavirus type 58 DNA sequence.";  
 RL Virology 185:424-427(1991).  
 CC -1- FUNCTION: Transcriptional transactivator. Binds double stranded  
 CC DNA (by similarity).

CC -1- SUBCELLULAR LOCATION: Nuclear matrix-associated (By similarity).  
 CC -1- SIMILARITY: Belongs to the papillomaviruses E6 protein family.  
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 CC -----  
 CC EMBL; D90400; BAA31845.1; -; Genomic DNA.  
 DR PIR; E36779; W6WL58.  
 DR InterPro; IPR001334; E6.  
 DR Pfam; PF00518; E6; 1.  
 KM Activator; DNA-binding; Early protein; Metal-binding; Nuclear protein;  
 KM Transcription; Transcription regulation; Zinc; Zinc-finger.  
 FT CHAIN 1 149  
 FT /Ftrd=PRO\_0000133374.  
 FT ZN\_FING 30 66 Potential\_  
 FT ZN\_FING 103 139 Potential.  
 SQ SEQUENCE 149 AA; 17794 MW; 79B3DC95831B158 CRC64;

Query Match 59.8%; Score 496; DB 1; Length 149;  
 Best Local Similarity 61.6%; Pred. No. 8.5e-41;  
 Matches 93; Conservative 20; Mismatches 36; Indels 2; Gaps 1;

Qy 1 MFQDPQRPRLPOLCTELQTTIHDIILECYCKQQLRREYVDFARFDLCIVYRDGPNY 60  
 Db 1 MFQDAEKPRTHLDCQALETSVHIELKVCCKKTLQRESEYDFVADLRIVYRDGNPF 60  
 Qy 61 AVXDCKKFKYSKISEYHACYSVYGTLEQYQNKPLCDLIRCIHXKPLCPCEKORHLD 120  
 Db 61 AVCVCLRLSKISEYHNYNSLYGNTLEQTLKKLEBILIRCIICQRLCPQEKGRHVD 120  
 Qy 121 KKORFHNIRGWRGCMSCCRSSRTRETOL 151  
 Db 121 LNKRFHNISGRWTRCAVCWMP--RRROTQV 149

## RESULT 75

0547M1 HPV58 PRELIMINARY; PRT; 149 AA.  
 ID 0547M1; Integrated into UniProtKB/TrEMBL.  
 AC 0547M1; Integrated into UniProtKB/TrEMBL.  
 DT 24-MAY-2005, sequence version 1.  
 DT 07-FEB-2006, entry version 6.  
 DE B6 protein.  
 GN Name=E6;  
 OS Human papillomavirus type 58.  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 OC Alphapapillomavirus.  
 NCBI\_TaxID=10598;  
 RN NUCLEOTIDE SEQUENCE.  
 RP STRAIN=E6/E7-HK-1, E6/E7-HK-10, E6/E7-HK-11, E6/E7-HK-12, E6/E7-HK-13,  
 RC E6/E7-HK-15, E6/E7-HK-16, E6/E7-HK-2, E6/E7-HK-4, E6/E7-HK-6,  
 RC E6/E7-HK-7, and E6/E7-HK-9;  
 RX MEDLINE=22176796; PubMed=12189229; DOI=10.1093/jnci/94.16.1249;  
 RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,  
 RA Cheung J.L.K., Cheng A.F.;  
 RT "Association of human papillomavirus type 58 variant with the risk of  
 cervical cancer.";  
 RT J. Natl. Cancer Inst. 94:1249-1253(2002).  
 RL [2]

RN NUCLEOTIDE SEQUENCE.  
 RP STRAIN=ED1710, ED1767, ED6197, HK2178, and OK332;  
 RC PubMed=16227283; DOI=10.1128/JVI.79.21.13630-13640.2005;  
 RA Calleja-Macias I.E., Villa L.L., Prado J.C., Kalamant M., Allan B.,  
 RA Williams A.L., Chung L.P., Collins R.J., Zuna R.E., Dunn S.T.,  
 RA Chu T.Y., Cudde H.A., Cuschieri K., von Knebel-Doeberitz M.,  
 RA Martinez C.R., Sanchez G.I., Bosch F.X., Munoz N., Bernard H.U.;  
 RT "Worldwide genomic diversity of the high-risk human papillomavirus  
 RT types 31, 35, 52, and 58, four close relatives of human papillomavirus  
 RT type 16.";  
 RL J. Virol. 79:13630-13640(2005).  
 RN [3]  
 RN NUCLEOTIDE SEQUENCE.

RC STRAIN-B6HK1:  
RA Chan P.K.S., Lam C.W., Li W.H., Chan M.Y.M., Cheung J.L.K.,  
RA Cheng A.F.;  
RT "Nucleotide sequence variation of the E6 gene of human papillomavirus  
RT type 58 from Chinese women with normal cervixes and cancerous  
RT lesions.";  
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
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CC -----  
DR EMBL: AF478150; AAL85395.1; -; Genomic DNA.  
DR EMBL: DQ057297; AAL85328.1; -; Genomic DNA.  
DR EMBL: DQ057298; AAY58329.1; -; Genomic DNA.  
DR EMBL: DQ057299; AAY58330.1; -; Genomic DNA.  
DR EMBL: DQ057301; AAY58332.1; -; Genomic DNA.  
DR EMBL: AF234529; AAF60305.1; -; Genomic DNA.  
DR EMBL: AF478151; AAL85396.1; -; Genomic DNA.  
DR EMBL: AF478153; AAL85398.1; -; Genomic DNA.  
DR EMBL: AF478155; AAL85400.1; -; Genomic DNA.  
DR EMBL: AF478156; AAL85401.1; -; Genomic DNA.  
DR EMBL: AF478158; AAL85403.1; -; Genomic DNA.  
DR EMBL: AF478159; AAL85404.1; -; Genomic DNA.  
DR EMBL: AF478161; AAL85405.1; -; Genomic DNA.  
DR EMBL: AF478162; AAL85406.1; -; Genomic DNA.  
DR EMBL: AF478164; AAL85409.1; -; Genomic DNA.  
DR EMBL: AF478165; AAL85410.1; -; Genomic DNA.  
DR EMBL: DQ057296; AAY58327.1; -; Genomic DNA.  
DR GO: GO:0042025; C:host cell nucleus; IEA.  
DR GO: GO:0003677; F:DNA binding; IEA.  
SQ SEQUENCE 149 AA; 17794 MW; 79B3DCC95831B158 CRC64;  
Query Match 59.8%; Score 496; DB 2; Length 149;  
Best Local Similarity 61.6%; Pred. No. 8.5e-41;  
Matches 93; Conservative 20; Mismatches 36; Indels 2; Gaps 1;  
QY 1 MFQDPQRPRLPOLCTELQTTTHDILIECYCQQLRREYVDFARFDLCIVRDGPNP 60  
DB 1 MFQDAEKPRTHLDCALLETSSVHEILKCECKTQRSEVDFVADLRIVRDGNPF 60  
QY 61 AVXDKCLKFKYSKISEYHYCYSVYGTTLLEQYNNKPLCDLLIRCNXKPLCPCEKORHLD 120  
DB 61 AVCVCLRLSKISEYHYNYSLYGTLEQTLKCLNEILIRCTICORPLCPQEKRHVD 120  
QY 121 KQRFNIRGRWTCRSCCSSRTRRETOL 151  
DB 121 LNKRFNISRGRWTCRCACWCRP--RRRQTV 149  
RESULT 76  
Q080H3 HPV58  
ID Q080H3 HPV58 PRELIMINARY; PRT; 149 AA.  
AC Q080H3;  
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.  
DT 01-JUN-2002, sequence version 1.  
DT 07-FEB-2006, entry version 14.  
DE E6 protein.  
OS Human Papillomavirus type 58.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Alphapapillomavirus.  
OX NCBI\_TaxID=10598;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=E6/E7-HK-17, and E6/E7-HK-18;  
RX MEDLINE=22176796; PubMed=12189229; DOI=10.1093/jnci/94.16.1249;  
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.H., Lo K.W.K., Chan M.Y.M.,  
RA Cheung J.L.K., Cheng A.F.;  
RT "Association of human papillomavirus type 58 variant with the risk of  
RT cervical cancer.";  
RL J. Natl. Cancer Inst. 94:1249-1253(2002).  
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CC -----  
CC EMBL: AF478166; AAL85411.1; -; Genomic DNA.  
CC EMBL: AF478167; AAL85412.1; -; Genomic DNA.  
DR GO: GO:0042025; C:host cell nucleus; IEA.  
DR GO: GO:0003677; F:DNA binding; IEA.  
DR InterPro: IPR001334; E6.  
DR Pfam: PF00518; E6; 1.  
SQ SEQUENCE 149 AA; 17808 MW; 7803DD78E831B159 CRC64;  
Query Match 59.8%; Score 496; DB 2; Length 149;  
Best Local Similarity 61.6%; Pred. No. 8.5e-41;  
Matches 93; Conservative 20; Mismatches 36; Indels 2; Gaps 1;  
QY 1 MFQDPQRPRLPOLCTELQTTTHDILIECYCQQLRREYVDFARFDLCIVRDGPNP 60  
DB 1 MFQDAEKPRTHLDCALLETSSVHEILKCECKTQRSEVDFVADLRIVRDGNPF 60  
QY 61 AVXDKCLKFKYSKISEYHYCYSVYGTTLLEQYNNKPLCDLLIRCNXKPLCPCEKORHLD 120  
DB 61 AVCVCLRLSKISEYHYNYSLYGTLEQTLKCLNEILIRCTICORPLCPQEKRHVD 120  
QY 121 KQRFNIRGRWTCRSCCSSRTRRETOL 151  
DB 121 LNKRFNISRGRWTCRCACWCRP--RRRQTV 149  
RESULT 77  
Q08087 9PAPI  
ID Q08087 9PAPI PRELIMINARY; PRT; 91 AA.  
AC Q08087;  
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.  
DT 01-NOV-1996, sequence version 1.  
DT 07-FEB-2006, entry version 25.  
DE E6 protein (fragment).  
OS Human papillomavirus.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Unclassified Papillomaviridae.  
OX NCBI\_TaxID=10586;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=HPV16; TISSUE=Cervical tissue;  
RA Haegert D.G., Galutira D.F., Younghusband B.H.;  
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.  
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CC -----  
DR EMBL: U14516; AAB60570.1; -; Genomic DNA.  
DR GO: GO:0042025; C:host cell nucleus; IEA.  
DR GO: GO:0003677; F:DNA binding; IEA.  
DR InterPro: IPR001334; E6.  
DR Pfam: PF00518; E6; 1.  
FT NON\_TER 1 1  
FT NON\_TER 91 91  
SQ SEQUENCE 91 AA; 11136 MW; 22FD3EA185ACBA7 CRC64;  
Query Match 59.6%; Score 495; DB 2; Length 91;  
Best Local Similarity 96.7%; Pred. No. 6.4e-41;  
Matches 88; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 42 VYDFARFDLCIVRDGPNYAVXDKCLKFKYSKISEYHYCYSVYGTTLLEQYNNKPLCDLLI 101  
DB 1 VYDFARFDLCIVRDGPNYAVXDKCLKFKYSKISEYHYCYSVYGTTLLEQYNNKPLCDLLI 60  
QY 102 RCINXKPLCPCEKORHLDKQRFNIRGRM 132  
DB 61 RCINXKPLCPCEKORHLDKQRFNIRGRM 91  
RESULT 78  
Q4TUH6 HPV52  
ID Q4TUH6 HPV52 PRELIMINARY; PRT; 148 AA.  
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AC 04TH6-2005, integrated into UniProtKB/TrEMBL.  
DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.  
DT 19-JUL-2005, sequence version 1.  
DT 07-FEB-2006, entry version 4.  
DE E6 protein.  
GN Name=E6;  
OS Human papillomavirus type 52.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
CC Alphapapillomavirus.  
OK NCBI\_taxid=10618;  
RN  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=HK151;  
RX PubMed:16227283; DOI=10.1128/JVI.79.21.13630-13640.2005;  
RA Calleja-Macias I.E., Villa L.L., Prado J.C., Kalantari M., Allan B.,  
RA Williamson A.L., Chung L.P., Collins R.J., Zuna R.E., Dunn S.T.,  
RA Chu T.Y., Cubie H.A., Cuschieri K., von Knebel-Doeberitz M.,  
RA Martins C.R., Sanchez G.I., Bosch F.X., Munoz N., Bernard H.U.;  
RT "Worldwide genomic diversity of the high-risk human papillomavirus  
RT types 16, 35, 52, and 58, four close relatives of human papillomavirus  
RT type 16,";  
RL J. Virol. 79:13630-13640(2005).  
RN  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=HK151;  
RA Calleja-Macias I.E., Kalantari M., Villa L.L., Prado J.C., Allan B.,  
RA Williamson A.L., Chung L.P., Collins R.J., Zuna R.E., Dunn T.,  
RA Chu T.Y., Cubie H.A., Cuschieri K., Knebel-Doeberitz M.V.,  
RA Sanchez G.I., Bosch X., Bernard H.-U.;  
RL Submitted (May-2005) to the EMBL/GenBank/DBJ databases.  
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CC  
EMBL: D0057292; AAY58323.1; -; Genomic DNA.  
DR GO: GO:0042025; C:host cell nucleus; IEA.  
DR GO: GO:0003677; F:DNA binding; IEA.  
DR  
SQ SEQUENCE 148 AA; 17913 MW; 2B89D590611AB0D4 CRC64;  
  
Query Match 59.3%; Score 492; DB 2; Length 148;  
Best Local Similarity 62.4%; Pred. No. 2,1e-40;  
Matches 88; Conservative 19; Mismatches 34; Indels 0; Gaps 0  
  
QY 1 MFQDPERPRKLPQLCTELQTTIHDIIECVYCKQQLRREYVDFPRDLCTVYDGNPY 60  
DB 1 MFEDATPRRTLHELCVELSEVSHIRLQCVCKKELQREYVKEFLFDLRIVYDNNPY 60  
QY 61 AYXDKLKFYSKISEYRHNYCVVGTLEQGXNKPCLDILLCINXQKPLCEEKRQRLD 120  
DB 61 GYCMICMLRPLSKISEYRHNYQVSLYKTLERVEKPLSEITTCICITQPLCEEKERNV 120  
QY 121 KKQRFHNIIGRWGTGRSCGCC 141  
DB 121 AKKRFHNIIGRWGTGRSCGCC 141  
  
RESULT 79  
ID V6\_HPV52 STANDARD; PRT; 148 AA.  
AC P36814;  
DT 01-JUN-1994, integrated into UniProtKB/Swiss-Prot.  
DT 01-JUN-1994, sequence version 1.  
DT 07-FEB-2006, entry version 27.  
DE Protein E6.  
GN Name=E6;  
OS Human papillomavirus type 52.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
CC Alphapapillomavirus.  
OK NCBI\_TaxID=10618;  
RN  
RP NUCLEOTIDE SEQUENCE (GENOMIC DNA).  
RC MEDLINE=94265501; PubMed=8205838;  
RX Delius H., Hofmann B.;

RT	"Primer-directed sequencing of human papillomavirus types.;"
RL	Curr. Top. Microbiol. Immunol. 186:13-31(1994)
CC	-1- FUNCTION: Transcriptional transactivator. Binds double stranded
CC	DNA (by similarity).
CC	-1- SUBCELLULAR LOCATION: Nuclear matrix-associated (by similarity).
CC	-1- SIMILARITY: Belongs to the papillomaviruses E6 protein family.
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CC	-----
DR	EMBL; X7481; GAA52585.1; -; Genomic_DNA.
DR	PIR; S36573; S36573.
DR	InterPro; IPR001334; E6.
DR	Pfam; PF00518; E6; 1.
KM	Activator; DNA-binding; Early protein; Metal-binding; Nuclear protein;
KM	Transcription; Transcription regulation; Zinc; Zinc-finger.
FT	CHAIN 1 148
FT	FTID=PRO_000013369.
FT	ZN FING 30 66
FT	ZN FING 103 139
FT	Potential.
FT	SEQUENCE 148 AA; 17898 MW; C5E9DCE341AB0DE CRC64;
SQL	
Query Match	58.7%; Score 487; DB 1; Length 148;
Best Local Similarity	61.7%; Pred. No. 6,6e-40;
Matches	87; Conservative 19; Mismatches 35; Indels 0; Gaps 0
OY	1 MFODPOEPRKLPOLCETELQTTIHIIIECYVCKOOLLRREYDPAFRLDCTIVARDGNY 60
DB	1 MFEDPATPRTHLHELCEVLEESVHEIRLQCVCKKELGRREYVKFLFDLRIYRDNMY 60
OY	61 AVXDCKLFYKISFYRYHCVSVGTTLEQYNNKPLCDLLIFNCIXQKPLCEBEKORHD 120
DB	61 GVCIMCFLFLKISFYRYHCVSVGTTLEQYNNKPLSEITTCICQPLCPBEKERHVN 120
OY	121 KKORPHNIRGRWTCGMSCCR 141
DB	121 ANKRFHIMGRWTCGSECWR 141
RESULT 80	
QATUH4_HPV52	
ID	QATUH4_HPV52 PRELIMINARY; PRT; 148 AA.
AC	QATUH4_
DT	19-JUL-2005, integrated into UniProtKB/TrEMBL.
DT	19-JUL-2005, sequence version 1.
DT	07-FEB-2006, entry version 6.
DE	E6 protein.
GN	Name=E6;
OS	Human papillomavirus type 52.
OC	Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC	Alphapapillomavirus.
OX	NCBI_TaxID=10618;
RN	[1]
RP	NUCLEOTIDE SEQUENCE.
RC	STRAIN=HK1243, and HK2571;
RC	PubMed=16227283; DOI=10.1128/JVI.79.21.13630-13640.2005;
RA	Calleja-Macias I.E., Villa L.L., Prado J.C., Kalantari M., Allan B.,
RA	Williamson A.L., Chung L.P., Collins R.U., Zuna R.E., Dunn S.T.,
RA	Chu T.Y., Cubie H.A., Cuschieri K., von Knebel-Doeberitz M.,
RA	Martins C.R., Sanchez G.I., Bosch F.X., Munoz N., Bernard H.V.;
RT	"Worldwide genomic diversity of the high-risk human papillomavirus
RT	types 31, 35, 52, and 58, four close relatives of human papillomavirus
RT	type 16.;"
RL	J. Virol. 79:13630-13640(2005).
RN	[2]
RP	NUCLEOTIDE SEQUENCE.
RC	STRAIN=HK1243, and HK2571;
RC	Calleja-Macias I.E., Kalantari M., Villa L.L., Prado J.C., Allan B.,
RA	Williamson A.L., Chung L.P., Collins R.U., Zuna R.E., Dunn T.,
RA	Chu T.Y., Cubie H.A., Cuschieri K., Knebel-Doeberitz M.V.,
RA	Sanchez G.I., Bosch X., Bernard H.-U.;
RT	Submitted (MAY-2005) to the EMBL/Genbank/DBJ databases.
CC	-----

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-----  
DR1 EMBL; DQ057294; AA58325.1; -; Genomic DNA.  
DR EMBL; DQ057293; AA58324.1; -; Genomic DNA.  
DR GO; GO:0042025; C:host cell nucleus; IEA.  
DR GO; GO:0003677; F:DNA binding; IEA.  
SQ SEQUENCE 148 AA; 17926 MW; 0CE9C7D7341AB0CD CRC64;  
  
Query Match 58.7%; Score 487; DB 2; Length 148;  
Best Local Similarity 61.7%; Pred. No. 6.6e-40;  
Matches 87; Conservative 19; Mismatches 35; Indels 0; Gaps 0;  
  
QY 1 MFQDPQERPRKLPOLCTELQTTIHDIIECYCKQQLRREYDPAFRLDCIVYRDGPNY 60  
DB 1 MFEDPARPRPTLHLCVLEESVHEIRLQCVQCKKELRREYVFLFTDLRIYVRDNNPY 60  
QY 61 AVXDKLKFYSKISEYRYHCYSVYGTTLLEQYNNKPLCDLLIRCIINXOKPLCPBEKORHL 120  
DB 61 GVCIMCLRFSLKISEYRYHCYSVYGTTLLEQYNNKPLCDLLIRCIINXOKPLCPBEKORHL 120  
QY 121 KQRFHNIRGWRGRCSCCR 141  
DB 121 ANKRFHNIRGWRGRCSCCR 141  
  
RESULT 81  
Q4TUH7 HPV52 PRELIMINARY; PRT; 148 AA.  
AC Q4TUH7  
DT 19-JUN-2005, integrated into UniProtKB/TrEMBL.  
DT 19-JUN-2005, sequence version 1.  
DT 07-FEB-2006, entry version 5.  
DE B6 protein.  
GN Name=B6;  
OS Human papillomavirus type 52.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Alphapapillomavirus.  
NCBI\_TaxId=10618;  
RX PubMed=16227283; DOI=10.1128/JVI.79.21.13630-13640.2005;  
RA Calleja-Macias I.E., Villa L.L., Prado J.C., Kalandari M., Allan B.,  
RA Williamson A.L., Chung L.P., Collins R.J., Zuna R.E., Dunn S.T.,  
RA Chu T.Y., Cubie H.A., Cuschieri K., von Knebel-Doeberitz M.,  
RA Martins G.R., Sanchez G.I., Bosch F.X., Munoz N., Bernard H.U.;  
RT "Worldwide genomic diversity of the high-risk human papillomavirus  
RT types 31, 35, 52, and 58, four close relatives of human papillomavirus  
RT type 16," J. Virol. 79:13630-13640(2005).  
RL J. Virol. 79:13630-13640(2005).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=BR0258, ED123, and ED18604;  
RX PubMed=16227283; DOI=10.1128/JVI.79.21.13630-13640.2005;  
RA Calleja-Macias I.E., Kalandari M., Villa L.L., Prado J.C., Allan B.,  
RA Williamson A.L., Chung L.P., Collins R.J., Zuna R.E., Dunn T.,  
RA Chu T.Y., Cubie H.A., Cuschieri K., Knebel-Doeberitz M.,  
RA Sanchez G.I., Bosch F.X., Bernard H.U.;  
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.  
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DR EMBL; DQ057291; AA58322.1; -; Genomic DNA.  
DR EMBL; DQ057290; AA58321.1; -; Genomic DNA.  
DR EMBL; DQ057289; AA58320.1; -; Genomic DNA.  
DR GO; GO:0042025; C:host cell nucleus; IEA.  
DR GO; GO:0003677; F:DNA binding; IEA.  
SQ SEQUENCE 148 AA; 17898 MW; C5E9DECE341AB0DE CRC64;  
  
Query Match 58.7%; Score 487; DB 2; Length 148;  
Best Local Similarity 61.7%; Pred. No. 6.6e-40;  
Matches 87; Conservative 19; Mismatches 35; Indels 0; Gaps 0;

QY 1 MFQDPQERPRKLPOLCTELQTTIHDIIECYCKQQLRREYDPAFRLDCIVYRDGPNY 60  
DB 1 MFEDPARPRPTLHLCVLEESVHEIRLQCVQCKKELRREYVFLFTDLRIYVRDNNPY 60  
QY 61 AVXDKLKFYSKISEYRYHCYSVYGTTLLEQYNNKPLCDLLIRCIINXOKPLCPBEKORHL 120  
DB 61 GVCIMCLRFSLKISEYRYHCYSVYGTTLLEQYNNKPLCDLLIRCIINXOKPLCPBEKORHL 120  
QY 121 KQRFHNIRGWRGRCSCCR 141  
DB 121 ANKRFHNIRGWRGRCSCCR 141  
  
RESULT 82  
VE6 HPV34 STANDARD; PRT; 148 AA.  
ID VE6 HPV34  
AC P36811;  
DT 01-JUN-1994, integrated into UniProtKB/Swiss-Prot.  
DT 01-JUN-1994, sequence version 1.  
DT 07-FEB-2006, entry version 28.  
DE Protein E6.  
GN Name=E6;  
OS Human papillomavirus type 34.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Alphapapillomavirus.  
NCBI\_TaxId=333764;  
RX PubMed=8205838;  
RA Delius H., Hofmann B.;  
RT Primer-directed sequencing of human papillomavirus types.";  
RL Curr. Top. Microbiol. Immunol. 186:13-31(1994).  
CC -1- FUNCTION: Transcriptional transactivator. Binds double stranded  
CC DNA (By similarity).  
CC -1- SUBCELLULAR LOCATION: Nuclear matrix-associated (By similarity).  
CC -1- SIMILARITY: Belongs to the papillomaviruses E6 protein family.  
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DR EMBL; X74476; CA52555.1; -; Genomic DNA.  
DR PIR; S36515; S36515.  
DR InterPro; IPR001334; E6.  
DR Pfam; PF00518; E6; 1.  
KW Activator; DNA-binding; Early protein; Metal-binding; Nuclear protein;  
KW Transcription; Transcription regulation; Zinc; Zinc-finger.  
FT CHAIN 1 148 /FTId=PRO\_0000133354.  
FT ZN\_FING 31 67 Potential.  
FT ZN\_FING 104 140 Potential.  
SQ SEQUENCE 148 AA; 17735 MW; E2FCC6B62BAF0DA CRC64;  
  
Query Match 58.3%; Score 484; DB 1; Length 148;  
Best Local Similarity 60.4%; Pred. No. 1.3e-39;  
Matches 87; Conservative 17; Mismatches 40; Indels 0; Gaps 0;  
  
QY 2 FQDPQERPRKLPOLCTELQTTIHDIIECYCKQQLRREYDPAFRLDCIVYRDGPNY 61  
DB 3 FPNDEPRPYKLPALCEVNISIHIEBLDCYACEROLYRCEYDRIFFDLGVYRKGRPLG 62  
QY 62 VXDCKLKFYSKISEYRYHCYSVYGTTLLEQYNNKPLCDLLIRCIINXOKPLCPBEKORHL 121  
DB 63 VQPCLLLFYSKISEYRYHCYSVYGTTLLEQYNNKPLCDLLIRCIINXOKPLCPBEKORHL 122  
QY 122 KQRFHNIRGWRGRCSCCRSRT 145  
DB 123 NKRPHQADQWGTGRCCTQCKRPSAT 146  
  
RESULT 83  
Q82005 HPV73 PRELIMINARY; PRT; 148 AA.  
ID Q82005 HPV73

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AC 082005;
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 23.
DE E6 protein.
OS Human Papillomavirus type 73.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=51033;
RN
  [1]
  NUCLEOTIDE SEQUENCE.
RX MEDLINE=96213783; PubMed=8635859;
RX DOI=10.1002/(SICI)1097-0215(19960516)66:4<453::AID-IJC7>3.0.CO;2-V;
RA Voelter C, He Y, Delius H, Roy-Burman A, Greenspan J.S.,
RA Greenspan D., de Villiers E.-M.;
RT "Novel HPV types present in oral papillomatous lesions from patients
  with HIV infection."
RL Int. J. Cancer 66:453-456(1996).
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CC -----
DR EMBL: X94165; CA63882.1; -; Genomic DNA.
DR GO: GO:0042025; C:host cell nucleus; IEA.
DR GO: GO:0003677; F:DNA binding; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
SQ SEQUENCE 148 AA; 17630 MW; F28E31E597ACCEDB CRC64;

Query Match 58.2%; Score 483; DB 2; Length 148;
Best Local Similarity 61.4%; Pred. No. 1.6e-39;
Matches 89; Conservative 16; Mismatches 40; Indels 0; Gaps 0;

QY 1 MFQDPQRPRLPOLCTELQTTIHDIIECYCKQQLRRVYDPAFDDLCIVRDGMPY 60
  : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 2 LFPNSEBPPYDQLQCDENVNISHDINDCVCFQKGLRSEYDFAFDLCIVRKDKPY 61
  : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 61 AVXKCKLFYSKISEYRHYCVSVGTTLEQYKNPKDCLIRCIIXKXKPLCPPEKQRIHD 120
  : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 62 GVCQPCPKLFYSKISEYRHYCVSVGTTLENTKNQKLCNHLIRCGKQKPLCPLEKQKVD 121
  : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 121 KKQRFHNRGRWTRGCMSCCSSRT 145
  : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 122 EKKRFHQIAEQWTRGTRCWRPSAT 146
  : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 84
Q80883_9PAPI PRELIMINARY; PRT; 90 AA.
AC 080883;
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 25.
DE E6 protein (fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Unclassified Papillomaviridae.
OX NCBI_TaxID=10566;
RN
  [1]
  NUCLEOTIDE SEQUENCE.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galutira D.F., Younghusband B.H.;
RA Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL: U14512; AAB60566.1; -; Genomic DNA.
DR GO: GO:0042025; C:host cell nucleus; IEA.
DR GO: GO:0003677; F:DNA binding; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
FT NON_TER 1
  1
  NUCLEOTIDE SEQUENCE.
  1
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FT NON TER 90
SQ SEQUENCE 90 AA; 10904 MW; 503ADF843AD6060B CRC64;

Query Match 58.0%; Score 481; DB 2; Length 90;
Best Local Similarity 95.6%; Pred. No. 1.5e-39;
Matches 86; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 42 VYDPAFDDLCIVRDGMPYAVXDCKLFYSKISEYRHYCVSVGTTLEQYKNPKDCLLI 101
  : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1 VYDPAFDDLCIVRDGMPYAVXDCKLFYSKISEYRHYCVSVGTTLEQYKNPKDCLLI 60
  : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 102 RCINXQKPLCPPEKQRIHDKKQRFHNRGR 131
  : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 61 RCINXQKPLCPPEKQRIHDKKQRFHNRGR 90
  : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 85
Q80885_9PAPI PRELIMINARY; PRT; 90 AA.
AC 080885;
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 25.
DE E6 protein (fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Unclassified Papillomaviridae.
OX NCBI_TaxID=10566;
RN
  [1]
  NUCLEOTIDE SEQUENCE.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galutira D.F., Younghusband B.H.;
RA Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL: U14514; AAB60568.2; -; Genomic DNA.
DR GO: GO:0042025; C:host cell nucleus; IEA.
DR GO: GO:0003677; F:DNA binding; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
FT NON_TER 1
  1
  NUCLEOTIDE SEQUENCE.
  1

Query Match 58.0%; Score 481; DB 2; Length 90;
Best Local Similarity 95.6%; Pred. No. 1.5e-39;
Matches 86; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 42 VYDPAFDDLCIVRDGMPYAVXDCKLFYSKISEYRHYCVSVGTTLEQYKNPKDCLLI 101
  : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1 VYDPAFDDLCIVRDGMPYAVXDCKLFYSKISEYRHYCVSVGTTLEQYKNPKDCLLI 60
  : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 102 RCINXQKPLCPPEKQRIHDKKQRFHNRGR 131
  : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 61 RCINXQKPLCPPEKQRIHDKKQRFHNRGR 90
  : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 86
Q80884_9PAPI PRELIMINARY; PRT; 90 AA.
AC 080884;
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 25.
DE E6 protein (fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Unclassified Papillomaviridae.
OX NCBI_TaxID=10566;
RN
  [1]
  NUCLEOTIDE SEQUENCE.
  1
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RC STRAIN=HPV16; TISSUE=Cervical tissue;  
RA Haegert D.G.; Galutira D.F.; Youngband B.H.;  
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.  
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CC -----  
DR EMBL; U14513; AAB60567.2; -, Genomic DNA.  
DR GO; GO:0042025; C:host cell nucleus; IEA.  
DR GO; GO:0003677; F:DNA binding; IEA.  
DR InterPro; IPR001334; B6.  
DR Pfam; PF00518; B6; 1.  
FT NON\_TER 1 1  
FT SEQUENCE 90 AA; 11021 MW; 47F42BBEFACCCC01 CRC64;  
SQ  
Query Match 57.3%; Score 476; DB 2; Length 90;  
Best Local Similarity 95.6%; Pred. No. 4.7e-39;  
Matches 86; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
QY 42 VYDFAPFDLCIVRDGNPYAVXDKLKYSKISYRHYCVYGTTLBEOYNKPLCDLLI 101  
DB 1 VYDFAPFDLWIVRDGNPYAVCDKLKYSKISYRHYCVSLYGTTLBEOYNKPLCDLLI 60  
QY 102 RCINXOKPLCEBKORHLDKKORFHNIRGR 131  
DB 61 RCINXOKPLCEBKORHLDKKORFHNIRGR 90  
RESULT 87  
VE6\_HP68 STANDARD; PRT; 158 AA.  
ID PS4667;  
DT 01-OCT-1996, integrated into UniProtKB/Swiss-Prot.  
DT 01-OCT-1996, sequence version 1.  
DT 07-FEB-2006, entry version 25.  
DE Protein B6.  
GN Name=B6;  
OS Human papillomavirus type 68.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Alphapapillomavirus.  
OX NCBI\_Taxid=45240;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
RX MEDLINE=97060129; PubMed=9904450;  
RA Longuet M., Beaudenon S., Orh G.;  
RT "Two novel genital human papillomavirus (HPV) types, HPV68 and HPV70,  
RT related to the potentially oncogenic HPV39.";  
RL J. Clin. Microbiol. 34:738-744(1996).  
CC -1- FUNCTION: Transcriptional transactivator. Binds double stranded  
CC DNA (By similarity).  
CC -1- SUBCELLULAR LOCATION: Nuclear matrix-associated (By similarity).  
CC -1- SIMILARITY: Belongs to the papillomaviruses B6 protein family.  
CC -----  
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CC -----  
DR EMBL; X67160; CAA47632.1; -, Genomic DNA.  
DR InterPro; IPR001334; B6.  
DR Pfam; PF00518; B6; 1.  
DR Activator; DNA-binding; Early protein; Metal-binding; Nuclear protein;  
KM Transcription; Transcription regulation; Zinc; Zinc-finger.  
FT CHAIN 1 158  
FT ZN\_FING 32 68  
FT ZN\_FING 105 141  
FT SEQUENCE 158 AA; 18796 MW; 46B37939CFBA6596 CRC64;  
SQ  
Query Match 56.4%; Score 468.5; DB 1; Length 158;  
Best Local Similarity 55.1%; Pred. No. 4.7e-38;  
Matches 86; Conservative 23; Mismatches 42; Indels 5; Gaps 1;  
QY 1 MFQDQBRPRRLPOLCTELQTTIHDIIECVYCKQQLRREVPYAFPRDLCTIVRDGNPY 60.

DB 3 LFHNPEBRPYKLPDLCTLTDTTLDHVTIDCVYCRQQRQREVEYEFASDLCVYRRDVPF 62  
QY 61 AYVXDKLKYSKISYRHYCVYGTTLBEOYNKPLCDLLIRCNKOKPLCEBKORHLD 120  
DB 63 AACQSCIKFYAKIRLHRYSVESVYATLTETITWTKLVNLLIRGMSCLKPLCPAEKLRHVT 122  
QY 121 KKQRFHNIRGRWYGRCSGCCRSS-----RTRRRTQL 151  
DB 123 TKRLHKRIAGNFTGQCHRCWTSKRDRRRRIQETOV 158  
RESULT 88  
VE6\_HP70 STANDARD; PRT; 158 AA.  
ID PS0804;  
DT 01-OCT-1996, integrated into UniProtKB/Swiss-Prot.  
DT 01-OCT-1996, sequence version 1.  
DT 07-FEB-2006, entry version 24.  
DE Protein B6.  
GN Name=B6;  
OS Human papillomavirus type 70.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Alphapapillomavirus.  
OX NCBI\_Taxid=39457;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
RX MEDLINE=96249586; PubMed=8815087;  
RA Forslund O., Hansson B.G.;  
RT "Human papillomavirus type 70 genome cloned from overlapping PCR  
RT products: complete nucleotide sequence and genomic organization.";  
RL J. Clin. Microbiol. 34:802-809(1996).  
RN [2]  
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
RX MEDLINE=97060129; PubMed=9904450;  
RA Longuet M., Beaudenon S., Orh G.;  
RT "Two novel genital human papillomavirus (HPV) types, HPV68 and HPV70,  
RT related to the potentially oncogenic HPV39.";  
RL J. Clin. Microbiol. 34:738-744(1996).  
CC -1- FUNCTION: Transcriptional transactivator. Binds double stranded  
CC DNA (By similarity).  
CC -1- SUBCELLULAR LOCATION: Nuclear matrix-associated (By similarity).  
CC -1- SIMILARITY: Belongs to the papillomaviruses B6 protein family.  
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CC -----  
DR EMBL; U21941; AAC54850.1; -, Genomic DNA.  
DR EMBL; U22461; AAC54880.1; -, Genomic DNA.  
DR InterPro; IPR001334; B6.  
DR Pfam; PF00518; B6; 1.  
DR Activator; DNA-binding; Early protein; Metal-binding; Nuclear protein;  
KM Transcription; Transcription regulation; Zinc; Zinc-finger.  
FT CHAIN 1 158  
FT ZN\_FING 32 68  
FT ZN\_FING 105 141  
FT CONFICT 100 100  
FT SEQUENCE 158 AA; 18617 MW; 6B610800D923D6DE CRC64;  
SQ  
Query Match 56.4%; Score 468.5; DB 1; Length 158;  
Best Local Similarity 56.8%; Pred. No. 4.7e-38;  
Matches 88; Conservative 21; Mismatches 41; Indels 5; Gaps 1;  
QY 2 FQDQBRPRRLPOLCTELQTTIHDIIECVYCKQQLRREVPYAFPRDLCTIVRDGNPYA 61  
DB 4 FPNPABRPRYKLPDLCTLTDTTLDHVTIDCVYCKQQLQGVTEYERAFSDLFIVRNGSPYA 63  
QY 62 VXDCLKFYSKISYRHYCVYGTTLBEOYNKPLCDLLIRCNKOKPLCEBKORHLDK 121  
DB 64 ACQSCIKFYAKIRLHRYSVNSVYATLTETITWTKLVNLLIRGMSCLKPLCPAEKLRHVT 123  
QY 122 KQRFHNIRGRWYGRCSGCCRSS-----RTRRRTQL 151

[illegible]

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CC      Distributed under the Creative Commons Attribution-NonDerivative license
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DR      EMBL; M62877; -, NOT_ANNOTATED_CDS; Genomic_DNA.
DR      PIR; E40415; M6WL51.
DR      InterPro; IPR001334; B6.
DR      Pfam; PF00518; B6; 1.
KW      Activator; DNA-binding; Early protein; Metal-binding; Nuclear protein;
KW      Transcription; Transcription regulation; Zinc; Zinc-finger.
FT      CHAIN   1             151
FT           /FTid=PRO_0000133368.
FT           Potential.
FT      ZN_FING 30             66
FT      ZN_FING 103           139
FT      ZN_FING 151 AA; 18134 MW; 578663BA1376478 CRC64;
SQ      SEQUENCE 151 AA; 18134 MW; 578663BA1376478 CRC64;

Query Match      55.4%; Score 460; DB 1; Length 151;
Best Local Similarity 57.0%; Pred. No. 3,1e-37;
Matches 86; Conservative 24; Mismatches 41; Indels 0; Gaps 0;

Oy      1 MFODPQSRPKLPOLCTELQTTIHDLLECVCYKQQLRREVYDPAFRLDCIYRDNQNP 60
          :::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      1 MFEDKRPRPTTHLCLCALVAMSHNIQVVCYCKELCRADYVNVAFTEIKIYYRDNNPY 60
          :::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

Oy      61 AVXDCKLCPYSKISERHYCYSYGTTLEQYNKPLCDLLIRCLNKKPLCPPEKQRHLD 120
          :::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      61 AVQCQCLLPFSKIREYRYSRYSVGTTLLEATITKSLYDLSIRCHRCORPLGPPEKKLVLD 120
          :::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

Oy      121 KKQRFHNRGRWTRGRCMCCRSSRTRRETOL 151
          ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      121 EKGRFHEIAGRWTQGCANCWRRTRQRETV 151
          ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 91
ID      V66_HPV45          STANDARD;          PRT;          158 AA.
AC      P21735.
DT      01-MAY-1991, integrated into UniProtKB/Swiss-Prot.
DT      01-JUN-1994, sequence version 2.
DT      07-FEB-2006, entry version 32.
DE      Protein B6.
GN      Name=B6;
OS      Human papillomavirus type 45.
OC      Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC      Alphapapillomavirus.
OX      NCBI_TaxID=10593;
RX      MEDLINE=94265501; PubMed=8205838;
RN      NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RA      MEDLINE=94265501; PubMed=8205838;
RA      Delling H., Hofmann B.;
RT      "Primer-directed sequencing of human papillomavirus types.",
RL      Curr. Top. Microbiol. Immunol. 186:13-31(1994).
RN      NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RP      Kaplan J.B., Burk R.D.;
RA      Submitted (AUG-1990) to the EMBL/GenBank/DBJ databases.
CC      -1- FUNCTION: Transcriptional transactivator. Binds double stranded
CC      DNA (By similarity).
CC      -1- FUNCTION: This protein has transforming activity in vitro.
CC      -1- SUBCELLULAR LOCATION: Nuclear matrix-associated (By similarity).
CC      -1- SIMILARITY: Belongs to the papillomaviruses B6 protein family.
CC      -----
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CC      -----
DR      EMBL; X74479; CAAS2573.1; -, Genomic_DNA.
DR      EMBL; M38198; AAA46973.1; -, Genomic_DNA.
DR      PIR; S36561.
DR      InterPro; IPR001334; B6.
DR      Pfam; PF00518; B6; 1.
KW      Activator; DNA-binding; Early protein; Metal-binding; Nuclear protein;
KW      Oncogene; Transcription; Transcription regulation; Zinc; Zinc-finger.
FT      CHAIN   1             158
FT           /FTid=PRO_0000133364.

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FT 2N FING 32 68 Potential.
FT 2N FING 105 141
FT CONFLICT 10 10 R -> P (in Ref. 2).
FT CONFLICT 30 30 I -> N (in Ref. 2).
FT CONFLICT 118 118 R -> A (in Ref. 2).
SQ SEQUENCE 158 AA; 18897 MW; FICFIDDD33AA4C3E CRC64;

Query Match 55.4%; Score 459.5; DB 1; Length 158;
Best Local Similarity 56.1%; Pred. No. 3.6e-37;
Matches 87; Conservative 22; Mismatches 41; Indels 5; Gaps 1;

QY 2 FQDQEPKRLPOLCTELQTTIHDIIEECVYCKQOLAREVYDFAFRDLCTIVRDGNPYA 61
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 4 PDDCKQRPKYKPDLCYTELNTSLQDSVSYCAKALETEYVYQFAFDLCIVRDCIAYA 63
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 62 VXDCKLAFYSKISERYHYCVSVYGTTEEQYNNKPLCDLLIRICNNKQPLCEBKQRHLDK 121
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 64 ACHKCIPIFYSHIRRELYRYSNVSGTLETKIINTLEYLNLLIRCLRCQKPLNPAEKRRHLKD 123
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 122 KQRFHNIRGRWTRGRMCSCCRSS-----RTRETLQ 151
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 124 KRRFHSIAGQYRGQCMTCCDARQERLRRRRETVQ 158
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 92
080882_9PAPI PRELIMINARY; PRT; 84 AA.
AC 080882;
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 25.
DE E6 protein (Fragment) .
OS Human Papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC unclassified Papillomaviridae.
OX NCBI_TaxID=10566;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HPV16; TISSUE=Cervical;
RA Haegert D.G., Galutira D.F., Younghuband B.H.;
RL Submitted (SEP-1994) to the EMBL/Genbank/DDbj databases.
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CC International License
CC EMBL: U14511; AAB60565.2; -; Genomic DNA.
DR GO: 0042025; C:host cell nucleus; IEA.
DR GO: 0003477; P:DNA binding; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 84
FT NON_TER 84
SQ SEQUENCE 84 AA; 10177 MW; 5AB6B996468E1CAAC CRC64;

Query Match 55.1%; Score 457; DB 2; Length 84;
Best Local Similarity 57.6%; Pred. No. 3.3e-37;
Matches 82; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 45 PAFRDLCTIVRDGNPYAVXDCKLAFYSKISERYHYCVSVYGTTEEQYNNKPLCDLLIRCI 104
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1 PAFRDLCTIVRDGNPYAVXDCKLAFYSKISERYHYCVSVYGTTEEQYNNKPLCDLLIRCI 60
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 105 NXQKPLCEBKQRHLDKQKRFHNI 128
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 61 NXQKPLCEBKQRHLDKQKRFHNI 84
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 93
VE6 HPV18 STANDARD; PRT; 158 AA.
AC P06463;
DT 01-JAN-1988, integrated into UniProtKB/Swiss-Prot.
DT 01-JAN-1988, sequence version 1.

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DT 07-FEB-2006, entry version 45.  
DE Protein E6.  
GN Name=E6;  
OS Human papillomavirus type 18.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Alphapapillomavirus.  
OX NCBI\_TaxId=333761;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
RX MEDLINE=87283882; PubMed=3039146;  
RA Cole S.T., Danos O.;  
RT "Nucleotide sequence and comparative analysis of the human  
papillomavirus type 18 genome. Phylogeny of papillomaviruses and  
repeated structure of the E6 and E7 gene products.";  
RL J. Mol. Biol. 193:599-608(1987).  
RL [2]  
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
RX MEDLINE=86306665; PubMed=3018129;  
RA Metlahevski G., Banks L., Wu-Liao J., Spence P., Pim D., Crawford L.,  
RT "The expression of human papillomavirus type 18 E6 protein in bacteria  
and the production of anti-E6 antibodies.";  
RL J. Gen. Virol. 67:1909-1916(1986).  
RN [3]  
RP NUCLEOTIDE SEQUENCE [MRNA].  
RX MEDLINE=88188247; PubMed=2833614;  
RA Inagaki Y., Tsunokawa Y., Takebe N., Nawa H., Nakanishi S., Terada M.,  
RT Suginura T.;  
RT "Nucleotide sequences of cDNAs for human papillomavirus type 18  
transcripts in HeLa cells.";  
RL J. Virol. 62:1640-1646(1988).  
RN [4]  
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
RX MEDLINE=87053870; PubMed=3023067;  
RA Schneider-Gaeddicke A., Schwartz E.;  
RT "Different human cervical carcinoma cell lines show similar  
transcription patterns of human papillomavirus type 18 early genes.";  
RL EMO J. 5:2285-2292(1986).  
RN [5]  
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
RX MEDLINE=87218459; PubMed=3045711;  
RA Seedorf K., Oltendorf T., Kraemer G., Roewekamp W.;  
RT "Identification of early proteins of the human papilloma viruses type  
16 (HPV 16) and type 18 (HPV 18) in cervical carcinoma cells.";  
RL EMO J. 6:139-144(1987).  
RN [6]  
RP ZINC-BINDING.  
RX MEDLINE=89385606; PubMed=2550872;  
RA Grossman S.R., Laimins L.A.;  
RT "E6 protein of human papillomavirus type 18 binds zinc.";  
RL Oncogene 4:1089-1093(1989).  
RN [7]  
RP INTERACTION WITH HUMAN TP53 PROTEIN.  
RX MEDLINE=94037097; PubMed=8221889; DOI=10.1016/0092-8674(93)90384-3;  
RA Scheffner M., Huibregtse J.M., Vierstra R.D., Howley P.M.;  
RT "The HPV-16 E6 and E6-AP complex functions as a ubiquitin-protein  
ligase in the ubiquitination of p53.";  
RL Cell 75:495-505(1993).  
RN [8]  
RP INTERACTION WITH HUMAN MEDZ, AND MUTAGENESIS OF 156-THR--VAL-158 AND  
VAL-158.  
RX MEDLINE=20457232; PubMed=11000240;  
DOI=10.1126/JVI.74.20.9680-9693.2000;  
RA Lee S.S., Glausinger B., Mactovani F., Banks L., Javler R.T.;  
RT "Multi-PDZ domain protein MUPP1 is a cellular target for both  
adenovirus E4-ORF1 and high-risk papillomavirus type 18 E6  
oncoproteins.";  
RL J. Virol. 74:9680-9693(2000).  
RN [9]  
RP INTERACTION WITH HUMAN PLIN1, AND INHIBITION OF E6-MEDIATED  
TRANSFORMATION.  
RX MEDLINE=22188366; PubMed=12200142; DOI=10.1016/S0006-291X(02)02041-7;  
RA Du M., Fan X., Hong E., Chen J.J.;  
RT "Interaction of oncogenic papillomavirus E6 proteins with fibulin-1.";  
RL

RL	Biochem. Biophys. Res. Commun.	296:962-969(2002).
CC	-1- FUNCTION: Transcriptional transactivator. Binds double stranded DNA (by similarity). Has transforming activity. Inactivates, with	
CC	E6-AP ubiquitin-protein ligase, the human TP53/p53 tumor	
CC	suppressor protein by targeting it to degradation. Binds and	
CC	targets human MDP1/MPDZ protein to degradation. Those two	
CC	functions presumably contribute to transforming activity.	
CC	Interaction with human FBXN1 protein also seems to be linked to	
CC	cell transformation.	
CC	-1- SUBUNIT: Forms a complex with E6-AP ubiquitin-protein ligase which	
CC	interacts with human p53. Binds to human FBXN1 and MDPZ.	
CC	-1- SUBCELLULAR LOCATION: Nuclear matrix-associated (by similarity).	
CC	-1- SIMILARITY: Belongs to the papillomavirus E6 protein family.	
CC	-----	
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CC	-----	
DR	EMBL; X04354; CAA27879.1; -; Genomic DNA.	
DR	EMBL; X05015; CAA28664.1; -; Genomic DNA.	
DR	EMBL; M20325; AAA99514.1; -; mRNA.	
DR	EMBL; M26798; AAA46946.1; -; Genomic DNA.	
DR	EMBL; X04773; CAA28466.1; -; Genomic DNA.	
DR	EMBL; A06324; CAA00539.1; -; Unassigned DNA.	
DR	EMBL; A06328; CAA00539.1; -; Unassigned RNA.	
DR	PIR; A26165; W6WL18.	
DR	InterPro; IPR001334; E6.	
DR	Pfam; PF00518; E6_1.	
KW	Activator; DNA-binding; Early protein; Metal-binding; Nuclear protein;	
KW	oncogene; transcription; transcription regulation; zinc; zinc-finger.	
KW	CHAIN	
FT	1	
FT	ZN_FING	
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FT	105 141	
FT	MOTIF	
FT	155 158	
FT	MUTAGEN	
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FT	22 22	
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FT	-----	
QY	Query Match	
QY	Best Local Similarity 54.9%; Score 455.5; DB 1; Length 158;	
QY	Matches 87; Conservative 21; Mismatches 42; Indels 5; Gaps 14	
QY	2 FODPQERPKLQPLCTELQTTIHDIILSCVYKQOOLRRREYVDFAPRLCTIYRDGNPYA 61	
QY	4 FEDPERRRYKLPDLCTELNTSLQDLEITICVYKQVLELVEVEEFAFKDLFVYVRSIHNA 63	
QY	62 VYDKCLKAYYSKISEYRHYCYSYGTTLEQYNNKPLCDLILRCINXQKPKLCEPKORHLDK 121	
QY	64 ACHKICIDYSEYRIRREIRHYSDSYVGDTLEKLTETTGYNLILRCIRCKQKPLNPAEKURHINE 123	
QY	122 KQPFNINRGWRGRCMCCSCRSR-----TRRETOL 151	
QY	124 KRPFNINRGYRGQCHSCCNRAQRERLQRRRETQV 158	
QY	-----	
QY	RESULT 94	
QY	076297 HPV18	
QY	076297 HPV18 PRELIMINARY; PRT; 158 AA.	
QY	076297	
QY	10-MAY-2005, integrated into UniProtKB/TrEMBL.	
QY	07-FEB-2006, entry version 4.	
QY	E6 protein.	
QY	Name=E6;	
QY	Human papillomavirus type 18.	
QY	VirusE6; GenDNA virusE6s, no RNA stage; Papillomaviridae;	
QY	Alphapapillomavirus.	
QY	NCBI_TaxID=333761;	
QY	(1)	
QY	NUCLEOTIDE SEQUENCE.	

RX PubMed:6306621; DOI=10.1128/JVI.79.24.15503-15510.2005;  
 RA Narechania A., Chen Z., Desalle R., Burk R.D.;  
 RT "Phylogenetic Incongruence among Oncogenic Genital Alpha Human  
 RL Papillomaviruses.";  
 CC J. Virol. 79:15503-15510(2005).  
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 CC  
 CC EMBL; AY262282; AAP20594.1; -; Genomic\_DNA.  
 DR GO; GO:0042025; C:host cell nucleus; IEA.  
 DR GO; GO:0003677; F:DNA binding; IEA.  
 DR InterPro; IPR001334; B6.  
 DR Pfam; PF00518; B6; 1.  
 SQ SEQUENCE 158 AA; 18872 MW; 5BFCF13CF43D157FA CRC64;  
  
 Query Match 54.9%; Score 455.5; DB 2; Length 158;  
 Best Local Similarity 56.1%; Pred. No. 9e-37;  
 Matches 87; Conservative 21; Mismatches 42; Indels 5; Gaps 1;  
  
 QY 2 FQDQSEPRKLPOLCTELQTTIHDIILCEYCKQQLRREYVAPAPDLCTVRRDNPYA 61  
 Db 4 FEDPRRRRYKLPDCTELNTSLQDIETCYCKVLELTVEFAFADLPVVRDLSLPA 63  
 QY 62 VXDCKLKFYSKISERYHYCVSVYGTLEQQYNKPLCDLLIRCNXKXKPLCPSEKORHLDK 121  
 Db 64 ACHKICIDPYSIRIRLRYHSDVSDYDTLEKLTNTGLYVLLIRLCRCQPLNPAEKRLRLNE 123  
 QY 122 KQREHNIRGRWTRGRCMSCCRSSR-----TYREQL 151  
 Db 124 KRPHNIAGHYRGQCHSCNRPARGRLQRRETRTV 158  
  
 RESULT 95  
 VF6\_HPVME STANDARD; PRT; 158 AA.  
 ID VF6\_HPVME  
 AC P27962;  
 DT 01-AUG-1992, integrated into UniProtKB/Swiss-Prot.  
 DT 01-AUG-1992, sequence version 1.  
 DT 07-FEB-2006, entry version 28.  
 DE Protein B6.  
 GN Name=B6;  
 OS Human papillomavirus type ME180.  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 OC Unclassified Papillomaviridae.  
 OX NCBI\_TaxID=10602;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE (GENOMIC DNA).  
 RX MEDLINE=91374616; PubMed=1716694.  
 RA Reuter S., Delius H., Kahn T., Hofmann B., Zur Hausen H., Schwarz E.;  
 RT "Characterization of a novel human papillomavirus DNA in the cervical  
 RL carcinoma cell line ME180.";  
 RL J. Virol. 65:5564-5568(1991).  
 CC -!- FUNCTION: Transcriptional transactivator. Binds double stranded  
 CC DNA (by similarity).  
 CC -!- SUBCELLULAR LOCATION: Nuclear matrix-associated (by similarity).  
 CC -!- SIMILARITY: Belongs to the papillomaviruses B6 protein family.  
 CC  
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 CC  
 CC EMBL; M73258; -; NOT\_ANNOTATED\_CDS; Genomic\_DNA.  
 DR PIR; C40509; M6WLPK.  
 DR InterPro; IPR001334; B6.  
 DR Pfam; PF00518; B6; 1.  
 KW Activator; DNA-binding; Early protein; Metal-binding; Nuclear protein;  
 KW Transcription; Transcription regulation; Zinc; Zinc-finger.  
 FT CHAIN 1 158 /Ftrid=PRO\_0000133318.  
 FT ZN\_FING 32 /Ftrid=PRO\_0000133318.  
 FT ZN\_FING 106 68 Potential.  
 FT ZN\_FING 141 Potential.  
 SQ SEQUENCE 158 AA; 18739 MW; 2B1F06B563F05FC CRC64;

Qy	Query Match	54.4%	Score 451.5;	DB 1;	Length 158;
Db	Best Local Similarity	55.1%	Pred. No. 2.2e-36;		
Matches	86;	Conservative	21;	Mismatches	44;
				Indels	5;
				Gaps	1;
Qy	1 MFODPQERPRKLPOLCTELQTTHIDIIIECYCKQQLLRREYDPAFEDLCIYRDGPNY	60			
Db	3 LFHNPEERPYKLPLDCRLTDLTDLTLDVITIDCVYCRQLQRTVEYEFAGFDLNVVRDGVPL	62			
Qy	61 AYXDKLFYSKISIEYRHVCYSVGTTLEQQYNKPLCDLLIRCNIXOKPLCPBEKQRHLD	120			
Db	63 AACSCIKIFAKIELRELARYSSSVATLETINTKLYDLDSIRCMCLPLSPAEXLRHLN	122			
Qy	121 KKORFNIRGRWTRGRCMSCRSS-----RTRRETOL	151			
Db	123 SKRRPHKIAGNFPGOCRCWCWSKEDRRRTROETOV	158			
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ID	Q7KYX8_HPV68	PRELIMINARY;	FRT;	158 AA.	
AC	Q7KYX8_				
DT	05-JUL-2004,	integrated into UniProtKB/TrEMBL.			
DT	05-JUL-2004,	sequence version 1.			
DT	07-FEB-2006,	entry version 12.			
OS	E6 protein.				
OS	Human papillomavirus type 68.				
OC	Viruses, dsDNA viruses, no RNA stage; Papillomaviridae;				
OC	Alphapapillomavirus.				
OX	NCBI_TaxID=45240;				
RN	[1]				
RP	NUCLEOTIDE SEQUENCE.				
RX	MEDLINE=91374616; PubMed=1716694;				
RA	Reuter S., Dellius H., Kahn T., Hofmann B., Zur Hausen H., Schwarz E.;				
RT	"Characterization of a novel human papillomavirus DNA in the cervical				
RL	carcinoma cell line ME180."				
J.	J. Virol. 65:5564-5568(1991).				
RN	[2]				
RP	NUCLEOTIDE SEQUENCE.				
RX	MEDLINE=98090644; PubMed=9427755; DOI=10.1093/emboj/17.1.215.				
RA	Reuter S., Bartelmann M., Vogt M., Geisen C., Napierköt I., Kahn T.,				
RA	Dellius H., Lichter P., Weitz S., Korn B., Schwarz E.;				
RT	"AEM-1, a novel human gene, identified by aberrant cotranscription				
RT	with papillomavirus oncogenes in aa cervical carcinoma cell line,				
RT	encodes a BTB/POZ-zinc finger protein with growth inhibitory				
activity".					
RL	EMBO J. 17:215-222(1998).				
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms				
CC	Distributed under the Creative Commons Attribution-NoDerivs license				
DR	EMBL: Y14591; CAAt74931.1; -; mRNA.				
DR	GO:0042025; C:host cell nucleus; IEA.				
DR	GO:0003677; F:DNA binding; IEA.				
DR	InterPro: IPR001334; E6.				
DR	Pfam: PF00518; E6; 1.				
SQ	SEQUENCE 158 AA; 18739 MW; 2B1FA06B563F05FC CRC64;				
Qy	Query Match	54.4%	Score 451.5;	DB 2;	Length 158;
Db	Best Local Similarity	55.1%	Pred. No. 2.2e-36;		
Matches	86;	Conservative	21;	Mismatches	44;
				Indels	5;
				Gaps	1;
Qy	1 MFODPQERPRKLPOLCTELQTTHIDIIIECYCKQQLLRREYDPAFEDLCIYRDGPNY	60			
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Qy	121 KKORFNIRGRWTRGRCMSCRSS-----RTRRETOL	151			
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AC 09UIZ3;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 07-FEB-2006, entry version 21.
DE E6.
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC unclassified Papillomaviridae.
OX NCBI_TaxID=10566;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=91374616; PubMed=1716694;
RA Reuter S., Bellus H., Kahn T., Hofmann B., Zur Hausen H., Schwarz E.;
RT "Characterization of a novel human papillomavirus DNA in the cervical
   carcinoma cell line ME180."
RL J. Virol. 65:5564-5568(1991).
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CC
CC EMBL; M73258; AAF14011.1; -; Genomic DNA.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; BC.
DR Pfam; PF00518; E6; 1.
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DT	01-MAR-1992,	sequence version 1.	
DT	07-FEB-2006,	entry version 30.	
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GN	Name=E6;		
OS	Human papillomavirus type 39.		
OC	Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;		
OC	Alphapapillomavirus.		
OX	NCBI_TaxID=10588;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE [GENOMIC DNA].		
RX	MEDLINE=91135017; PubMed=1847266;		
RA	Volpert C., Strebeck R.E.;		
RT	"Genome organization and nucleotide sequence of human papillomavirus		
RT	type 39.";		
RL	Virolology 181:419-423(1991).		
CC	-1- FUNCTION: Transcriptional transactivator. Binds double stranded		
CC	DNA (By similarity).		
CC	-1- FUNCTION: This protein may be involved in the oncogenic potential		
CC	of this virus (cervical neoplasia-associated virus).		
CC	-1- SUBCELLULAR LOCATION: Nuclear matrix-associated (By similarity).		

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CC -1- SIMILARITY: Belongs to the papillomaviruses E6 protein family.
CC -----
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CC Distributed under the Creative Commons Attribution-NonDerivs License
CC -----
DR EMBL; M62849; AAA47050.1; -; Genomic_DNA.
DR PIR; A38502; M6M139.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
KW Activator; DNA-binding; Early protein; Metal-binding; Nuclear protein;
KW Oncogene; Transcription; Transcription regulation; Zinc; Zinc-finger.
FT CHAIN 1 158 /FtId=PRO_0000133358.
FT ZN FING 32 68 Potential.
FT ZN FING 105 141 Potential.
SQ SEQUENCE 158 AA; 18727 MW; 1B5E9D55BC1B662E CRC64;

Query Match 54.2%; Score 449.5; DB 1; Length 158;
Best Local Similarity 55.5%; Pred. No. 3.5e-36;
Matches 86; Conservative 19; Mismatches 45; Indels 5; Gaps 1;

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DB 4 FHNPAERPYKLPDLCTLTDTLQDTTACVYCRBPLOQTEVEYEFASDLVYVYRDGEPLA 63
QY 62 VXDCKLFYSKISEYRHYCVSYVGTLEQYNNKPLCDLLIRGINXOKPLCPBEKQRHLDK 121
DB 64 ACGSCIFVAKIRRLRYSDSVVATLTLENITNTKLYNLLIRCMCKLRKCPAEKLRHLNS 123
QY 122 KORFHNIRGRWGTGRCMSCCRSSR-----TRRETQL 151
DB 124 KRREHKIAGHYRGCHSCNRRARQRRRTQV 158

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DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 07-FEB-2006, entry version 17.
DE E6 protein.
OS Human papillomavirus type 18.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxId=333761;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Laaseri M., Gul'ko L., Vinokurova S., Kissel'jova N., Veiko V.,
RA Kissel'jev F.;
RT "Cloning of E6 and E7 Genes of Human Papilloma Virus Type 18 and
RT Transformation Potential of E7 Gene and its Mutants.";
RL Virus Genes 182:139-149(1999).
RN [2]
RN NUCLEOTIDE SEQUENCE.
RA Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RA Veiko V.P.;
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CC -----
DR EMBL; Y18491; CAB53096.1; -; Genomic_DNA.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 158 AA; 18886 MW; 5BCF13CF43D407AF CRC64;

Query Match 54.2%; Score 449.5; DB 2; Length 158;
Best Local Similarity 55.5%; Pred. No. 3.5e-36;
Matches 86; Conservative 21; Mismatches 43; Indels 5; Gaps 1;

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DB 64 ACHKCIDFYRIRLRYSDSVYGDTEKLTNGLYNLLIRCMCKLRKCPAEKLRHLNE 123
QY 122 KORFHNIRGRWGTGRCMSCCRSSR-----TRRETQL 151
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ID Q994A0 HPV82 PRELIMINARY; PRT; 151 AA.
AC Q994A0;
DT 01-JUN-2001, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2001, sequence version 1.
DT 07-FEB-2006, entry version 17.
DE Putative transforming protein E6.
GN Name=E6;
OS Human papillomavirus type 82.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxId=129724;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=16306621; DOI=10.1128/JVI.79.24.15503-15510.2005;
RA Narechania A., Chen Z., Desalle R., Burk R.D.;
RT "Phylogenetic Incongruence among Oncogenic Genital Alpha Human
RT Papillomaviruses.";
RL J. Virol. 79:15503-15510(2005).
RN [2]
RN NUCLEOTIDE SEQUENCE.
RA Teraai M., Burk R.D.;
RT "Cervical HPV's in Evolution; Genomic Sequence of IS39/82, a Subtype
RT of Oncogenic HPV 82 (W13B).";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AF293961; AAK28449.1; -; Genomic_DNA.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
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DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18071 MW; 5BDC340E467CF75D CRC64;

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QY 61 AYVDCKLFYSKISEYRHYCVSYVGTLEQYNNKPLCDLLIRGINXOKPLCPBEKQRHL 120
DB 61 AVCKKICLIFYRIRLRYSDSVYGDTEKLTNGLYNLLIRCMCKLRKCPAEKLRKQVVD 120
QY 121 KORFHNIRGRWGTGRCMSCCRSSRTRRETQL 151
DB 121 DKCRPFHEIAGRWGTGQCANCRNTARQSESTQV 151

Search completed: May 27, 2006, 05:16:23
Job time : 238.867 secs
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OM protein - protein search, using sw model

Run on: May 27, 2006, 05:33:17 ; Search time 157.064 Seconds  
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445.330 Million cell updates/sec

Title: US-10-530-253-13ED  
Perfect score: 830  
Sequence: 1 MFQDPQERPRKLPQLCELDQ.....MTGRCMSCCRRTRRRTQL 151

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Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : Published Applications AA Main:  
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2: /EMC\_Celestra\_SIDS3/ptodata/2/pubppaa/US08\_PUBCOMB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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4	826	99.5	151	5	US-10-484-063-27
5	826	99.5	151	5	US-10-530-253-13
6	826	99.5	151	5	US-10-530-253-1
7	823	99.2	158	5	US-10-858-384-2
8	823	99.2	158	5	US-10-367-057-16
9	823	99.2	158	6	US-11-021-949-13
10	823	99.2	158	6	US-11-021-949-13
11	823	99.2	171	4	US-10-472-724-2
12	823	99.2	248	5	US-10-530-253-9
13	823	99.2	248	5	US-10-530-253-11
14	823	99.2	256	6	US-11-192-923A-2
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16	823	99.2	273	4	US-10-000-903-4
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20	823	99.2	371	5	US-10-000-903-6
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29	523	63.0	149	5	US-10-530-253-16	Sequence 16, Appl
30	523	63.0	149	5	US-11-021-949-18	Sequence 18, Appl
31	520	62.7	149	5	US-10-530-253-17	Sequence 17, Appl
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33	498	60.0	149	6	US-11-021-949-36	Sequence 36, Appl
34	496	59.8	149	5	US-10-530-253-24	Sequence 24, Appl
35	496	59.8	149	6	US-11-021-949-15	Sequence 15, Appl
36	487	58.7	148	5	US-10-530-253-22	Sequence 22, Appl
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38	484	58.3	148	6	US-11-021-949-39	Sequence 39, Appl
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41	468.5	56.4	158	6	US-11-021-949-31	Sequence 31, Appl
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46	455.5	54.9	158	5	US-10-530-253-15	Sequence 15, Appl
47	455.5	54.9	158	6	US-11-021-949-28	Sequence 28, Appl
48	455.5	54.9	172	4	US-10-472-724-6	Sequence 6, Appl
49	455.5	54.9	278	4	US-10-000-903-21	Sequence 21, Appl
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51	455.5	54.9	383	4	US-10-000-903-23	Sequence 23, Appl
52	455.5	54.9	383	5	US-10-899-771-23	Sequence 23, Appl
53	451.5	54.4	162	6	US-11-021-949-31	Sequence 31, Appl
54	451.5	54.4	158	5	US-10-800-023-27	Sequence 27, Appl
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56	449.5	54.2	158	6	US-10-530-253-19	Sequence 19, Appl
57	449.5	54.2	151	6	US-11-021-949-25	Sequence 25, Appl
58	449.5	54.1	151	6	US-11-021-949-25	Sequence 25, Appl
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60	426.5	51.4	155	5	US-11-021-949-22	Sequence 22, Appl
61	421	50.7	152	5	US-10-530-253-39	Sequence 39, Appl
62	415.5	50.1	160	5	US-10-530-253-25	Sequence 25, Appl
63	415.5	50.1	160	6	US-11-021-949-32	Sequence 32, Appl
64	415	50.0	151	6	US-11-021-949-26	Sequence 26, Appl
65	385.5	46.4	153	6	US-11-021-949-20	Sequence 20, Appl
66	379	44.7	154	6	US-11-021-949-21	Sequence 21, Appl
67	372.5	44.9	155	6	US-11-021-949-23	Sequence 23, Appl
68	333	40.1	117	5	US-10-751-845-16	Sequence 16, Appl
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70	333	40.1	237	5	US-10-751-845-158	Sequence 158, Appl
71	333	40.1	261	5	US-10-751-845-160	Sequence 160, Appl
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73	323	38.9	536	4	US-10-368-046-10	Sequence 10, Appl
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75	323	38.9	536	5	US-10-918-337-11	Sequence 11, Appl
76	294	35.4	150	5	US-10-367-057-11	Sequence 11, Appl
77	189	22.8	119	5	US-10-751-845-159	Sequence 159, Appl
78	177	21.3	32	4	US-10-476-570-19	Sequence 19, Appl
79	172	20.7	32	4	US-10-476-570-9	Sequence 9, Appl
80	163	19.6	30	5	US-10-476-570-53	Sequence 53, Appl
81	163	19.6	30	5	US-10-858-384-4	Sequence 4, Appl
82	159	19.2	29	4	US-10-476-570-55	Sequence 55, Appl
83	159	19.2	29	5	US-10-858-384-8	Sequence 8, Appl
84	157	18.9	29	4	US-10-476-570-13	Sequence 13, Appl
85	146	17.6	24	6	US-11-021-949-5	Sequence 5, Appl
86	136.5	16.4	140	6	US-11-021-949-23	Sequence 23, Appl
87	136	16.4	25	6	US-11-021-949-1	Sequence 1, Appl
88	135	16.3	23	4	US-10-476-570-40	Sequence 40, Appl
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90	132	15.9	22	4	US-10-751-845-65	Sequence 65, Appl
91	130	15.7	22	4	US-10-476-570-56	Sequence 56, Appl
92	130	15.7	22	5	US-10-476-570-56	Sequence 56, Appl
93	130	15.7	42	5	US-10-751-845-10	Sequence 10, Appl
94	126	15.2	23	5	US-10-751-845-152	Sequence 152, Appl
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97	115.5	13.9	23	4	US-10-476-570-27	Sequence 27, Appl
98	115	13.9	20	5	US-10-938-249-513	Sequence 513, Appl
99	114	13.7	20	4	US-10-476-570-41	Sequence 41, Appl
100	114	13.7	22	4	US-10-612-818-4	Sequence 4, Appl

## ALIGNMENTS

## RESULT 1

US-10-530-253-3  
; Sequence 3, Application US/10530253  
; Publication No. US20060014926A1  
; GENERAL INFORMATION:  
; APPLICANT: Cassecci, Maria C.  
; APPLICANT: Smith, Larry  
; APPLICANT: Jeffrey K. Pullen  
; APPLICANT: Susan P. McElhinney  
; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS  
; FILE REFERENCE: 00630/100M137-US2  
; CURRENT APPLICATION NUMBER: US/10/530,253  
; PRIOR FILING DATE: 2005-04-04  
; PRIOR APPLICATION NUMBER: PCT/US2003/031726  
; PRIOR FILING DATE: 2003-10-02  
; PRIOR APPLICATION NUMBER: US 60/415,929  
; PRIOR FILING DATE: 2002-10-03  
; NUMBER OF SEQ ID NOS: 65  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 248  
; TYPE: PRT  
; ORGANISM: Human papillomavirus type 16  
US-10-530-253-3

## Query Match

Best Local Similarity 99.8%; Score 828; DB 5; Length 248;  
Matches 149; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFQDPQERPRKLPOLCTELQTTIHDIILECVYCKQQLRREYVDFAFRDLCTIVYRDGNPY 60  
DB 1 MFQDPQERPRKLPOLCTELQTTIHDIILECVYCKQQLRREYVDFAFRDLCTIVYRDGNPY 60  
QY 61 AYXDKCLKFYSKISSEYRHYCVSYGTTLEQYNNKPLCDLLIRICINXOKPLCPBEKQRHLD 120  
DB 61 AYXDKCLKFYSKISSEYRHYCVSYGTTLEQYNNKPLCDLLIRICINXOKPLCPBEKQRHLD 120  
QY 121 KQRFHNIRGRWTGRCMSCCRSSRTTRRETOL 151  
DB 121 KQRFHNIRGRWTGRCMSCCRSSRTTRRETOL 151

## RESULT 2

US-10-530-253-5  
; Sequence 5, Application US/10530253  
; Publication No. US20060014926A1  
; GENERAL INFORMATION:  
; APPLICANT: Cassecci, Maria C.  
; APPLICANT: Smith, Larry  
; APPLICANT: Jeffrey K. Pullen  
; APPLICANT: Susan P. McElhinney  
; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS  
; FILE REFERENCE: 00630/100M137-US2  
; CURRENT APPLICATION NUMBER: US/10/530,253  
; PRIOR FILING DATE: 2005-04-04  
; PRIOR APPLICATION NUMBER: PCT/US2003/031726  
; PRIOR FILING DATE: 2003-10-02  
; PRIOR APPLICATION NUMBER: US 60/415,929  
; PRIOR FILING DATE: 2002-10-03  
; NUMBER OF SEQ ID NOS: 65  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5  
; LENGTH: 248  
; TYPE: PRT  
; ORGANISM: Human papillomavirus type 16  
US-10-530-253-5

## Query Match

99.8%; Score 828; DB 5; Length 248;

Best Local Similarity 98.7%; Pred. No. 6.5e-81;  
Matches 149; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFQDPQERPRKLPOLCTELQTTIHDIILECVYCKQQLRREYVDFAFRDLCTIVYRDGNPY 60  
DB 1 MFQDPQERPRKLPOLCTELQTTIHDIILECVYCKQQLRREYVDFAFRDLCTIVYRDGNPY 60  
QY 61 AYXDKCLKFYSKISSEYRHYCVSYGTTLEQYNNKPLCDLLIRICINXOKPLCPBEKQRHLD 120  
DB 61 AYXDKCLKFYSKISSEYRHYCVSYGTTLEQYNNKPLCDLLIRICINXOKPLCPBEKQRHLD 120  
QY 121 KQRFHNIRGRWTGRCMSCCRSSRTTRRETOL 151  
DB 121 KQRFHNIRGRWTGRCMSCCRSSRTTRRETOL 151

## RESULT 3

US-10-484-063-20  
; Sequence 20, Application US/10484063  
; Publication No. US20050048467A1  
; GENERAL INFORMATION:  
; APPLICANT: SASTRY, K. JAGANNADHA  
; APPLICANT: TORTOLERO-LUNA, GUILTERMO  
; APPLICANT: FOLLEN, MICHAEL  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED  
; FILE REFERENCE: UTSC:560US  
; CURRENT APPLICATION NUMBER: US/10/484,063  
; PRIOR FILING DATE: 2004-01-16  
; PRIOR APPLICATION NUMBER: PCT/US02/23198  
; PRIOR FILING DATE: 2002-07-19  
; PRIOR APPLICATION NUMBER: 60/306,809  
; PRIOR FILING DATE: 2001-07-20  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 20  
; LENGTH: 151  
; TYPE: PRT  
; ORGANISM: Human papillomavirus  
US-10-484-063-20

## Query Match

Best Local Similarity 99.5%; Score 826; DB 5; Length 151;  
Matches 149; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFQDPQERPRKLPOLCTELQTTIHDIILECVYCKQQLRREYVDFAFRDLCTIVYRDGNPY 60  
DB 1 MFQDPQERPRKLPOLCTELQTTIHDIILECVYCKQQLRREYVDFAFRDLCTIVYRDGNPY 60  
QY 61 AYXDKCLKFYSKISSEYRHYCVSYGTTLEQYNNKPLCDLLIRICINXOKPLCPBEKQRHLD 120  
DB 61 AYXDKCLKFYSKISSEYRHYCVSYGTTLEQYNNKPLCDLLIRICINXOKPLCPBEKQRHLD 120  
QY 121 KQRFHNIRGRWTGRCMSCCRSSRTTRRETOL 151  
DB 121 KQRFHNIRGRWTGRCMSCCRSSRTTRRETOL 151

## RESULT 4

US-10-484-063-27  
; Sequence 27, Application US/10484063  
; Publication No. US20050048467A1  
; GENERAL INFORMATION:  
; APPLICANT: SASTRY, K. JAGANNADHA  
; APPLICANT: TORTOLERO-LUNA, GUILTERMO  
; APPLICANT: FOLLEN, MICHAEL  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED  
; FILE REFERENCE: UTSC:560US  
; CURRENT APPLICATION NUMBER: US/10/484,063  
; PRIOR FILING DATE: 2004-01-16  
; PRIOR APPLICATION NUMBER: PCT/US02/23198  
; PRIOR FILING DATE: 2002-07-19

; PRIOR APPLICATION NUMBER: 60/306,809  
; PRIOR FILING DATE: 2001-07-20  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 27  
; LENGTH: 151  
; TYPE: PRT  
; ORGANISM: Human papillomavirus type 16  
US-10-484-063-27

Query Match 99.5%; Score 826; DB 5; Length 151;  
Best Local Similarity 98.7%; Pred. No. 6e-81;  
Matches 149; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFODPQERPRKLPOLCTELQTTTHDIIIECYCKQQLIRREYVDFAFRDLCTIVRDGPNY 60  
DB 1 MFODPQERPRKLPOLCTELQTTTHDIIIECYCKQQLIRREYVDFAFRDLCTIVRDGPNY 60  
QY 61 AVXDKCLKFYSKISEYHYCYSVYGTLEQYNNKPLCDLLIRCNXOKPLCPBEKQRLD 126  
DB 61 AVXDKCLKFYSKISEYHYCYSVYGTLEQYNNKPLCDLLIRCNXOKPLCPBEKQRLD 120  
QY 121 KKQRFHNIRGWTGRCMSCCRSSRTRETOL 151  
DB 121 KKQRFHNIRGWTGRCMSCCRSSRTRETOL 151

## RESULT 5

US-10-530-253-13  
; Sequence 13, Application US/10530253  
; Publication No. US20060014926A1  
; GENERAL INFORMATION:  
; APPLICANT: Casasetti, Maria C.  
; APPLICANT: Smith, Larry  
; APPLICANT: Jeffrey K. Pullen  
; APPLICANT: Susan P. McElhinney  
; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS  
; FILE REFERENCE: 00630/100M137-US2  
; CURRENT APPLICATION NUMBER: US/10/530, 253  
; PRIOR FILING DATE: 2005-04-04  
; PRIOR APPLICATION NUMBER: PCT/US2003/031726  
; PRIOR FILING DATE: 2003-10-02  
; PRIOR APPLICATION NUMBER: US 60/415, 929  
; PRIOR FILING DATE: 2002-10-03  
; NUMBER OF SEQ ID NOS: 65  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 13  
; LENGTH: 151  
; TYPE: PRT  
; ORGANISM: Human papillomavirus type 16  
US-10-530-253-13

Query Match 99.5%; Score 826; DB 5; Length 151;  
Best Local Similarity 98.7%; Pred. No. 6e-81;  
Matches 149; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFODPQERPRKLPOLCTELQTTTHDIIIECYCKQQLIRREYVDFAFRDLCTIVRDGPNY 60  
DB 1 MFODPQERPRKLPOLCTELQTTTHDIIIECYCKQQLIRREYVDFAFRDLCTIVRDGPNY 60  
QY 61 AVXDKCLKFYSKISEYHYCYSVYGTLEQYNNKPLCDLLIRCNXOKPLCPBEKQRLD 120  
DB 61 AVXDKCLKFYSKISEYHYCYSVYGTLEQYNNKPLCDLLIRCNXOKPLCPBEKQRLD 120  
QY 121 KKQRFHNIRGWTGRCMSCCRSSRTRETOL 151  
DB 121 KKQRFHNIRGWTGRCMSCCRSSRTRETOL 151

RESULT 6  
US-10-530-253-1  
; Sequence 1, Application US/10530253  
; Publication No. US20060014926A1

; GENERAL INFORMATION:  
; APPLICANT: Casasetti, Maria C.  
; APPLICANT: Smith, Larry  
; APPLICANT: Jeffrey K. Pullen  
; APPLICANT: Susan P. McElhinney  
; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS  
; FILE REFERENCE: 00630/100M137-US2  
; CURRENT APPLICATION NUMBER: US/10/530, 253  
; PRIOR FILING DATE: 2005-04-04  
; PRIOR APPLICATION NUMBER: PCT/US2003/031726  
; PRIOR FILING DATE: 2003-10-02  
; PRIOR APPLICATION NUMBER: US 60/415, 929  
; PRIOR FILING DATE: 2002-10-03  
; NUMBER OF SEQ ID NOS: 65  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 248  
; TYPE: PRT  
; ORGANISM: Human papillomavirus type 16  
US-10-530-253-1

Query Match 99.5%; Score 826; DB 5; Length 248;  
Best Local Similarity 98.7%; Pred. No. 1.1e-80;  
Matches 149; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFODPQERPRKLPOLCTELQTTTHDIIIECYCKQQLIRREYVDFAFRDLCTIVRDGPNY 60  
DB 1 MFODPQERPRKLPOLCTELQTTTHDIIIECYCKQQLIRREYVDFAFRDLCTIVRDGPNY 60  
QY 61 AVXDKCLKFYSKISEYHYCYSVYGTLEQYNNKPLCDLLIRCNXOKPLCPBEKQRLD 120  
DB 61 AVXDKCLKFYSKISEYHYCYSVYGTLEQYNNKPLCDLLIRCNXOKPLCPBEKQRLD 120  
QY 121 KKQRFHNIRGWTGRCMSCCRSSRTRETOL 151  
DB 121 KKQRFHNIRGWTGRCMSCCRSSRTRETOL 151

## RESULT 7

US-10-858-384-2  
; Sequence 2, Application US/10858384  
; Publication No. US2005003025A1  
; GENERAL INFORMATION:  
; APPLICANT: CHOPPIN, JEANNINE  
; APPLICANT: BOURGAULT VILADA, ISABELLE  
; APPLICANT: GUILLET, JEAN-GERARD  
; APPLICANT: CONNAN, FRANCINE  
; APPLICANT: FERRIES, ESTELLE  
; TITLE OF INVENTION: POLYPEPTOPIC PROTEIN FRAGMENTS OF THE E6 PROTEIN  
; TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE  
; FILE REFERENCE: 0508-1037-1  
; CURRENT APPLICATION NUMBER: US/10/858, 384  
; PRIOR FILING DATE: 2004-06-02  
; PRIOR APPLICATION NUMBER: FR 9907012  
; PRIOR FILING DATE: 1999-06-03  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 2  
; LENGTH: 158  
; TYPE: PRT  
; ORGANISM: Human Papillomavirus  
US-10-858-384-2

Query Match 99.2%; Score 823; DB 5; Length 158;  
Best Local Similarity 98.0%; Pred. No. 1.3e-80;  
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFODPQERPRKLPOLCTELQTTTHDIIIECYCKQQLIRREYVDFAFRDLCTIVRDGPNY 60  
DB 8 MFODPQERPRKLPOLCTELQTTTHDIIIECYCKQQLIRREYVDFAFRDLCTIVRDGPNY 67  
QY 61 AVXDKCLKFYSKISEYHYCYSVYGTLEQYNNKPLCDLLIRCNXOKPLCPBEKQRLD 120

```
|||||:|||||
Db      68 AVCDKCLFYSKISYRHYCYSLYGTLEEQYNKPLCDLLIRICINCQKPLCPBEKQRHLD 127
Qy      121 KKQRFNIRGRWTCRMSCCRSSRTRETOL 151
Db      128 KKQRFNIRGRWTCRMSCCRSSRTRETOL 158
```

RESULT 8  
US-10-367-057-16  
; Sequence 16, Application US/10367057  
; Publication No. US20050100554A1  
; GENERAL INFORMATION:  
; APPLICANT: Cuthill, Scott;  
; APPLICANT: Jackson, Amanda;  
; APPLICANT: Lewin, David A.;  
; APPLICANT: Ooi, Chean Eng;  
; TITLE OF INVENTION: Complexes and Methods of Using Same  
; FILE REFERENCE: 21402-559  
; CURRENT APPLICATION NUMBER: US/10/367,057  
; CURRENT FILING DATE: 2003-02-14  
; PRIOR APPLICATION NUMBER: 60/256,911  
; PRIOR FILING DATE: 2002-02-14  
; NUMBER OF SEQ ID NOS: 198  
; SOFTWARE: Curoseq1st version 0.1  
; SEQ ID NO 16  
; LENGTH: 158  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-367-057-16

Query Match 99.2%; Score 823; DB 5; Length 158;  
Best Local Similarity 98.0%; Pred. No. 1.3e-80;  
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```
Qy      1 MFQDPQERPRKLPOLCTELQTTIHDIIECYVCKQQLRREYDPAFRLDCTVYRDGNPY 60
Db      8 MFQDPQERPRKLPOLCTELQTTIHDIIECYVCKQQLRREYDPAFRLDCTVYRDGNPY 67
Qy      61 AVXDCKLKFYSKISYRHYCYSVYGTLEEQYNKPLCDLLIRICINXQKPLCPBEKQRHLD 120
Db      68 AVXDCKLKFYSKISYRHYCYSLYGTLEEQYNKPLCDLLIRICINCQKPLCPBEKQRHLD 127
Qy      121 KKQRFNIRGRWTCRMSCCRSSRTRETOL 151
Db      128 KKQRFNIRGRWTCRMSCCRSSRTRETOL 158
```

RESULT 9  
US-11-021-949-13  
; Sequence 13, Application US/11021949  
; Publication No. US20050142541A1  
; GENERAL INFORMATION:  
; APPLICANT: LU, PETER  
; APPLICANT: GARMAN, JONATHAN DAVID  
; APPLICANT: BELMARES, MICHAEL P.  
; APPLICANT: DIAZ-SAMIENTO, CHAMORRO SOKOZA  
; APPLICANT: SCHWEIZER, JOHANNES  
; TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRAINS OF HPV  
; FILE REFERENCE: VITA-012  
; CURRENT APPLICATION NUMBER: US/11/021,949  
; CURRENT FILING DATE: 2004-12-23  
; PRIOR APPLICATION NUMBER: 60/532,373  
; PRIOR FILING DATE: 2003-12-23  
; NUMBER OF SEQ ID NOS: 361  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13  
; LENGTH: 158  
; TYPE: PRT  
; ORGANISM: human papilloma virus (HPV)  
US-11-021-949-13

Query Match 99.2%; Score 823; DB 6; Length 158;  
Best Local Similarity 98.0%; Pred. No. 1.3e-80;  
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```
Qy      1 MFQDPQERPRKLPOLCTELQTTIHDIIECYVCKQQLRREYDPAFRLDCTVYRDGNPY 60
Db      8 MFQDPQERPRKLPOLCTELQTTIHDIIECYVCKQQLRREYDPAFRLDCTVYRDGNPY 67
Qy      61 AVXDCKLKFYSKISYRHYCYSVYGTLEEQYNKPLCDLLIRICINXQKPLCPBEKQRHLD 120
Db      68 AVXDCKLKFYSKISYRHYCYSLYGTLEEQYNKPLCDLLIRICINCQKPLCPBEKQRHLD 127
Qy      121 KKQRFNIRGRWTCRMSCCRSSRTRETOL 151
Db      128 KKQRFNIRGRWTCRMSCCRSSRTRETOL 158
```

RESULT 10  
US-11-206-138-3  
; Sequence 3, Application US/11206138  
; Publication No. US20060039919A1  
; GENERAL INFORMATION:  
; APPLICANT: Healthbake Biotech CO. LTD.  
; TITLE OF INVENTION: Fusion protein for inhibiting cervical cancer  
; FILE REFERENCE: P7819/0613  
; CURRENT APPLICATION NUMBER: US/11/206,138  
; CURRENT FILING DATE: 2005-08-18  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: Patentin version 3.3  
; SEQ ID NO 3  
; LENGTH: 158  
; TYPE: PRT  
; ORGANISM: Human papillomavirus type 16  
US-11-206-138-3

Query Match 99.2%; Score 823; DB 6; Length 158;  
Best Local Similarity 98.0%; Pred. No. 1.3e-80;  
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```
Qy      1 MFQDPQERPRKLPOLCTELQTTIHDIIECYVCKQQLRREYDPAFRLDCTVYRDGNPY 60
Db      8 MFQDPQERPRKLPOLCTELQTTIHDIIECYVCKQQLRREYDPAFRLDCTVYRDGNPY 67
Qy      61 AVXDCKLKFYSKISYRHYCYSVYGTLEEQYNKPLCDLLIRICINXQKPLCPBEKQRHLD 120
Db      68 AVXDCKLKFYSKISYRHYCYSLYGTLEEQYNKPLCDLLIRICINCQKPLCPBEKQRHLD 127
Qy      121 KKQRFNIRGRWTCRMSCCRSSRTRETOL 151
Db      128 KKQRFNIRGRWTCRMSCCRSSRTRETOL 158
```

RESULT 11  
US-10-472-724-2  
; Sequence 2, Application US/10472724  
; Publication No. US20040171806A1  
; GENERAL INFORMATION:  
; APPLICANT: Cid-Arregui, Angel  
; APPLICANT: Zur Hausen, Harald  
; TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination  
; FILE REFERENCE: 4121-154  
; CURRENT APPLICATION NUMBER: US/10/472,724  
; CURRENT FILING DATE: 2003-09-17  
; PRIOR APPLICATION NUMBER: PCT/EP02/03271  
; PRIOR FILING DATE: 2002-03-22  
; PRIOR APPLICATION NUMBER: EP 01107271.7  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: Patentin version 3.2  
; SEQ ID NO 2  
; LENGTH: 171  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
US-10-472-724-2

```
FEATURE:
OTHER INFORMATION: Synthetic Construct
US-10-472-724-2

Query Match          99.2%; Score 823; DB 4; Length 171;
Best Local Similarity 98.0%; Pred. No. 1.5e-80;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFODPQERPRKLPOLCTELQTTIHDIIECYCKQQLRREYDPAFRDLCTIVRDGNPY 60
DB 13 MFODPQERPRKLPOLCTELQTTIHDIIECYCKQQLRREYDPAFRDLCTIVRDGNPY 72
QY 61 AVXDKLKFYSKISEYRHVCYSVGTTLBQOYNKPLCDLLIRCIINXOKPLCPEEKQRHLD 120
DB 73 AVCDKCLKFYSKISEYRHVCYSVGTTLBQOYNKPLCDLLIRCIINXOKPLCPEEKQRHLD 132
QY 121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151
DB 133 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 163

RESULT 12
US-10-530-253-9
Sequence 9, Application US/10530253
Publication No. US20060014926A1
GENERAL INFORMATION:
APPLICANT: Casasetti, Maria C.
APPLICANT: Smith, Larry
APPLICANT: Jeffrey K. Pullen
APPLICANT: Susan P. McElhinney
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 00630/100M137-US2
CURRENT APPLICATION NUMBER: US/10/530,253
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PCT/US2003/031726
PRIOR FILING DATE: 2003-10-02
PRIOR APPLICATION NUMBER: US 60/415,929
PRIOR FILING DATE: 2002-10-03
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PatentIn version 3.1
SEQ ID NO 9
LENGTH: 248
TYPE: PRT
ORGANISM: Human papillomavirus type 16
US-10-530-253-9

Query Match          99.2%; Score 823; DB 5; Length 248;
Best Local Similarity 98.7%; Pred. No. 2.2e-80;
Matches 148; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 FQDPQERPRKLPOLCTELQTTIHDIIECYCKQQLRREYDPAFRDLCTIVRDGNPY 61
DB 99 FQDPQERPRKLPOLCTELQTTIHDIIECYCKQQLRREYDPAFRDLCTIVRDGNPY 158
QY 62 VXDCKLKFYSKISEYRHVCYSVGTTLBQOYNKPLCDLLIRCIINXOKPLCPEEKQRHLD 121
DB 159 VGDCKLKFYSKISEYRHVCYSVGTTLBQOYNKPLCDLLIRCIINXOKPLCPEEKQRHLD 218
QY 122 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151
DB 219 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 248

RESULT 13
US-10-530-253-11
Sequence 11, Application US/10530253
Publication No. US20060014926A1
GENERAL INFORMATION:
APPLICANT: Casasetti, Maria C.
APPLICANT: Smith, Larry
APPLICANT: Jeffrey K. Pullen
APPLICANT: Susan P. McElhinney
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
```

```
FILE REFERENCE: 00630/100M137-US2
CURRENT APPLICATION NUMBER: US/10/530,253
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PCT/US2003/031726
PRIOR FILING DATE: 2003-10-02
PRIOR APPLICATION NUMBER: US 60/415,929
PRIOR FILING DATE: 2002-10-03
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PatentIn version 3.1
SEQ ID NO 11
LENGTH: 248
TYPE: PRT
ORGANISM: Human papillomavirus type 16
US-10-530-253-11

Query Match          99.2%; Score 823; DB 5; Length 248;
Best Local Similarity 98.7%; Pred. No. 2.2e-80;
Matches 148; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 FQDPQERPRKLPOLCTELQTTIHDIIECYCKQQLRREYDPAFRDLCTIVRDGNPY 61
DB 99 FQDPQERPRKLPOLCTELQTTIHDIIECYCKQQLRREYDPAFRDLCTIVRDGNPY 158
QY 62 VXDCKLKFYSKISEYRHVCYSVGTTLBQOYNKPLCDLLIRCIINXOKPLCPEEKQRHLD 121
DB 159 VGDCKLKFYSKISEYRHVCYSVGTTLBQOYNKPLCDLLIRCIINXOKPLCPEEKQRHLD 218
QY 122 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151
DB 219 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 248

RESULT 14
US-11-192-923A-2
Sequence 2, Application US/11192923A
Publication No. US20060018928A1
GENERAL INFORMATION:
APPLICANT: PANQ, XIAOMU
TITLE OF INVENTION: VIRUS-LIKE PARTICLE CONTAINING A DENGUE VIRUS
FILE REFERENCE: 116620-003
CURRENT APPLICATION NUMBER: US/11/192,923A
CURRENT FILING DATE: 2005-07-29
PRIOR APPLICATION NUMBER: CN 03115272.4
PRIOR FILING DATE: 2003-01-30
PRIOR APPLICATION NUMBER: CN 03115273.2
PRIOR FILING DATE: 2003-01-30
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 2
LENGTH: 256
TYPE: PRT
ORGANISM: Human papillomavirus
US-11-192-923A-2

Query Match          99.2%; Score 823; DB 6; Length 256;
Best Local Similarity 98.0%; Pred. No. 2.3e-80;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFODPQERPRKLPOLCTELQTTIHDIIECYCKQQLRREYDPAFRDLCTIVRDGNPY 60
DB 106 MFODPQERPRKLPOLCTELQTTIHDIIECYCKQQLRREYDPAFRDLCTIVRDGNPY 165
QY 61 AVXDKLKFYSKISEYRHVCYSVGTTLBQOYNKPLCDLLIRCIINXOKPLCPEEKQRHLD 120
DB 166 AVCDKCLKFYSKISEYRHVCYSVGTTLBQOYNKPLCDLLIRCIINXOKPLCPEEKQRHLD 225
QY 121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151
DB 226 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 256

RESULT 15
```

US-09-367-309A-1  
; Sequence 1, Application US/09367309A  
; Publication No. US20020081329A1  
; GENERAL INFORMATION:  
; APPLICANT: MACFARLAN, RODERICK I.  
; APPLICANT: MALIAROS, JIM  
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES  
; FILE REFERENCE: 017227/0149  
; CURRENT APPLICATION NUMBER: US/09/367,309A  
; CURRENT FILING DATE: 1999-08-11  
; PRIOR APPLICATION NUMBER: PCT/AU98/00080  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: AU PO 5178  
; PRIOR FILING DATE: 1997-02-19  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 266  
; TYPE: PRT  
; ORGANISM: Human papillomavirus type 16  
US-09-367-309A-1

Query Match 99.2%; Score 823; DB 3; Length 266;  
Best Local Similarity 98.0%; Pred. No. 2.4e-80;  
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFODPQERPRKLPOLCTELQTTIHDIIECYCKQOLLREYVDPAFRDLCTVYRDGPNY 60  
DB 8 MFODPQERPRKLPOLCTELQTTIHDIIECYCKQOLLREYVDPAFRDLCTVYRDGPNY 67  
QY 61 AVXDCKLKFYSKISSEYRHVCYVGTTLLEQYNNKPLCDLLIRICINXOKPLCPPEEKQRHLD 120  
DB 68 AVCDCKLKFYSKISSEYRHVCYVGTTLLEQYNNKPLCDLLIRICINXOKPLCPPEEKQRHLD 127  
QY 121 KKORFHNIRGWTGRCMSCCRSSRTRETOL 151  
DB 128 KKORFHNIRGWTGRCMSCCRSSRTRETOL 158

RESULT 16  
US-10-000-903-4  
; Sequence 4, Application US/10000903  
; Publication No. US20020182221A1  
; GENERAL INFORMATION:  
; APPLICANT: Bruck, Claudine  
; APPLICANT: Cabazon Silva, Teresa  
; APPLICANT: Delisse, Anne-Marie Eva Bernande  
; APPLICANT: Gerard, Catherine Marie Ghislaine  
; APPLICANT: Lombardo-Bencheikh, Angela  
; TITLE OF INVENTION: Vaccine  
; FILE REFERENCE: B45107  
; CURRENT APPLICATION NUMBER: US/10/000,903  
; CURRENT FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: PCT/EP98/05285  
; PRIOR FILING DATE: 1998-08-17  
; PRIOR APPLICATION NUMBER: GB 9717953.5  
; PRIOR FILING DATE: 1997-08-22  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 4  
; LENGTH: 273  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-10-000-903-4

Query Match 99.2%; Score 823; DB 4; Length 273;  
Best Local Similarity 98.0%; Pred. No. 2.5e-80;  
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFODPQERPRKLPOLCTELQTTIHDIIECYCKQOLLREYVDPAFRDLCTVYRDGPNY 60  
DB 114 MFODPQERPRKLPOLCTELQTTIHDIIECYCKQOLLREYVDPAFRDLCTVYRDGPNY 173

QY 61 AVXDCKLKFYSKISSEYRHVCYVGTTLLEQYNNKPLCDLLIRICINXOKPLCPPEEKQRHLD 120  
DB 174 AVCDCKLKFYSKISSEYRHVCYVGTTLLEQYNNKPLCDLLIRICINXOKPLCPPEEKQRHLD 233  
QY 121 KKORFHNIRGWTGRCMSCCRSSRTRETOL 151  
DB 234 KKORFHNIRGWTGRCMSCCRSSRTRETOL 264

RESULT 17  
US-10-899-771-4  
; Sequence 4, Application US/10899771  
; Publication No. US20050031638A1  
; GENERAL INFORMATION:  
; APPLICANT: Dalemans, Wilfried L.J.  
; APPLICANT: Gerard, Catherine Marie Ghislaine  
; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins  
; FILE REFERENCE: B45124  
; CURRENT APPLICATION NUMBER: US/10/899,771  
; CURRENT FILING DATE: 2004-07-27  
; PRIOR APPLICATION NUMBER: US/09/581,976  
; PRIOR FILING DATE: 2000-06-20  
; PRIOR APPLICATION NUMBER: PCT/EP98/08563  
; PRIOR FILING DATE: 1998-12-18  
; PRIOR APPLICATION NUMBER: GB 9727262.9  
; PRIOR FILING DATE: 1997-12-24  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 4  
; LENGTH: 273  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Chimaeic protein (protein D from Haemophilus  
; OTHER INFORMATION: Influenzae B and B6 from Human papilloma virus type  
; OTHER INFORMATION: 16)  
US-10-899-771-4

Query Match 99.2%; Score 823; DB 5; Length 273;  
Best Local Similarity 98.0%; Pred. No. 2.5e-80;  
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFODPQERPRKLPOLCTELQTTIHDIIECYCKQOLLREYVDPAFRDLCTVYRDGPNY 60  
DB 114 MFODPQERPRKLPOLCTELQTTIHDIIECYCKQOLLREYVDPAFRDLCTVYRDGPNY 173  
QY 61 AVXDCKLKFYSKISSEYRHVCYVGTTLLEQYNNKPLCDLLIRICINXOKPLCPPEEKQRHLD 120  
DB 174 AVCDCKLKFYSKISSEYRHVCYVGTTLLEQYNNKPLCDLLIRICINXOKPLCPPEEKQRHLD 233  
QY 121 KKORFHNIRGWTGRCMSCCRSSRTRETOL 151  
DB 234 KKORFHNIRGWTGRCMSCCRSSRTRETOL 264

RESULT 18  
US-10-000-903-10  
; Sequence 10, Application US/10000903  
; Publication No. US20020182221A1  
; GENERAL INFORMATION:  
; APPLICANT: Bruck, Claudine  
; APPLICANT: Cabazon Silva, Teresa  
; APPLICANT: Delisse, Anne-Marie Eva Bernande  
; APPLICANT: Gerard, Catherine Marie Ghislaine  
; APPLICANT: Lombardo-Bencheikh, Angela  
; TITLE OF INVENTION: Vaccine  
; FILE REFERENCE: B45107  
; CURRENT APPLICATION NUMBER: US/10/000,903  
; CURRENT FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: PCT/EP98/05285  
; PRIOR FILING DATE: 1998-08-17  
; PRIOR APPLICATION NUMBER: GB 9717953.5

PRIOR FILING DATE: 1997-08-22  
NUMBER OF SEQ ID NOS: 23  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 10  
LENGTH: 292  
TYPE: PRT  
ORGANISM: Homo sapien  
US-10-000-903-10

Query Match 99.2%; Score 823; DB 4; Length 292;  
Best Local Similarity 98.0%; Pred. No. 2.7e-80;  
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFODPOBPRRLPOLCTELQTTIHDIIECYCKQQLRRVYDFAFRDLCTVRRDGPY 60  
DB 133 MFODPOBPRRLPOLCTELQTTIHDIIECYCKQQLRRVYDFAFRDLCTVRRDGPY 192  
QY 61 AVXDKLKFYSKISEYHYCYSVYGTLEQOYNKPLCDLIRCTINXQKPLCPBEKQRHLD 120  
DB 193 AVXDKLKFYSKISEYHYCTSLXGTTLEQOYNKPLCDLIRCTINXQKPLCPBEKQRHLD 252  
QY 121 KKORFHNIRGWTGRCMSCSSRRTRRETOL 151  
DB 253 KKORFHNIRGWTGRCMSCSSRRTRRETOL 283

RESULT 19  
US-10-899-771-10  
Sequence 10, Application US/10899771  
Publication No. US20050031638A1  
GENERAL INFORMATION:  
APPLICANT: Dalemans, Wilfried L.J.  
APPLICANT: Gerard, Catherine Marie Ghislaine  
TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins  
FILE REFERENCE: B45124  
CURRENT APPLICATION NUMBER: US/10/899,771  
CURRENT FILING DATE: 2004-07-27  
PRIOR APPLICATION NUMBER: US/09/581,976  
PRIOR FILING DATE: 2000-06-20  
PRIOR APPLICATION NUMBER: PCT/EP98/08563  
PRIOR FILING DATE: 1998-12-18  
PRIOR APPLICATION NUMBER: GB 9727262.9  
PRIOR FILING DATE: 1997-12-24  
NUMBER OF SEQ ID NOS: 28  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 10  
LENGTH: 292  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Chimeric protein (Clyta from Streptococcus  
OTHER INFORMATION: pneumoniae and E6 from Human papilloma virus type  
US-10-899-771-10

Query Match 99.2%; Score 823; DB 5; Length 292;  
Best Local Similarity 98.0%; Pred. No. 2.7e-80;  
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFODPOBPRRLPOLCTELQTTIHDIIECYCKQQLRRVYDFAFRDLCTVRRDGPY 60  
DB 133 MFODPOBPRRLPOLCTELQTTIHDIIECYCKQQLRRVYDFAFRDLCTVRRDGPY 192  
QY 61 AVXDKLKFYSKISEYHYCYSVYGTLEQOYNKPLCDLIRCTINXQKPLCPBEKQRHLD 120  
DB 193 AVXDKLKFYSKISEYHYCTSLXGTTLEQOYNKPLCDLIRCTINXQKPLCPBEKQRHLD 252  
QY 121 KKORFHNIRGWTGRCMSCSSRRTRRETOL 151  
DB 253 KKORFHNIRGWTGRCMSCSSRRTRRETOL 283

RESULT 20  
US-10-000-903-6  
Sequence 6, Application US/10000903  
Publication No. US20020182221A1  
GENERAL INFORMATION:  
APPLICANT: Bruck, Claudine  
APPLICANT: Cabezon Silva, Teresa  
APPLICANT: Delisse, Anne-Marie Eva Bernarde  
APPLICANT: Gerard, Catherine Marie Ghislaine  
TITLE OF INVENTION: Vaccine  
FILE REFERENCE: B45107  
CURRENT APPLICATION NUMBER: US/10/000,903  
CURRENT FILING DATE: 2001-10-01  
PRIOR APPLICATION NUMBER: PCT/EP98/05285  
PRIOR FILING DATE: 1998-08-17  
PRIOR APPLICATION NUMBER: GB 9717953.5  
PRIOR FILING DATE: 1997-08-22  
NUMBER OF SEQ ID NOS: 23  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 6  
LENGTH: 371  
TYPE: PRT  
ORGANISM: Homo sapien  
US-10-000-903-6

Query Match 99.2%; Score 823; DB 4; Length 371;  
Best Local Similarity 98.0%; Pred. No. 3.6e-80;  
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFODPOBPRRLPOLCTELQTTIHDIIECYCKQQLRRVYDFAFRDLCTVRRDGPY 60  
DB 114 MFODPOBPRRLPOLCTELQTTIHDIIECYCKQQLRRVYDFAFRDLCTVRRDGPY 173  
QY 61 AVXDKLKFYSKISEYHYCYSVYGTLEQOYNKPLCDLIRCTINXQKPLCPBEKQRHLD 120  
DB 174 AVXDKLKFYSKISEYHYCTSLXGTTLEQOYNKPLCDLIRCTINXQKPLCPBEKQRHLD 233  
QY 121 KKORFHNIRGWTGRCMSCSSRRTRRETOL 151  
DB 234 KKORFHNIRGWTGRCMSCSSRRTRRETOL 264

RESULT 21  
US-10-899-771-6  
Sequence 6, Application US/10899771  
Publication No. US20050031638A1  
GENERAL INFORMATION:  
APPLICANT: Dalemans, Wilfried L.J.  
APPLICANT: Gerard, Catherine Marie Ghislaine  
TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins  
FILE REFERENCE: B45124  
CURRENT APPLICATION NUMBER: US/10/899,771  
CURRENT FILING DATE: 2004-07-27  
PRIOR APPLICATION NUMBER: US/09/581,976  
PRIOR FILING DATE: 2000-06-20  
PRIOR APPLICATION NUMBER: PCT/EP98/08563  
PRIOR FILING DATE: 1998-12-18  
PRIOR APPLICATION NUMBER: GB 9727262.9  
PRIOR FILING DATE: 1997-12-24  
NUMBER OF SEQ ID NOS: 28  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 6  
LENGTH: 371  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Chimeric protein (protein D from Haemophilus  
OTHER INFORMATION: influenzae B and B6E7 fusion from Human papilloma  
US-10-899-771-6

```
Query Match          99.2%; Score 823; DB 5; Length 371;
Best Local Similarity 98.0%; Pred. No. 3.6e-80;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 1 MFODPQERPRKLPOLCTELQTTIHDIIECVYCKQQLRREYDPAFRDLCTVYRDGMPY 60
Db 114 MFODPQERPRKLPOLCTELQTTIHDIIECVYCKQQLRREYDPAFRDLCTVYRDGMPY 173
Oy 61 AVXDCKLKFYSKISSEYRHYCVSVGTTLLEQYNNKPLCDLLIRNCINXQKPLCEEKQRHLD 120
Db 174 AVXDCKLKFYSKISSEYRHYCVSVGTTLLEQYNNKPLCDLLIRNCINXQKPLCEEKQRHLD 233
Oy 121 KKQRFHNIRGRWTGRCMSCRSSRTRRETOL 151
Db 234 KKQRFHNIRGRWTGRCMSCRSSRTRRETOL 264

RESULT 22
US-10-000-903-14
; Sequence 14, Application US/10000903
; Publication No. US2002018221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-14

Query Match          99.2%; Score 823; DB 4; Length 390;
Best Local Similarity 98.0%; Pred. No. 3.8e-80;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 1 MFODPQERPRKLPOLCTELQTTIHDIIECVYCKQQLRREYDPAFRDLCTVYRDGMPY 60
Db 133 MFODPQERPRKLPOLCTELQTTIHDIIECVYCKQQLRREYDPAFRDLCTVYRDGMPY 192
Oy 61 AVXDCKLKFYSKISSEYRHYCVSVGTTLLEQYNNKPLCDLLIRNCINXQKPLCEEKQRHLD 120
Db 193 AVXDCKLKFYSKISSEYRHYCVSVGTTLLEQYNNKPLCDLLIRNCINXQKPLCEEKQRHLD 252
Oy 121 KKQRFHNIRGRWTGRCMSCRSSRTRRETOL 151
Db 253 KKQRFHNIRGRWTGRCMSCRSSRTRRETOL 283

RESULT 23
US-10-899-771-14
; Sequence 14, Application US/10899771
; Publication No. US20050031638A1
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.
; APPLICANT: Gerard, Catherine Marie Ghislaine
; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
; TITLE OF INVENTION: and Fusion Proteins Adjuncted with a Cpg Oligonucleotide
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/10/899,771
; CURRENT FILING DATE: 2004-07-27
; PRIOR APPLICATION NUMBER: US/09/581,976

; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/08563
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: GB 9727262.9
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimaeic protein (C)lyta from Streptococcus
; OTHER INFORMATION: pneumoniae and E6E7 fusion from Human papilloma
; OTHER INFORMATION: virus type 16
US-10-899-771-14

Query Match          99.2%; Score 823; DB 5; Length 390;
Best Local Similarity 98.0%; Pred. No. 3.8e-80;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 1 MFODPQERPRKLPOLCTELQTTIHDIIECVYCKQQLRREYDPAFRDLCTVYRDGMPY 60
Db 133 MFODPQERPRKLPOLCTELQTTIHDIIECVYCKQQLRREYDPAFRDLCTVYRDGMPY 192
Oy 61 AVXDCKLKFYSKISSEYRHYCVSVGTTLLEQYNNKPLCDLLIRNCINXQKPLCEEKQRHLD 120
Db 193 AVXDCKLKFYSKISSEYRHYCVSVGTTLLEQYNNKPLCDLLIRNCINXQKPLCEEKQRHLD 252
Oy 121 KKQRFHNIRGRWTGRCMSCRSSRTRRETOL 151
Db 253 KKQRFHNIRGRWTGRCMSCRSSRTRRETOL 283

RESULT 24
US-10-530-253-7
; Sequence 7, Application US/10530253
; Publication No. US20060014926A1
; GENERAL INFORMATION:
; APPLICANT: Casagetti, Maria C.
; APPLICANT: Smith, Larry
; APPLICANT: Jeffrey K. Pullen
; APPLICANT: Susan P. McElhinney
; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
; FILE REFERENCE: 00630/100M137-US2
; CURRENT APPLICATION NUMBER: US/10/530,253
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US2003/031726
; PRIOR FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/415,929
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-530-253-7

Query Match          98.9%; Score 821; DB 5; Length 248;
Best Local Similarity 98.7%; Pred. No. 3.7e-80;
Matches 148; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 FODPQERPRKLPOLCTELQTTIHDIIECVYCKQQLRREYDPAFRDLCTVYRDGMPY 61
Db 99 FODPQERPRKLPOLCTELQTTIHDIIECVYCKQQLRREYDPAFRDLCTVYRDGMPY 158
Oy 62 VXDCKLKFYSKISSEYRHYCVSVGTTLLEQYNNKPLCDLLIRNCINXQKPLCEEKQRHLD 121
Db 159 VXDCKLKFYSKISSEYRHYCVSVGTTLLEQYNNKPLCDLLIRNCINXQKPLCEEKQRHLD 218
Oy 122 KORFHNIRGRWTGRCMSCRSSRTRRETOL 151
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Db 219 KORFHNIRGWTGRCMSCCRSSRTRETOL 248

## RESULT 25

US-10-177-390-6  
; Sequence 6, Application US/10177390  
; Publication No. US20030143743A1  
; GENERAL INFORMATION:  
; APPLICANT: Schuler, Gerold  
; APPLICANT: N.V. Antwerpse Innovatiecentrum  
; TITLE OF INVENTION: Improved transfection of Eucaryotic Cells with linear  
; FILE REFERENCE: 021505wo/JH/ml  
; CURRENT APPLICATION NUMBER: US/10/177,390  
; CURRENT FILING DATE: 2002-06-20  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 151  
; TYPE: PRT  
; ORGANISM: Human papillomavirus type 16  
US-10-177-390-6

Query Match Best Local Similarity 98.7%; Score 819; DB 4; Length 151;  
Matches 148; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MFODPQERPRKLPOLCTELQTTTHDIILECYCKQQLLRREVDPAFRDLCTIVRDGPNY 60  
Db 1 MFODPQERPRKLPOLCTELQTTTHDIILECYCKQQLLRREVDPAFRDLCTIVRDGPNY 60  
Qy 61 AVXKCLKFKYSKISEYRHVCYSVGTTLLEQYKNRPLCDLLIRCNXQKPLCPBEKORHLD 120  
Db 61 AVXKCLKFKYSKISEYRHVCYSVGTTLLEQYKNRPLCDLLIRCNXQKPLCPBEKORHLD 120  
Qy 121 KORFHNIRGWTGRCMSCCRSSRTRETOL 151  
Db 121 KORFHNIRGWTGRCMSCCRSSRTRETOL 151

## RESULT 26

US-11-072-288-1  
; Sequence 1, Application US/11072288  
; Publication No. US20050159386A1  
; GENERAL INFORMATION:  
; APPLICANT: KIENY, Marie-Paule  
; APPLICANT: BALLOUT, Jean-Marc  
; APPLICANT: BIZOUARNE, Nadine  
; TITLE OF INVENTION: ANTITUMORAL COMPOSITION BASED ON IMMUNOGENIC  
; FILE REFERENCE: 017753-122  
; CURRENT APPLICATION NUMBER: US/11/072,288  
; CURRENT FILING DATE: 2005-03-07  
; PRIOR APPLICATION NUMBER: US/09/462,993  
; PRIOR FILING DATE: 2000-04-17  
; PRIOR APPLICATION NUMBER: PCT/FR98/01576  
; PRIOR FILING DATE: 1998-07-17  
; PRIOR APPLICATION NUMBER: FR 97/09152  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn Ver. 2.2  
; SEQ ID NO 1  
; LENGTH: 243  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Derived from  
; OTHER INFORMATION: human papillomavirus, strain HPV-16, E6 protein  
; OTHER INFORMATION: fused F protein signals, Clone E6\*TWf.  
US-11-072-288-1

Query Match Best Local Similarity 93.9%; Score 779.5; DB 6; Length 243;  
Matches 94.7%; Pred. No. 1.1e-75;

Matches 143; Conservative 1; Mismatches 2; Indels 5; Gaps 1;

Qy 1 MFODPQERPRKLPOLCTELQTTTHDIILECYCKQQLLRREVDPAFRDLCTIVRDGPNY 60  
Db 36 MFODPQERPRKLPOLCTELQTTTHDIILECYCKQQLLRREVDPAFRDLCTIVRDGPNY 95  
Qy 61 AVXKCLKFKYSKISEYRHVCYSVGTTLLEQYKNRPLCDLLIRCNXQKPLCPBEKORHLD 120  
Db 96 AVXKCLKFKYSKISEYRHVCYSVGTTLLEQYKNRPLCDLLIRCNXQKPLCPBEKORHLD 150  
Qy 121 KORFHNIRGWTGRCMSCCRSSRTRETOL 151  
Db 151 KORFHNIRGWTGRCMSCCRSSRTRETOL 181

## RESULT 27

US-10-530-253-18  
; Sequence 18, Application US/10530253  
; Publication No. US20060014926A1  
; GENERAL INFORMATION:  
; APPLICANT: Cassecci, Maria C.  
; APPLICANT: Smith, Larry  
; APPLICANT: Jeffrey K. Pullen  
; APPLICANT: Susan P. McShinney  
; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS  
; FILE REFERENCE: 00630/100M137-US2  
; CURRENT APPLICATION NUMBER: US/10/530,253  
; CURRENT FILING DATE: 2005-04-04  
; PRIOR APPLICATION NUMBER: PCT/US2003/031726  
; PRIOR FILING DATE: 2003-10-02  
; PRIOR APPLICATION NUMBER: US 60/415,929  
; PRIOR FILING DATE: 2002-10-03  
; NUMBER OF SEQ ID NOS: 65  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 18  
; LENGTH: 149  
; TYPE: PRT  
; ORGANISM: Human papillomavirus type 35  
US-10-530-253-18

Query Match Best Local Similarity 69.6%; Score 578; DB 5; Length 149;  
Matches 108; Conservative 13; Mismatches 28; Indels 2; Gaps 1;

Qy 1 MFODPQERPRKLPOLCTELQTTTHDIILECYCKQQLLRREVDPAFRDLCTIVRDGPNY 60  
Db 1 MFODPQERPRKLPOLCTELQTTTHDIILECYCKQQLLRSEVDPAFYDLCTIVREGOPY 60  
Qy 61 AVXKCLKFKYSKISEYRHVCYSVGTTLLEQYKNRPLCDLLIRCNXQKPLCPBEKORHLD 120  
Db 61 GVCCKLKFKYSKISEYRWYRSVGTTLLEQYKNRPLCDLLIRCTTCQKPLCPVEKORHLD 120  
Qy 121 KORFHNIRGWTGRCMSCCRSSRTRETOL 151  
Db 121 EKRPFHNIRGWTGRCMSCWKP--TRRETEV 149

## RESULT 28

US-11-021-949-14  
; Sequence 14, Application US/11021949  
; Publication No. US20050142541A1  
; GENERAL INFORMATION:  
; APPLICANT: LU, PETER  
; APPLICANT: GARMAN, JONATHAN DAVID  
; APPLICANT: BELMARES, MICHAEL P.  
; APPLICANT: DIAZ-SARMIENTO, CHAMORRO SOMOZA  
; APPLICANT: SCHWEIZER, JOHANNES  
; TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRAINS OF HPV  
; FILE REFERENCE: VITA-012  
; CURRENT APPLICATION NUMBER: US/11/021,949  
; CURRENT FILING DATE: 2004-12-23  
; PRIOR APPLICATION NUMBER: 60/532,373

;; PRIOR FILING DATE: 2003-12-23  
;; NUMBER OF SEQ ID NOS: 361  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 14  
;; LENGTH: 149  
;; TYPE: PRT  
;; ORGANISM: human papilloma virus (HPV)  
US-11-021-949-14

Query Match 69.6%; Score 578; DB 6; Length 149;  
Best Local Similarity 71.5%; Pred. No. 3.6e-54;  
Matches 108; Conservative 13; Mismatches 28; Indels 2; Gaps 1;

QY 1 MFODPQERPRKLPOLCTELQTTIHDIIECYCKQQLRREYVDFAFRDLCTIVRDGPNY 60  
DB 1 MFODPQERPRKLPOLCTELQTTIHDIIECYCKQQLRREYVDFAFRDLCTIVRDGPNY 60  
QY 61 AVXDCKLKFYSKISRYHYCYSVYGTLEQOYNKPLCDLLIRICINXQKPLCPBEKQRHLD 120  
DB 61 GVCCKLKFYSKISRYHYCYSVYGTLEQOYNKPLCDLLIRICINXQKPLCPBEKQRHLD 120  
QY 121 KKQRFNIRGRWTCGMSCCSSRRRTETOL 151  
DB 121 KKQRFNIRGRWTCGMSCCSSRRRTETOL 151

RESULT 29  
US-10-530-253-16

;; Sequence 16, Application US/10530253  
;; Publication No. US20060014926A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Casasetti, Maria C.  
;; APPLICANT: Smith, Larry  
;; APPLICANT: Jeffrey K. McElhinney  
;; APPLICANT: Susan P. McElhinney  
;; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS  
;; FILE REFERENCE: 00630/100M137-US2  
;; CURRENT APPLICATION NUMBER: US/10/530,253  
;; PRIOR FILING DATE: 2005-04-04  
;; PRIOR APPLICATION NUMBER: PCT/US2003/031726  
;; PRIOR FILING DATE: 2003-10-02  
;; PRIOR APPLICATION NUMBER: US 60/415,929  
;; PRIOR FILING DATE: 2002-10-03  
;; NUMBER OF SEQ ID NOS: 65  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 16  
;; LENGTH: 149  
;; TYPE: PRT  
;; ORGANISM: Human papillomavirus type 31  
US-10-530-253-16

Query Match 63.0%; Score 523; DB 5; Length 149;  
Best Local Similarity 64.9%; Pred. No. 3.2e-48;  
Matches 98; Conservative 18; Mismatches 33; Indels 2; Gaps 1;

QY 1 MFODPQERPRKLPOLCTELQTTIHDIIECYCKQQLRREYVDFAFRDLCTIVRDGPNY 60  
DB 1 MFODPQERPRKLPOLCTELQTTIHDIIECYCKQQLRREYVDFAFRDLCTIVRDGPNY 60  
QY 61 AVXDCKLKFYSKISRYHYCYSVYGTLEQOYNKPLCDLLIRICINXQKPLCPBEKQRHLD 120  
DB 61 GVCCKLKFYSKISRYHYCYSVYGTLEQOYNKPLCDLLIRICINXQKPLCPBEKQRHLD 120  
QY 121 KKQRFNIRGRWTCGMSCCSSRRRTETOL 151  
DB 121 KKQRFNIRGRWTCGMSCCSSRRRTETOL 151

RESULT 30  
US-11-021-949-18  
;; Sequence 18, Application US/11021949  
;; Publication No. US20050142541A1  
;; GENERAL INFORMATION:

;; APPLICANT: LU, PETER  
;; APPLICANT: GARMAN, JONATHAN DAVID  
;; APPLICANT: BELMARES, MICHAEL P  
;; APPLICANT: DIAZ-SANTIAGO, CHAMORRO SOMOZA  
;; APPLICANT: SCHWEIZER, JOHANNES  
;; TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRAINS OF HPV  
;; FILE REFERENCE: VITA-012  
;; CURRENT APPLICATION NUMBER: US/11/021,949  
;; PRIOR FILING DATE: 2004-12-23  
;; PRIOR APPLICATION NUMBER: 60/532,373  
;; PRIOR FILING DATE: 2003-12-23  
;; NUMBER OF SEQ ID NOS: 361  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 18  
;; LENGTH: 149  
;; TYPE: PRT  
;; ORGANISM: human papilloma virus (HPV)  
US-11-021-949-18

Query Match 63.0%; Score 523; DB 6; Length 149;  
Best Local Similarity 64.9%; Pred. No. 3.2e-48;  
Matches 98; Conservative 18; Mismatches 33; Indels 2; Gaps 1;

QY 1 MFODPQERPRKLPOLCTELQTTIHDIIECYCKQQLRREYVDFAFRDLCTIVRDGPNY 60  
DB 1 MFODPQERPRKLPOLCTELQTTIHDIIECYCKQQLRREYVDFAFRDLCTIVRDGPNY 60  
QY 61 AVXDCKLKFYSKISRYHYCYSVYGTLEQOYNKPLCDLLIRICINXQKPLCPBEKQRHLD 120  
DB 61 GVCCKLKFYSKISRYHYCYSVYGTLEQOYNKPLCDLLIRICINXQKPLCPBEKQRHLD 120  
QY 121 KKQRFNIRGRWTCGMSCCSSRRRTETOL 151  
DB 121 KKQRFNIRGRWTCGMSCCSSRRRTETOL 151

RESULT 31  
US-10-530-253-17

;; Sequence 17, Application US/10530253  
;; Publication No. US20060014926A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Casasetti, Maria C.  
;; APPLICANT: Smith, Larry  
;; APPLICANT: Jeffrey K. McElhinney  
;; APPLICANT: Susan P. McElhinney  
;; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS  
;; FILE REFERENCE: 00630/100M137-US2  
;; CURRENT APPLICATION NUMBER: US/10/530,253  
;; PRIOR FILING DATE: 2005-04-04  
;; PRIOR APPLICATION NUMBER: PCT/US2003/031726  
;; PRIOR FILING DATE: 2003-10-02  
;; PRIOR APPLICATION NUMBER: US 60/415,929  
;; PRIOR FILING DATE: 2002-10-03  
;; NUMBER OF SEQ ID NOS: 65  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 17  
;; LENGTH: 149  
;; TYPE: PRT  
;; ORGANISM: Human papillomavirus type 33  
US-10-530-253-17

Query Match 62.7%; Score 520; DB 5; Length 149;  
Best Local Similarity 63.6%; Pred. No. 6.7e-48;  
Matches 96; Conservative 19; Mismatches 34; Indels 2; Gaps 1;

QY 1 MFODPQERPRKLPOLCTELQTTIHDIIECYCKQQLRREYVDFAFRDLCTIVRDGPNY 60  
DB 1 MFODPQERPRKLPOLCTELQTTIHDIIECYCKQQLRREYVDFAFRDLCTIVRDGPNY 60  
QY 61 AVXDCKLKFYSKISRYHYCYSVYGTLEQOYNKPLCDLLIRICINXQKPLCPBEKQRHLD 120  
DB 61 GVCCKLKFYSKISRYHYCYSVYGTLEQOYNKPLCDLLIRICINXQKPLCPBEKQRHLD 120

Oy 121 KKORFHNIRGWTGRCSGCCSSRTRETOL 151  
Db 121 LNKRFHNISGRWAGRCACWRS--RRRETAL 149

## RESULT 32

US-11-021-949-16  
; Sequence 16, Application US/11021949  
; Publication No. US20050142541A1  
; GENERAL INFORMATION:  
; APPLICANT: LU, PETER  
; APPLICANT: GARMAN, JONATHAN DAVID  
; APPLICANT: BELMARES, MICHAEL P.  
; APPLICANT: DIAZ-SARMIENTO, CHAMORRO SOMOZA  
; APPLICANT: SCHWEIZER, JOHANNES  
; TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRAINS OF HPV  
; FILE REFERENCE: VITA-012  
; CURRENT APPLICATION NUMBER: US/11/021,949  
; CURRENT FILING DATE: 2004-12-23  
; PRIOR APPLICATION NUMBER: 60/532,373  
; PRIOR FILING DATE: 2003-12-23  
; NUMBER OF SEQ ID NOS: 361  
; SOFTWARE: PASTSEQ for Windows Version 4.0  
; SEQ ID NO 16  
; LENGTH: 149  
; TYPE: PRT  
; ORGANISM: human papilloma virus (HPV)  
US-11-021-949-16

Query Match 62.7%; Score 520; DB 6; Length 149;  
Best Local Similarity 63.6%; Pred. No. 6.7e-48;  
Matches 96; Conservative 19; Mismatches 34; Indels 2; Gaps 1;

Oy 1 MFODPOERPRKLPOLCTELQTTIHDIIECYVCKQQLRRVYDFAFRDLCTVYRDGPNY 60  
Db 1 MFODTEKPRHLHDLQALETTHINIELQVCECKKPLRSEVDFAPADLIVYRREGNPF 60  
Oy 61 AVXDCKLFYSKISEYRHVCYVGTTLQOYNKPLCDLLIRCNXOKPLCPBEKORHLD 120  
Db 61 GICGLCFRLSKISEYRHVCYVGTTLQOYNKPLCDLLIRCNXOKPLCPBEKORHLD 120  
Oy 121 KKORFHNIRGWTGRCSGCCSSRTRETOL 151  
Db 121 LNKRFHNISGRWAGRCACWRS--RRRETAL 149

## RESULT 33

US-11-021-949-360  
; Sequence 360, Application US/11021949  
; Publication No. US20050142541A1  
; GENERAL INFORMATION:  
; APPLICANT: LU, PETER  
; APPLICANT: GARMAN, JONATHAN DAVID  
; APPLICANT: BELMARES, MICHAEL P.  
; APPLICANT: DIAZ-SARMIENTO, CHAMORRO SOMOZA  
; APPLICANT: SCHWEIZER, JOHANNES  
; TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRAINS OF HPV  
; FILE REFERENCE: VITA-012  
; CURRENT APPLICATION NUMBER: US/11/021,949  
; CURRENT FILING DATE: 2004-12-23  
; PRIOR APPLICATION NUMBER: 60/532,373  
; PRIOR FILING DATE: 2003-12-23  
; NUMBER OF SEQ ID NOS: 361  
; SOFTWARE: PASTSEQ for Windows Version 4.0  
; SEQ ID NO 360  
; LENGTH: 149  
; TYPE: PRT  
; ORGANISM: human papilloma virus (HPV)  
US-11-021-949-360

Query Match 60.0%; Score 498; DB 6; Length 149;  
Best Local Similarity 60.1%; Pred. No. 1.6e-45;  
Matches 89; Conservative 22; Mismatches 37; Indels 0; Gaps 0;

Oy 1 MFODPOERPRKLPOLCTELQTTIHDIIECYVCKQQLRRVYDFAFRDLCTVYRDGPNY 60  
Db 1 MFODTEKPRHLHDLQALETTHINIELQVCECKKPLRSEVDFAPADLIVYRREGNPF 60  
Oy 61 AVXDCKLFYSKISEYRHVCYVGTTLQOYNKPLCDLLIRCNXOKPLCPBEKORHLD 120  
Db 61 GVCCKQLRLSKISEYRHVCYVGTTLQOYNKPLCDLLIRCNXOKPLCPBEKORHLD 120  
Oy 121 KKORFHNIRGWTGRCSGCCSSRTRETOL 148  
Db 121 LNKRFHNISGRWAGRCACWRS--RRRETAL 149

## RESULT 34

US-10-530-253-24  
; Sequence 24, Application US/10530253  
; Publication No. US20060014926A1  
; GENERAL INFORMATION:  
; APPLICANT: Casaccia, Maria C.  
; APPLICANT: Smith, Larry  
; APPLICANT: Jeffrey K. Pullen  
; APPLICANT: Susan P. McElhinney  
; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS  
; FILE REFERENCE: 00630/100M137-US2  
; CURRENT APPLICATION NUMBER: US/10/530,253  
; CURRENT FILING DATE: 2005-04-04  
; PRIOR APPLICATION NUMBER: PCT/US2003/031726  
; PRIOR FILING DATE: 2003-10-02  
; PRIOR APPLICATION NUMBER: US 60/415,929  
; PRIOR FILING DATE: 2002-10-03  
; NUMBER OF SEQ ID NOS: 65  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 24  
; LENGTH: 149  
; TYPE: PRT  
; ORGANISM: Human papillomavirus type 58  
US-10-530-253-24

Query Match 59.8%; Score 496; DB 5; Length 149;  
Best Local Similarity 61.6%; Pred. No. 2.6e-45;  
Matches 93; Conservative 20; Mismatches 36; Indels 2; Gaps 1;

Oy 1 MFODPOERPRKLPOLCTELQTTIHDIIECYVCKQQLRRVYDFAFRDLCTVYRDGPNY 60  
Db 1 MFODTEKPRHLHDLQALETTHINIELQVCECKKPLRSEVDFAPADLIVYRREGNPF 60  
Oy 61 AVXDCKLFYSKISEYRHVCYVGTTLQOYNKPLCDLLIRCNXOKPLCPBEKORHLD 120  
Db 61 AVCKVCLRLSKISEYRHVCYVGTTLQOYNKPLCDLLIRCNXOKPLCPBEKORHLD 120  
Oy 121 KKORFHNIRGWTGRCSGCCSSRTRETOL 151  
Db 121 LNKRFHNISGRWAGRCACWRS--RRRETAL 149

## RESULT 35

US-11-021-949-15  
; Sequence 15, Application US/11021949  
; Publication No. US20050142541A1  
; GENERAL INFORMATION:  
; APPLICANT: LU, PETER  
; APPLICANT: GARMAN, JONATHAN DAVID  
; APPLICANT: BELMARES, MICHAEL P.  
; APPLICANT: DIAZ-SARMIENTO, CHAMORRO SOMOZA  
; APPLICANT: SCHWEIZER, JOHANNES  
; TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRAINS OF HPV  
; FILE REFERENCE: VITA-012  
; CURRENT APPLICATION NUMBER: US/11/021,949

```

; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: 60/532,373
; PRIOR FILING DATE: 2003-12-23
; NUMBER OF SEQ ID NOS: 361
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 149
; TYPE: PRT
; ORGANISM: human papilloma virus (HPV)
US-11-021-949-15

Query Match          59.8%; Score 496; DB 6; Length 149;
Best Local Similarity 61.6%; Pred. No. 2.6e-45;
Matches 93; Conservative 20; Mismatches 36; Indels 2; Gaps 1;

QY 1 MFODPQERPKLPOLCTELQTTIHDIIECVYCKQQLLRREYDFAFRDLCTVYRDGNPY 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MFODAEKRPRLHDICQALETSVEHEIKVCCKKTLQSRSEYDVFADLRIVYRDGNPF 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 AVXDCKLFYSKISEYRHAYCVSVGTLEQYNNKPLCDLLIRICINXOKPLCPBEKORHLD 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 AVCKVCLRLSKISSEYRHAYNSLYGDTLEQTLKKCLNELIRICICQPLCPBEKORHVD 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 KKORFHNIIRGWTGRCSGCCRRSRRRTFOL 151
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 LNKRFHNIISGRWTGRCAVCWMP--RRQTOV 149
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 36
US-10-530-253-22
; Sequence 22, Application US/10530253
; Publication No. US20060014926A1
; GENERAL INFORMATION:
; APPLICANT: Casasetti, Maria C.
; APPLICANT: Smith, Larry
; APPLICANT: Jeffrey K. Pullen
; APPLICANT: Susan P. McElhinney
; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
; FILE REFERENCE: 00630/100M137-US2
; CURRENT APPLICATION NUMBER: US/10/530,253
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US2003/031726
; PRIOR FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/415,929
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 148
; TYPE: PRT
; ORGANISM: Human papillomavirus type 52
US-10-530-253-22

Query Match          58.7%; Score 487; DB 5; Length 148;
Best Local Similarity 61.7%; Pred. No. 2.4e-44;
Matches 87; Conservative 19; Mismatches 35; Indels 0; Gaps 0;

QY 1 MFODQERPKLPOLCTELQTTIHDIIECVYCKQQLLRREYDFAFRDLCTVYRDGNPY 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MFEDATRPRLTHELCEVLESVHEIRLQCVCKKELORREYKFLFTDLRIYVRDNNPY 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 AVXDCKLFYSKISEYRHAYCVSVGTLEQYNNKPLCDLLIRICINXOKPLCPBEKORHLD 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 GVCIMCLRLSKISSEYRHAYSLYKGTLEBRVKKPLSEITTRICICQPLCPBEKERRHV 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 KKORFHNIIRGWTGRCSGCCRR 141
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 ANKRFHNIIRGWTGRCSGCCRR 141
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 37
US-11-021-949-17
; Sequence 17, Application US/11021949
```

```

; Publication No. US20050142541A1
; GENERAL INFORMATION:
; APPLICANT: LU, PETER
; APPLICANT: GARMAN, JONATHAN DAVID
; APPLICANT: BELMARES, MICHAEL P.
; APPLICANT: DIAZ-SARMIENTO, CHAMORRO SOMOZA
; APPLICANT: SCHWEIZER, JOHANNES
; TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRAINS OF HPV
; FILE REFERENCE: VITA-012
; CURRENT APPLICATION NUMBER: US/11/021,949
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: 60/532,373
; PRIOR FILING DATE: 2003-12-23
; NUMBER OF SEQ ID NOS: 361
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 148
; TYPE: PRT
; ORGANISM: human papilloma virus (HPV)
US-11-021-949-17

Query Match          58.7%; Score 487; DB 6; Length 148;
Best Local Similarity 61.7%; Pred. No. 2.4e-44;
Matches 87; Conservative 19; Mismatches 35; Indels 0; Gaps 0;

QY 1 MFODPQERPKLPOLCTELQTTIHDIIECVYCKQQLLRREYDFAFRDLCTVYRDGNPY 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MFEDATRPRLTHELCEVLESVHEIRLQCVCKKELORREYKFLFTDLRIYVRDNNPY 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 AVXDCKLFYSKISEYRHAYCVSVGTLEQYNNKPLCDLLIRICINXOKPLCPBEKORHLD 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 GVCIMCLRLSKISSEYRHAYSLYKGTLEBRVKKPLSEITTRICICQPLCPBEKERRHV 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 KKORFHNIIRGWTGRCSGCCRR 141
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 ANKRFHNIIRGWTGRCSGCCRR 141
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 38
US-11-021-949-359
; Sequence 359, Application US/11021949
; Publication No. US20050142541A1
; GENERAL INFORMATION:
; APPLICANT: LU, PETER
; APPLICANT: GARMAN, JONATHAN DAVID
; APPLICANT: BELMARES, MICHAEL P.
; APPLICANT: DIAZ-SARMIENTO, CHAMORRO SOMOZA
; APPLICANT: SCHWEIZER, JOHANNES
; TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRAINS OF HPV
; FILE REFERENCE: VITA-012
; CURRENT APPLICATION NUMBER: US/11/021,949
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: 60/532,373
; PRIOR FILING DATE: 2003-12-23
; NUMBER OF SEQ ID NOS: 361
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 359
; LENGTH: 148
; TYPE: PRT
; ORGANISM: human papilloma virus (HPV)
US-11-021-949-359

Query Match          58.3%; Score 484; DB 6; Length 148;
Best Local Similarity 60.4%; Pred. No. 5.1e-44;
Matches 87; Conservative 17; Mismatches 40; Indels 0; Gaps 0;

QY 2 FODPQERPKLPOLCTELQTTIHDIIECVYCKQQLLRREYDFAFRDLCTVYRDGNPY 61
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 FPNBERPKLPALCEVNIISHEILDVYCEBOLYKCEYVDYFIRDLCTVYRKGRKLG 62
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 62 VXDCKLFYSKISEYRHAYCVSVGTLEQYNNKPLCDLLIRICINXOKPLCPBEKORHLD 121
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

Db 63 VCPCLLFISKQYRYNOSYGRITLLEMLTKOLCNILIRGCKQKQKFLCELEQRHAYDE 122

Qy 122 KQFHNIRGWTGRCSGCCRSRT 145

Db 123 NKRFHQIADQWTRCTQCMRPSAT 146

```

RESULT 39
US-11-021-949-19
; Sequence 19, Application US/11021949
; Publication No. US20050142541A1
; GENERAL INFORMATION:
; APPLICANT: LV, PETER
; APPLICANT: GARMAN, JONATHAN DAVID
; APPLICANT: BEAURES, MICHAEL P.
; APPLICANT: DIAZ-SARMIENTO, CHAMORRO SOMOLA
; APPLICANT: SCHWEIZER, JOHANNES
; TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRAINS OF HPV
; TITLE OF INVENTION: AND METHODS OF THEIR USE
; FILE REFERENCE: VITA-012
; CURRENT APPLICATION NUMBER: US/11/021,949
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: 60/532,373
; PRIOR FILING DATE: 2003-12-23
; NUMBER OF SEQ ID NOS: 361
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 148
; TYPE: PR1
; ORGANISM: human papilloma virus (HPV)
US-11-021-949-19

```

Query Match	58.2%	Score 483	DB 6	Length 148
Best Local Similarity	61.4%	Pred. NO. 6.6e-44		
Matches 89, Conservative	16	Mismatches 40	Indels 0	Gaps 0

Qy	MPDOPRPERKLEPOLCTELOTTHIDHIIIEVCYKQOOLREYDYDPAFRILCIVADGAPY	60
Dy	2 LFNSEERPYKQALDDEVANISHIDINDCVCFOGRLSYSEVYDPAFSDLCIVRRKDPY	61
Qy	AYNDCKLCKEFSKISEVRHVCYVYGTLEDOQYKPLCDLIRICMXOKPLGSEMKORLD	120
Dy	62 GVCPCLCKEFSKIRERHRYQSVYGTLENTKOLCNILRCGKQKPLCEKQKAVD	121
Qy	121 KQRFNHRGRMTGRCMSCCRSSRT	145
Dy	122 EKRRFHQIAQWGTGRCTRCWRPSAT	146

```

RESULT 40
US-10-530-253-26
; Sequence 26, Application US/10530253
; Publication No. US20060014926A1
GENERAL INFORMATION:
; APPLICANT: Cassecci, Maria C.
; APPLICANT: Smith, Larry
; APPLICANT: Jeffrey K. Pullen
; APPLICANT: Susan P. McElhinney
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
; FILE REFERENCE: 06630/100M137-US2
; CURRENT APPLICATION NUMBER: US/10/530,253
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US2003/031726
; PRIOR FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/415,929
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human papillomavirus type 68

```

US-10-530-253-26

Query Match	56.4%;	Score 468.5;	DB 5;	Length 158;
Best Local Similarity	55.1%;	Pred. No. 2.6e-42;		
Matches	86;	Conservative	23;	Mismatches 42;
			Indels	5;
			Gaps	1.

```
Oy      1 MEOPDQEBPRKLPOLCETELQTTIHIIIEECVACSKOOLLREYVDFAFBLCLVYRGNPY 60
       : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      3 LFHNPBEPYPKLPDLCRLTLDITLHAVTIIDCVYCRQLQRTLEYEERPFSLDCVYIRGVPE 62
Oy      61 AVXDCKLFYSKISSEYRHVCYSVGTLLEEQYNKEPLCDLLILRCINXOKPILCEBKORHLID 120
       | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      63 AACGSCIFAYAKIRLRYYSESVAATLETINTNLNMLNICMGLCKPLCPAEKLRHLT 122
Oy      121 KKQRFHNIRGWTCRMCSCRRS-----RTRRETQL 151
       | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      123 TKRRLHKAGNFTGCRCRWCTSKREDRRRIKETOV 158
```

```

RESULT 41
US-11-021-949-361
Sequence 361, Application US/11021949
Publication No. US20050142541A1
GENERAL INFORMATION:
APPLICANT: LU, PETER
APPLICANT: GARMAN, JONATHAN DAVID
APPLICANT: BELMARES, MICHAEL P.
APPLICANT: DIAZ-SABRMENTO, CHAMORRO SOMOZA
APPLICANT: SCHEWEIZER, JOHANNES
TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRAINS OF HPV
TITLE OF INVENTION: ANTIBODIES FOR THEIR USE
FILE REFERENCE: VITA-012
CURRENT APPLICATION NUMBER: US/11/021,949
CURRENT FILING DATE: 2004-12-23
PRIOR APPLICATION NUMBER: 60/532,373
PRIOR FILING DATE: 2003-12-23
NUMBER OF SEQ ID NOS: 361
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 361
LENGTH: 158
TYPE: PRT
ORGANISM: human papilloma virus (HPV)
US-11-021-949-361

```

Query Match	56.4%	Score 468.5;	DB 6;	Length 158;
Best Local Similarity	56.8%	Pred. No. 2.6e-42;		
Matches 88;	Conservative 21;	Mismatches 41;	Indels 5;	Gaps 1

```

QY 2 QODPERPKPQLQTELOTTIHDIIECVYCKOOLREBYVDFAFRDICTIVRODGNPYA 61
Db 4 FPNPAPERYKLPDLCTALDITLHDITTDICVYCKTQLOQCEVEYEFASDLPFIVRNGEPIA 63
QY 62 VXDCKLAEYSKISERYHCYSVGTTLLEQYNNKPLCDLLIRICINXOKPLCPKEKORHLDK 121
Db 64 ACQKIKTHAKRELRHYSNSVYATILBSITNTKLYNLSIRCMSCILCPAEKLRHVT 122
QY 122 KORFENIRGMRGCMSCCRSS-----RRRRETOL 151
Db 124 KRPFHOLAGSYTGCRCHCWTNRBDRRRRIRRETQV 158

```

```

RESULT 42
US-10-530-253-21
; Sequence 21, Application US/10530253
; Publication No. US20060014926A1
;
GENERAL INFORMATION:
;
APPLICANT: Cassetti, Maria C.
;
APPLICANT: Smith, Larry
;
APPLICANT: Jeffrey K. Pullen
;
APPLICANT: Susan P. McElhinney
;
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
;
FILE REFERENCE: 00630/100M137-US2
;
CURRENT APPLICATION NUMBER: US/10/530.253

```

```

1 CURRENT FILING DATE: 2005-04-04
2
3 PRIOR APPLICATION NUMBER: PCT/US2003/031726
4
5 PRIOR FILING DATE: 2003-10-02
6
7 PRIOR APPLICATION NUMBER: US 60/415, 929
8
9 PRIOR FILING DATE: 2002-10-03
10
11 NUMBER OF SEQ ID NOS: 65
12
13 SOFTWARE: PatentIn version 3.1
14
15 SEQ ID NO 21
16
17 LENGTH: 151
18
19 TYPE: prt
20
21 ORGANISM: Human papillomavirus type 51
22
23 US-10-530-253-21

```

Query Match	55.4%	Score	460	DB	5	Length	151
Best Local Similarity	57.0%	Pred. No.	2.1e-41				
Matches	86	Conservative	24	Mismatches	41	Indels	0
						Gaps	0

Qy	1	MEODPOEBPRXJ.POLCETELQOTIHIHILECYCKOOLLREAYDFAFBDICITVYRGPNP	60
		: : : : :     : : : : :     : : : : :     : : : : :	
Db	1	MFEDGGRPRTHLEALNVSMMNIQVVCVCKEELCPADYVNAFTEKIYIRDNBP	60
Qy	61	AVXDKCLFXYKISEYRHYCYVYGTLEEQYNKPLCDLLIRCNXQKPLCPBEKORHLD	120
		: : : : :     : : : : :     : : : : :     : : : : :	
Db	61	AVCKCLLFYSXIRERRYRSRVYGTLLAITYKSLDYLSIRCHCORPLGPEEKOLVD	120
Qy	121	KKOREFHTIRGWTGRCMSCCRSRTRETOJL	151
		: : : : :     : : : : :     : : : : :     : : : : :	
Db	121	EKRFEHTIAGRMTGOCANCORTROBNEHOV	151

```

RESULT 43
US-11-021-949-24
? Sequence 24, Application US/11021949
? Publication No. US20050142541A1
? GENERAL INFORMATION:
? APPLICANT: LU, PETER
? APPLICANT: GARMAN, JONATHAN DAVID
? APPLICANT: BELMARES, MICHAEL P.
? APPLICANT: DIAZ-SARMIENTO, CHAORRO SOMOZA
? APPLICANT: SCHWEIZER, JOHANNES
? TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRAINS OF HPV
? TITLE OF INVENTION: ANTIBODIES FOR THEIR USE
? FILE REFERENCE: VITA-012
? CURRENT APPLICATION NUMBER: US/11/021,949
? CURRENT FILING DATE: 2004-12-23
? PRIOR APPLICATION NUMBER: 60/532,373
? PRIOR FILING DATE: 2003-12-23
? NUMBER OF SEQ ID NOS: 361
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 24
? LENGTH: 151
? TYPE: PRT
? ORGANISM: human papilloma virus (HPV)
US-11-021-949-24

```

Query Match	55.4%	Score	460	DB	6	Length	151
Best Local Similarity	57.0%	Pred.	No. 2.1e-41				
Matches	86	Conservative	41	Indels	0	Gaps	0

[illegible]

**RESULT 44**

```

US-10-530-253-20
; Sequence 20, Application US/10530253
; Publication No. US20060014926A1
; GENERAL INFORMATION:
; APPLICANT: Cassetti, Maria C.
; APPLICANT: Smith, Larry
; APPLICANT: Jeffrey K. Pullen
; APPLICANT: Susan P. McElhinney
; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
; FILE REFERENCE: 00630/100M137-US2
; CURRENT APPLICATION NUMBER: US/10/530,253
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US2003/031726
; PRIOR FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/445,929
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
;
; LENGTH: 158
;
; TYPE: PRT
; ORGANISM: Human papillomavirus type 45
US-10-530-253-20

```

Query Match	55.4%	Score 459.5;	DB 5;	Length 158;
Best Local Similarity	56.1%;	Pred. No. 2.5e-41;		
Matches	87;	Conservative	22;	Mismatches 41;
			Indels	5;
			Gaps	1;

[illegible]

```
Qy      122 KQRFHNIGRWTRCWSCCRSS---RTRETOL 151  
         |::|::|::|::|::|::|::|::|::|:  
Db      124 KRPFHSIAGQYRGQCNTCCDQAQRERLRRRRETOV 156
```

```

RESULT 45
US-11-021-949-29
; Sequence 29, Application US/11021949
; Publication No. US20050142541A1
; GENERAL INFORMATION:
; APPLICANT: LU, PETER
; APPLICANT: GARMAN, JONATHAN DAVID
; APPLICANT: BELMARES, MICHAEL P.
; APPLICANT: DIAZ-SARMIENTO, CHANORRO SOMOLA
; APPLICANT: SCHEIDLER, JOHANNES
; TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRAINS OF HPV
; FILE REFERENCE: VIRA-012
; CURRENT APPLICATION NUMBER: US/11/021,949
; PRIOR FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: 60/6532,373
; PRIOR FILING DATE: 2003-12-23
; NUMBER OF SEQ ID NOS: 361
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 158
; TYPE: PRT
; ORGANISM: human papilloma virus (HPV)
US-11-021-949-29

```

Query Match	55.4%;	Score 459.5;	DB 6;	Length 158;
Best Local Similarity	56.1%;	Pred. No. 2.5e-41;		
Matches	87;	Conservative	22;	Mismatches 41;
			Indels	5;
			Gaps	1

**Qy**      2 FQDPQERPKRLPQLCTELQTTHDIIIEGVCYCKQDLRREVVYDFARFLCTIVRDGNPYA 61  
| | : : | | | | | : : : | | | | | | | | | |  
**Db**      4 FDDPKRPYPKLPDLCTELNTSLQDVSIACVYCCKTLERTVEVYQFAFKDLCTIVRDCIAYA 61

```

; TYPE: PRT
; ORGANISM: human papilloma virus (HPV)
US-11-021-949-28
Query Match
Best Local Similarity 54.9%; Score 455.5; DB 5; Length 158;
Matches 87; Conservative 21; Mismatches 42; Indels 5; Gaps 1;

Qy 2 FQDQERPRKLPOLCTELQTTIHDIIECYCKQQLRREYDPAFRLDLCIVRDGNPYA 61
Db 4 FEDPTRRPRYKLPDLCTELNTSLQDIEITCYCKTVLETFEFAFQDLFVYVYDSIPHA 63

Qy 62 VXDCKLFYSKISRYRYCYSVYGTLEQYNNKPLCDLLIRCIYXOKPLCEBQKRLHDK 121
Db 64 ACHKCIDFYSRIRLRYSDSVYGDTEKLTNTGLVNLIRCLRCQKPLNPAEKRLHNE 123

Qy 122 KQRFHNIRGWTGRCMSCCRSSR-----TRRETOL 151
Db 124 KRFRHNLAGHYRGQCHSCCNRAQERLQRRETQV 158

RESULT 47
US-11-021-949-28
; Sequence 28, Application US/11021949
; Publication No. US20050142541A1
; GENERAL INFORMATION:
; APPLICANT: LU, PETER
; APPLICANT: GARMAN, JONATHAN DAVID
; APPLICANT: BELMARES, MICHAEL P.
; APPLICANT: DIAZ-SABRIMIENTO, CHAMORRO SOMOZA
; APPLICANT: SCHMEIZER, JOHANNES
; TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRAINS OF HPV
; TITLE OF INVENTION: AND METHODS OF THEIR USE
; FILE REFERENCE: VITA-012
; CURRENT APPLICATION NUMBER: US/11/021.949
; PRIOR FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: 60/532,373
; NUMBER OF SEQ ID NOS: 361
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 158

```

```

; TYPE: PRT
; ORGANISM: human papilloma virus (HPV)
US-11-021-949-28
Query Match
Best Local Similarity 54.9%; Score 455.5; DB 6; Length 158;
Matches 87; Conservative 21; Mismatches 42; Indels 5; Gaps 1;

Qy 2 FQDQERPRKLPOLCTELQTTIHDIIECYCKQQLRREYDPAFRLDLCIVRDGNPYA 61
Db 4 FEDPTRRPRYKLPDLCTELNTSLQDIEITCYCKTVLETFEFAFQDLFVYVYDSIPHA 63

Qy 62 VXDCKLFYSKISRYRYCYSVYGTLEQYNNKPLCDLLIRCIYXOKPLCEBQKRLHDK 121
Db 64 ACHKCIDFYSRIRLRYSDSVYGDTEKLTNTGLVNLIRCLRCQKPLNPAEKRLHNE 123

Qy 122 KQRFHNIRGWTGRCMSCCRSSR-----TRRETOL 151
Db 130 KRFRHNLAGHYRGQCHSCCNRAQERLQRRETQV 164

RESULT 49
US-10-000-903-21
; Sequence 21, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Christaline
; APPLICANT: Lombardo-Bencheikh, Angela

```

```

; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-21

Query Match      54.9%; Score 455.5; DB 4; Length 278;
Best Local Similarity 56.1%; Pred. No. 1.3e-40;
Matches 87; Conservative 21; Mismatches 42; Indels 5; Gaps 1;

Oy      2 FODPQERPKLPOLCTELQTTIHDIILIECVYCKQOQLRREYVDFAFRDLGIYVRDGNPYA 61
      115 FEDPTRRYPKLPDCTELNTSLQDIETVCYCKTVLETFEVEFAFADLFVVRDSIFA 174
Db      62 VXDCKLKFYSKISRYRHYCVSYGTTLEQOYNKPLCDLLIRCIYNQKPLCEBEKORHLDK 121
      175 ACHKCIDFYSIRIRLRYHSDSVYGDTEKLTNTGLYNLLIRCLRCQKPLNPAEKLRHLNE 234

Oy      122 KORFHNIRGWRWTCGMSCCRSSR-----TRRETQL 151
      235 KRRFHNIRAGHYRGQCHSCCNRAKORERLQRRRETV 269
Db

RESULT 50
US-10-899-771-21
; Sequence 21, Application US/10899771
; Publication No. US20050031638A1
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.
; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
; TITLE OF INVENTION: and Fusion Proteins Adjuncted with a CpG Oligonucleotide
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/10/899,771
; CURRENT FILING DATE: 2004-07-27
; PRIOR APPLICATION NUMBER: US/09/581,976
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/08563
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: GB 9727262.9
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimeric protein (protein D from Haemophilus
; OTHER INFORMATION: influenzae B and B6 from Human papilloma virus type
; OTHER INFORMATION: 18)
US-10-899-771-21

Query Match      54.9%; Score 455.5; DB 5; Length 278;
Best Local Similarity 56.1%; Pred. No. 1.3e-40;
Matches 87; Conservative 21; Mismatches 42; Indels 5; Gaps 1;

Oy      2 FODPQERPKLPOLCTELQTTIHDIILIECVYCKQOQLRREYVDFAFRDLGIYVRDGNPYA 61
      115 FEDPTRRYPKLPDCTELNTSLQDIETVCYCKTVLETFEVEFAFADLFVVRDSIFA 174
Db      62 VXDCKLKFYSKISRYRHYCVSYGTTLEQOYNKPLCDLLIRCIYNQKPLCEBEKORHLDK 121
      175 ACHKCIDFYSIRIRLRYHSDSVYGDTEKLTNTGLYNLLIRCLRCQKPLNPAEKLRHLNE 234

Oy      122 KORFHNIRGWRWTCGMSCCRSSR-----TRRETQL 151
      235 KRRFHNIRAGHYRGQCHSCCNRAKORERLQRRRETV 269
Db
```

```

Db      175 ACHKCIDFYSIRIRLRYHSDSVYGDTEKLTNTGLYNLLIRCLRCQKPLNPAEKLRHLNE 234
Oy      122 KORFHNIRGWRWTCGMSCCRSSR-----TRRETQL 151
      235 KRRFHNIRAGHYRGQCHSCCNRAKORERLQRRRETV 269
Db

RESULT 51
US-10-000-903-23
; Sequence 23, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Bernarde
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-23

Query Match      54.9%; Score 455.5; DB 4; Length 383;
Best Local Similarity 56.1%; Pred. No. 1.8e-40;
Matches 87; Conservative 21; Mismatches 42; Indels 5; Gaps 1;

Oy      2 FODPQERPKLPOLCTELQTTIHDIILIECVYCKQOQLRREYVDFAFRDLGIYVRDGNPYA 61
      115 FEDPTRRYPKLPDCTELNTSLQDIETVCYCKTVLETFEVEFAFADLFVVRDSIFA 174
Db      62 VXDCKLKFYSKISRYRHYCVSYGTTLEQOYNKPLCDLLIRCIYNQKPLCEBEKORHLDK 121
      175 ACHKCIDFYSIRIRLRYHSDSVYGDTEKLTNTGLYNLLIRCLRCQKPLNPAEKLRHLNE 234

Oy      122 KORFHNIRGWRWTCGMSCCRSSR-----TRRETQL 151
      235 KRRFHNIRAGHYRGQCHSCCNRAKORERLQRRRETV 269
Db

RESULT 52
US-10-899-771-23
; Sequence 23, Application US/10899771
; Publication No. US20050031638A1
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.
; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
; TITLE OF INVENTION: and Fusion Proteins Adjuncted with a CpG Oligonucleotide
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/10/899,771
; CURRENT FILING DATE: 2004-07-27
; PRIOR APPLICATION NUMBER: US/09/581,976
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/08563
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: GB 9727262.9
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 383
; TYPE: PRT
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chinaeric protein (proteins D from Haemophilus
; OTHER INFORMATION: influenzae B and B67 fusion from Human papilloma
; OTHER INFORMATION: virus type 18)
US-10-899-771-23
```

```
Query Match          54.9%; Score 455.5; DB 5; Length 383;
Best Local Similarity 56.1%; Pred. No. 1.8e-40;
Matches 87; Conservative 21; Mismatches 42; Indels 5; Gaps 1;
```

```
QY 2 FODPQERPKLPOLCTELQTTIHDIIECYCKQOQLRREYDPAFRLCIYVRDGNPYA 61
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 115 FEDTRRPYKLPDLCTELNTSLQDIETCYCKVLELTFEFAFRLDLYVVRDSDIPA 174
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 62 VDKCKLFYSKISEYRHYCYVYGTLEQOYNKPLCDLLIRCLNXXQPLCPPEKORLIDK 121
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 175 ACHKCIDFYSRIELRHSYSDVYGDLEKLTNTGLYNLLIRCLRCQKPLPAEKLRLINE 234
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 122 KQRFNIRGRMTGRMCCSSR-----TRRETOL 151
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 235 KRPFNIRAGHYRQCHSCCNRAQERLQRRRETQV 269
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

```
RESULT 53
US-11-021-949-31
; Sequence 31, Application US/11021949
; Publication No. US20050142541A1
; GENERAL INFORMATION:
; APPLICANT: LU, PETER
; APPLICANT: GARMAN, JONATHAN DAVID
; APPLICANT: BELMARES, MICHAEL P.
; APPLICANT: DIAZ-SARMIENTO, CHAMORRO SOMOZA
; APPLICANT: SCHWEIZER, JOHANNES
; TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRAINS OF HPV
; TITLE OF INVENTION: AND METHODS OF THEIR USE
; FILE REFERENCE: VITA-012
; CURRENT APPLICATION NUMBER: US/11/021,949
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: 60/532,373
; PRIOR FILING DATE: 2003-12-23
; NUMBER OF SEQ ID NOS: 361
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 162
; TYPE: PRT
; ORGANISM: human papilloma virus (HPV)
US-11-021-949-31
```

```
Query Match          54.4%; Score 451.5; DB 6; Length 162;
Best Local Similarity 55.1%; Pred. No. 1.8e-40;
Matches 86; Conservative 21; Mismatches 44; Indels 5; Gaps 1;
```

```
QY 1 MFQDQERPKLPOLCTELQTTIHDIIECYCKQOQLRREYDPAFRLCIYVRDGNPY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 7 LFHNPBRPKLPDLCTELTDTTIDVTIDCYCKRQORREVEFAAGDLNAYVRDGVPL 66
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 AVXDKCLFYSKISEYRHYCYVYGTLEQOYNKPLCDLLIRCLNXXQPLCPPEKORLID 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 67 AACQSCIKFYAKIRLELHYSESYYATLETITNTKLDLSIRCMCCPKLSPAEKLAHIN 126
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 KQRFNIRGRMTGRMCCSSR-----TRRETOL 151
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 127 SKRPFNIRAGHYRQCHSCCNRAQERLQRRRETQV 162
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

```
RESULT 54
US-10-800-023-27
; Sequence 27, Application US/10800023
; Publication No. US20040258688A1
; GENERAL INFORMATION:
; APPLICANT: Steinman, Ralph
; APPLICANT: Nussenzweig, Michel
```

```
; APPLICANT: Hawiger, Daniel
; APPLICANT: Bonifaz, Laura
; TITLE OF INVENTION: Enhanced Antigen Delivery and Modulation
; TITLE OF INVENTION: Of the Immune Response Therefrom
; FILE REFERENCE: 600-1-081CONCIP1
; CURRENT APPLICATION NUMBER: US/10/800,023
; CURRENT FILING DATE: 2004-03-14
; PRIOR APPLICATION NUMBER: 09/925,284
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/586,704
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: PCT/US96/01383
; PRIOR FILING DATE: 1996-01-31
; PRIOR APPLICATION NUMBER: 08/381,528
; PRIOR FILING DATE: 1995-01-31
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 158
; TYPE: PRT
; ORGANISM: human papilloma virus E6 protein
US-10-800-023-27
```

```
Query Match          54.2%; Score 449.5; DB 5; Length 158;
Best Local Similarity 55.5%; Pred. No. 3e-40;
Matches 86; Conservative 21; Mismatches 43; Indels 5; Gaps 1;
```

```
QY 2 FODPQERPKLPOLCTELQTTIHDIIECYCKQOQLRREYDPAFRLCIYVRDGNPYA 61
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 4 FEDTRRPYKLPDLCTELNTSLQDIETCYCKVLELTFEFAFRLDLYVVRDSDIPA 63
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 62 VDKCKLFYSKISEYRHYCYVYGTLEQOYNKPLCDLLIRCLNXXQPLCPPEKORLIDK 121
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 64 ACHKCIDFYSRIELRHSYSDVYGDLEKLTNTGLYNLLIRCLRCQKPLPAEKLRLINE 123
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 122 KQRFNIRGRMTGRMCCSSR-----TRRETOL 151
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 124 KRPFNIRAGHYRQCHSCCNRAQERLQRRRETQV 158
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

```
RESULT 55
US-10-530-253-19
; Sequence 19, Application US/10530253
; Publication No. US20060014926A1
; GENERAL INFORMATION:
; APPLICANT: Casasetti, Maria C.
; APPLICANT: Smith, Larry
; APPLICANT: Jeffrey K. Pullen
; APPLICANT: Susan P. McElhinney
; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
; FILE REFERENCE: 00630/100M137-US2
; CURRENT APPLICATION NUMBER: US/10/530,253
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US2003/031726
; PRIOR FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/415,929
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human papillomavirus type 39
US-10-530-253-19
```

```
Query Match          54.2%; Score 449.5; DB 5; Length 158;
Best Local Similarity 55.5%; Pred. No. 3e-40;
Matches 86; Conservative 19; Mismatches 45; Indels 5; Gaps 1;
```

```
QY 2 FODPQERPKLPOLCTELQTTIHDIIECYCKQOQLRREYDPAFRLCIYVRDGNPYA 61
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 4 FHNPAERPKLPDLCTELTDTTIDVTIDCYCKRQORREVEFAAGDLNAYVRDGVPLA 63
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```









US-10-751-845-157

Query Match 40.1%; Score 333; DB 5; Length 236;  
Best Local Similarity 65.3%; Pred. No. 1.8e-27;  
Matches 66; Conservative 4; Mismatches 3; Indels 28; Gaps 2;

Qy 1 MFODPQERPRKLPOLCTELQTTIHDIILECVYCKQQLLRREYVDFAFRDLCIYVRDGNPY 60  
Db 2 MFODPQERPRKLPOLCTEL-----LLRREYVDFAFRDLCIYVRDGNPY 44  
Qy 61 AVXDCKLFYSKISEYRHVCYSYVGTLEQQYNKPLCDLLI 101  
Db 45 -----KISEYRHVCYSYVGTLEQQYNKTLHEMYL 74

RESULT 70

US-10-751-845-158  
; Sequence 158, Application US/10751845  
; Publication No. US20050100928A1  
; GENERAL INFORMATION:  
; APPLICANT: Hedley, Mary Lynne  
; APPLICANT: Urban, Robert G.  
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES  
; FILE REFERENCE: 08191-013001  
; CURRENT APPLICATION NUMBER: US/10/751,845  
; PRIOR FILING DATE: 2004-01-05  
; PRIOR APPLICATION NUMBER: US/09/664,225  
; PRIOR FILING DATE: 2000-08-18  
; PRIOR APPLICATION NUMBER: US 60/169,846  
; PRIOR FILING DATE: 1999-12-09  
; PRIOR APPLICATION NUMBER: US 60/154,665  
; PRIOR FILING DATE: 1999-09-16  
; NUMBER OF SEQ ID NOS: 163  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 158  
; LENGTH: 237  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Artificial fusion sequence  
US-10-751-845-158

Query Match 40.1%; Score 333; DB 5; Length 237;  
Best Local Similarity 65.3%; Pred. No. 1.8e-27;  
Matches 66; Conservative 4; Mismatches 3; Indels 28; Gaps 2;

Qy 1 MFODPQERPRKLPOLCTELQTTIHDIILECVYCKQQLLRREYVDFAFRDLCIYVRDGNPY 60  
Db 3 MFODPQERPRKLPOLCTEL-----LLRREYVDFAFRDLCIYVRDGNPY 45  
Qy 61 AVXDCKLFYSKISEYRHVCYSYVGTLEQQYNKPLCDLLI 101  
Db 46 -----KISEYRHVCYSYVGTLEQQYNKTLHEMYL 75

RESULT 71

US-10-751-845-160  
; Sequence 160, Application US/10751845  
; Publication No. US20050100928A1  
; GENERAL INFORMATION:  
; APPLICANT: Hedley, Mary Lynne  
; APPLICANT: Urban, Robert G.  
; APPLICANT: Chiciz, Roman M.  
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES  
; FILE REFERENCE: 08191-013001  
; CURRENT APPLICATION NUMBER: US/10/751,845  
; PRIOR FILING DATE: 2004-01-05  
; PRIOR APPLICATION NUMBER: US/09/664,225  
; PRIOR FILING DATE: 2000-08-18  
; PRIOR APPLICATION NUMBER: US 60/169,846  
; PRIOR FILING DATE: 1999-12-09  
; PRIOR APPLICATION NUMBER: US 60/154,665

; PRIOR FILING DATE: 1999-09-16  
; NUMBER OF SEQ ID NOS: 163  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 160  
; LENGTH: 261  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Artificial fusion sequence  
US-10-751-845-160

Query Match 40.1%; Score 333; DB 5; Length 261;  
Best Local Similarity 65.3%; Pred. No. 2e-27;  
Matches 66; Conservative 4; Mismatches 3; Indels 28; Gaps 2;

Qy 1 MFODPQERPRKLPOLCTELQTTIHDIILECVYCKQQLLRREYVDFAFRDLCIYVRDGNPY 60  
Db 27 MFODPQERPRKLPOLCTEL-----LLRREYVDFAFRDLCIYVRDGNPY 69  
Qy 61 AVXDCKLFYSKISEYRHVCYSYVGTLEQQYNKPLCDLLI 101  
Db 70 -----KISEYRHVCYSYVGTLEQQYNKTLHEMYL 99

RESULT 72

US-10-367-095-10  
; Sequence 10, Application US/10367095  
; Publication No. US20030228696A1  
; GENERAL INFORMATION:  
; APPLICANT: Robin A. Robinson  
; TITLE OF INVENTION: No. US20030228696A1 Insect Cell Line  
; FILE REFERENCE: 44149-1US1  
; CURRENT APPLICATION NUMBER: US/10/367,095  
; PRIOR FILING DATE: 2003-02-14  
; PRIOR APPLICATION NUMBER: US 60/356,119  
; PRIOR FILING DATE: 2002-02-14  
; PRIOR APPLICATION NUMBER: US 60/356,161  
; PRIOR FILING DATE: 2002-02-14  
; PRIOR APPLICATION NUMBER: US 60/356,118  
; PRIOR FILING DATE: 2002-02-14  
; PRIOR APPLICATION NUMBER: US 60/356,133  
; PRIOR FILING DATE: 2002-02-14  
; PRIOR APPLICATION NUMBER: US 60/356,157  
; PRIOR FILING DATE: 2002-02-14  
; PRIOR APPLICATION NUMBER: US 60/356,156  
; PRIOR FILING DATE: 2002-02-14  
; PRIOR APPLICATION NUMBER: US 60/356,123  
; PRIOR FILING DATE: 2002-02-14  
; PRIOR APPLICATION NUMBER: US 60/356,113  
; PRIOR FILING DATE: 2002-02-14  
; PRIOR APPLICATION NUMBER: US 60/356,154  
; PRIOR FILING DATE: 2002-02-14  
; PRIOR APPLICATION NUMBER: US 60/356,135  
; PRIOR FILING DATE: 2002-02-14  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 536  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: HPV-16 L2/E6 fusion protein  
US-10-367-095-10

Query Match 38.9%; Score 323; DB 4; Length 536;  
Best Local Similarity 100.0%; Pred. No. 5.5e-26;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFODPQERPRKLPOLCTELQTTIHDIILECVYCKQQLLRREYVDFAFRDLCIYVRDGNPY 59  
Db 478 MFODPQERPRKLPOLCTELQTTIHDIILECVYCKQQLLRREYVDFAFRDLCIYVRDGNPY 536

```
RESULT 73
US-10-368-046-10
; Sequence 10, Application US/10368046
; Publication No. US20040063188A1
; GENERAL INFORMATION:
; APPLICANT: Robin A. Robinson
; APPLICANT: Victoria Cioce
; TITLE OF INVENTION: Method for Isolation and Purification of
; FILE REFERENCE: 44149-3US1
; CURRENT APPLICATION NUMBER: US/10/368,046
; PRIOR APPLICATION NUMBER: US 60/356,119
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,161
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,118
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,133
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,157
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,156
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,123
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,113
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,154
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,135
; PRIOR FILING DATE: 2002-02-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HPV-16 L2/E6 fusion protein
US-10-368-046-10

Query Match      38.9%; Score 323; DB 4; Length 536;
Best Local Similarity 100.0%; Pred. No. 5,5e-26;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MFDDPQRRPKLPLQCTELQTTIHDIILECVCKQQLLRREYVDFAFRDLCIYRDGNP 59
Db      478 MFDDPQRRPKLPLQCTELQTTIHDIILECVCKQQLLRREYVDFAFRDLCIYRDGNP 536

RESULT 74
US-10-367-367-10
; Sequence 10, Application US/10367367
; Publication No. US20040121465A1
; GENERAL INFORMATION:
; APPLICANT: Robin A. Robinson
; APPLICANT: Robin A. Robinson
; TITLE OF INVENTION: Optimization of Gene Sequences of
; FILE REFERENCE: 44149-2US1
; CURRENT APPLICATION NUMBER: US/10/367,367
; PRIOR APPLICATION NUMBER: US 60/356,119
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,161
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,118
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,133
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,157
```

```
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,156
; PRIOR FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HPV-16 L2/E6 fusion protein
US-10-367-367-10

Query Match      38.9%; Score 323; DB 4; Length 536;
Best Local Similarity 100.0%; Pred. No. 5,5e-26;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MFDDPQRRPKLPLQCTELQTTIHDIILECVCKQQLLRREYVDFAFRDLCIYRDGNP 59
Db      478 MFDDPQRRPKLPLQCTELQTTIHDIILECVCKQQLLRREYVDFAFRDLCIYRDGNP 536

RESULT 75
US-10-918-337-10
; Sequence 10, Application US/10918337
; Publication No. US20050118191A1
; GENERAL INFORMATION:
; APPLICANT: NOVAVAX, INC., et al.
; TITLE OF INVENTION: Optimization of Gene Sequences of
; FILE REFERENCE: 19065/2132
; CURRENT APPLICATION NUMBER: US/10/918,337
; PRIOR FILING DATE: 2004-08-13
; PRIOR APPLICATION NUMBER: PCT/US03/04473
; PRIOR FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 60/356,119
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,161
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,118
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,133
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,157
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,156
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,154
; PRIOR FILING DATE: 2002-02-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HPV-16 L2/E6 fusion protein
US-10-918-337-10

Query Match      38.9%; Score 323; DB 5; Length 536;
Best Local Similarity 100.0%; Pred. No. 5,5e-26;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MFDDPQRRPKLPLQCTELQTTIHDIILECVCKQQLLRREYVDFAFRDLCIYRDGNP 59
Db      478 MFDDPQRRPKLPLQCTELQTTIHDIILECVCKQQLLRREYVDFAFRDLCIYRDGNP 536
```

```

RESULT 76
US-10-367-057-11
; Sequence 11, Application US/10367057
; Publication No. US20050100554A1
; GENERAL INFORMATION:
; APPLICANT: Cuthill, Scott;
; APPLICANT: Jackson, Amanda;
; APPLICANT: Lewin, David A.;
; APPLICANT: Ooi, Chean Eng
; TITLE OF INVENTION: Complexes of Using Same
; FILE REFERENCE: 21402-559
; CURRENT APPLICATION NUMBER: US/10/367,057
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/7256,911
; PRIOR FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 198
; SOFTWARE: Curoseqqlst version 0.1
; SEQ ID NO 11
; LENGTH: 150
; TYPE: PR1
; ORGANISM: Homo sapiens
; US-10-367-057-11

```

```

RESULT 77
US-10-751-845-159
; Sequence 159, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chicz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751, 845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 159
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial fusion sequence
; US-10-751-845-159

```

Query Match 22.8%; Score 189; DB 5; Length 119;  
 Best Local Similarity 35.3%; Pred. NO. 2.9e-12;  
 Matches 48; Conservative 14; Mismatches 32; Indels 42; Gaps 4;  
 8 RPKRLPOLCTELQTTIHDIIEECVYCKQQLRRREYDAPFDLCIVYDGNPYAVXDKL 67

Db 2 RPYKLPDLCTELANTSPQDIEITCVCKTVALBELTEVEPEFAK-----42  
 QY 68 KFSKSKSEIYHNYCYSYGTLEEQYNNKPLCDLLIRINQKELCEBEKHIDKKRF--12  
 Db 43 -----SYGDTLEKLTNTGTGYNLLIRCLRQKKATLQDVLVHLEPONEIPV 88  
 QY 126 HNRGRWTRCWSCCR 141  
 Db 89 H-----TMLCM-CKK 97

```

RESULT 78
US-10-476-570-19
; Sequence 19, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; TITLE OF INVENTION: papillomavirus proteins and uses thereof
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 33
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 14-46
US-10-476-570-19

```

Query Match	21.3%;	Score 177;	DB 4;	Length 33;
Best Local Similarity	100.0%;	Pred. No. 1,3e-11;		
Matches	33;	Conservative	0;	Mismatches 0;
				Indels 0;
				Gaps 0;
QY	7	ERPRKLPOLCTELQTTIHDIILLECVCYKQOILRR	39	
Db	1	ERPRKLPOLCTELQTTIHDIILLECVCYKQOILRR	33	

```

, RESULT 79
, US-10-476-570-9
, Sequence 9, Application US/10476570
, Publication No. US20040170644A1
, GENERAL INFORMATION:
, APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
, APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
, APPLICANT: MAILLIERE, Bernard
, APPLICANT: BOURGAULT-VILLADA, Isabelle
, APPLICANT: POUVELLE-MORATILLE, Sandra
, APPLICANT: GUILLET, Jean-Geard
, TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
, FILE OF INVENTION: papillomavirus proteins and uses thereof
, PILE REFERENCE: 45636-5071-US
, CURRENT APPLICATION NUMBER: US/10/476,570
, CURRENT FILING DATE: 2003-11-04
, PRIOR APPLICATION NUMBER: PCT/FR02/01533
, PRIOR FILING DATE: 2002-05-03
, PRIOR APPLICATION NUMBER: FR 01 05980
, PRIOR FILING DATE: 2001-05-04
, NUMBER OF SEQ ID NOS: 63
, SOFTWARE: PatentIn Ver. 2.1

```

```
; SEQ ID NO 9
; LENGTH: 32
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 14-45
US-10-476-570-9
```

```
Query Match      20.7%; Score 172; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.5e-11;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      7 ERRKLPOLCTELQTTIHDIILCEVCYCKQQL 38
Db      1 ERRKLPOLCTELQTTIHDIILCEVCYCKQQL 32
```

```
RESULT 80
US-10-476-570-53
; Sequence 53, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; TITLE OF INVENTION: Papillomavirus proteins and uses thereof
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; PRIOR FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 53
; LENGTH: 30
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 15-44
US-10-476-570-53
```

```
Query Match      19.6%; Score 163; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.9e-10;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      8 RPRKLPOLCTELQTTIHDIILCEVCYCKQQL 37
Db      1 RPRKLPOLCTELQTTIHDIILCEVCYCKQQL 30
```

```
RESULT 81
US-10-858-384-4
; Sequence 4, Application US/10858384
; Publication No. US20050033025A1
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT-VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
; TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
; FILE REFERENCE: 0508-1037-1
; CURRENT APPLICATION NUMBER: US/10/858,384
; PRIOR FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: FR 9907012
```

```
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin Ver. 3.2
; SEQ ID NO 4
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of the Artificial Sequence: Peptide fragment
; OTHER INFORMATION: for E6 of HPV
US-10-858-384-4
```

```
Query Match      19.6%; Score 163; DB 5; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.9e-10;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      8 RPRKLPOLCTELQTTIHDIILCEVCYCKQQL 37
Db      1 RPRKLPOLCTELQTTIHDIILCEVCYCKQQL 30
```

```
RESULT 82
US-10-476-570-55
; Sequence 55, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; TITLE OF INVENTION: Papillomavirus proteins and uses thereof
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; PRIOR FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 55
; LENGTH: 29
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 80-108
US-10-476-570-55
```

```
Query Match      19.2%; Score 159; DB 4; Length 29;
Best Local Similarity 96.6%; Pred. No. 1e-09;
Matches 28; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      73 ISEYRHYCVSYGTTLEQQYNKPLCDLLI 101
Db      1 ISEYRHYCVSYGTTLEQQYNKPLCDLLI 29
```

```
RESULT 83
US-10-858-384-8
; Sequence 8, Application US/10858384
; Publication No. US20050033025A1
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT-VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
; TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
```

```
; FILE REFERENCE: 0508-1037-1
; CURRENT APPLICATION NUMBER: US/10/858,384
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: FR 9907012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin Ver. 3.2
; SEQ ID NO 8
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of the Artificial Sequence: Peptide fragment
; OTHER INFORMATION: for E6 of HPV
US-10-858-384-8

Query Match      19.2%; Score 159; DB 5; Length 29;
Best Local Similarity 96.6%; Pred. No. 1e-09;
Matches 28; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      73 ISEYRHVCYSYGTTLEQYNNKPLCDLLI 101
Db      1 ISEYRHVCYSLYGTTLEQYNNKPLCDLLI 29

RESULT 84
US-10-476-570-13
; Sequence 13, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIER, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUELLE-MORATILLE, Sandra
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; FILE REFERENCE: 4536-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 13
; LENGTH: 29
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 91-119
US-10-476-570-13

Query Match      18.9%; Score 157; DB 4; Length 29;
Best Local Similarity 96.6%; Pred. No. 1.7e-09;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      84 YGTTLEQYNNKPLCDLLIRICINXKPLCP 112
Db      1 YGTTLEQYNNKPLCDLLIRICINXKPLCP 29

RESULT 85
US-11-021-949-5
; Sequence 5, Application US/11021949
; Publication No. US20050142541A1
; GENERAL INFORMATION:
; APPLICANT: LU PETER
; APPLICANT: GARMAN, JONATHAN DAVID
; APPLICANT: BELMARES, MICHAEL P.
; APPLICANT: DIAZ-SARMIENTO, CHAMORRO SOMOZA
```

```
; APPLICANT: SCHWEIZER, JOHANNES
; TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRAINS OF HPV
; FILE REFERENCE: VITA-012
; CURRENT APPLICATION NUMBER: US/11/021,949
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: 60/532,373
; PRIOR FILING DATE: 2003-12-23
; NUMBER OF SEQ ID NOS: 361
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 24
; TYPE: PRT
; ORGANISM: human papilloma virus (HPV)
US-11-021-949-5

Query Match      17.6%; Score 146; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.1e-08;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      117 RHLDKQRFPHNRGRWTRCSCC 140
Db      1 RHLDKQRFPHNRGRWTRCSCC 24

RESULT 86
US-10-367-057-23
; Sequence 23, Application US/10367057
; Publication No. US20050100554A1
; GENERAL INFORMATION:
; APPLICANT: Cuthill, Scott;
; APPLICANT: Jackson, Amanda;
; APPLICANT: Lewin, David A.;
; APPLICANT: Ooi, Chean Eng
; TITLE OF INVENTION: Complexes and Methods of Using Same
; FILE REFERENCE: 21402-559
; CURRENT APPLICATION NUMBER: US/10/367,057
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/256,911
; PRIOR FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 198
; SOFTWARE: CuroseqList version 0.1
; SEQ ID NO 23
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-367-057-23

Query Match      16.4%; Score 136.5; DB 5; Length 140;
Best Local Similarity 28.0%; Pred. No. 1.7e-06;
Matches 37; Conservative 21; Mismatches 73; Indels 1; Gaps 1;

Qy      10 RKLQCLTELQTTIHDIILECVYCKQQLRREYDFRPLCIYRDGNFYAXDKLKF 69
Db      6 RTVQQLSESLCIPYIDVLLPCNFCNYSNAEKLLFHPDLHLYWRNVLVFGCCGCAAT 65

Qy      70 YSKISEYRHVCYSYGTTLEQYNNKPLCDLLIRICINXKPLCEPEKORHLDKORFNIR 129
Db      66 VSLIEFVLYQESYEVEIEIIDRPLQIELKCVTICKLSVAEKLEVSNGERHVR 125

Qy      130 GRWTRCSCCR 141
Db      126 NRLKAKC-SLCR 136

RESULT 87
US-11-021-949-1
; Sequence 1, Application US/11021949
; Publication No. US20050142541A1
; GENERAL INFORMATION:
; APPLICANT: LU, PETER
; APPLICANT: GARMAN, JONATHAN DAVID
; APPLICANT: BELMARES, MICHAEL P.
```

```

; APPLICANT: DIAZ-SABMIENTO, CHAMORO SOMOZA
; APPLICANT: SCHWEIZER, JOHANNES
; TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRAINS OF HPV
; TITLE OF INVENTION: AND METHODS OF THEIR USE
; FILE REFERENCE: VITA-012
; CURRENT APPLICATION NUMBER: US/11/021,949
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: 60/532,373
; PRIOR FILING DATE: 2003-12-23
; NUMBER OF SEQ ID NOS: 361
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 25
; TYPE: PRT
; ORGANISM: human papilloma virus (HPV)
US-11-021-949-1

Query Match          16.4%; Score 136; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.6e-07;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 FODPQERPRRLPOLCTELQTTIHDI 26
Db      1 FODPQERPRRLPOLCTELQTTIHDI 25

RESULT 89
US-10-476-570-40
; Sequence 40, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MILLERE, Bernard
; APPLICANT: BOURGault-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from B6 and/or E7
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 23
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 118-140
US-10-476-570-40

Query Match          16.3%; Score 135; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 3e-07;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      111 CPEKORHLDKORFHNIRGRWT 133
Db      1 CPEKORHLDKORFHNIRGRWT 23

RESULT 89
US-10-476-570-44
; Sequence 44, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MILLERE, Bernard
```

```

; APPLICANT: BOURGault-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from B6 and/or E7
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
; LENGTH: 24
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 135-158
US-10-476-570-44

Query Match          16.3%; Score 135; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 3.2e-07;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      128 IGRMTGRCMCCRSRTTRRRTQL 151
Db      1 IGRMTGRCMCCRSRTTRRRTQL 24

RESULT 90
US-10-751-845-65
; Sequence 65, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Human Papilloma virus
US-10-751-845-65

Query Match          15.9%; Score 132; DB 5; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.7e-07;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      37 LIRREYVDPAFRDLCTVIRGDNFY 60
Db      1 LIRREYVDPAFRDLCTVIRGDNFY 24

RESULT 91
US-10-476-570-56
; Sequence 56, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
```

```
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
; LENGTH: 22
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 118-139
US-10-476-570-56
```

```
Query Match 15.7%; Score 130; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 1e-06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 111 CPEKQRHLDKKQRFHNIRGM 132
Db 1 CPEKQRHLDKKQRFHNIRGM 22
```

```
RESULT 92
US-10-858-384-10
; Sequence 10, Application US/10858384
; Publication No. US2005003025A1
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCES
; APPLICANT: FERRIS, ESTELLE
; TITLE OF INVENTION: POLYPEPTIDE PROTEIN FRAGMENTS OF THE E6 PROTEIN
; TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
; FILE REFERENCE: 0508-1037-1
; CURRENT APPLICATION NUMBER: US/10/858,384
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: FR 9907012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 10
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of the Artificial Sequence: Peptide fragment
US-10-858-384-10
```

```
Query Match 15.7%; Score 130; DB 5; Length 22;
Best Local Similarity 100.0%; Pred. No. 1e-06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 111 CPEKQRHLDKKQRFHNIRGM 132
Db 1 CPEKQRHLDKKQRFHNIRGM 22
```

```
RESULT 93
US-10-751-845-152
; Sequence 152, Application US/10751845
```

```
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chicz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 152
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Human Papilloma virus
US-10-751-845-152
```

```
Query Match 15.7%; Score 130; DB 5; Length 42;
Best Local Similarity 58.5%; Pred. No. 2.1e-06;
Matches 24; Conservative 6; Mismatches 11; Indels 0; Gaps 0;
```

```
OY 8 RPRKLPOLCTELQTHIDILCEVCYCKQDLREYVDFAR 48
Db 2 RPYKLPOLCTELNTSLQDILITCVYCTVLETFEFAFK 42
```

```
RESULT 94
US-10-751-845-66
; Sequence 66, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chicz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Human Papilloma virus
US-10-751-845-66
```

```
Query Match 15.2%; Score 126; DB 5; Length 23;
Best Local Similarity 95.7%; Pred. No. 2.9e-06;
Matches 22; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 72 KISEYRHYCYSVYGTLEQYNNK 94
Db 1 KISEYRHYCYSLYGTLEQYNNK 23
```

```
RESULT 95
US-10-858-384-6
; Sequence 6, Application US/10858384
; Publication No. US2005003025A1
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
```

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; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCES
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIDIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
; TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: 0508-1037-1
; CURRENT APPLICATION NUMBER: US/10/858,384
; PRIOR FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: FR 9907012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin Ver. 3.2
; SEQ ID NO 6
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of the Artificial Sequence: Peptide fragment
; US-10-858-384-6

Query Match          14.9%; Score 124; DB 5; Length 22;
Best Local Similarity 100.0%; Pred. No. 4.5e-06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 RREYDFAFRDLCIVYRDGNPY 60
DB 1 RREYDFAFRDLCIVYRDGNPY 22

RESULT 96
US-11-021-949-3
; Sequence 3, Application US/11021949
; Publication No. US20050142541A1
; GENERAL INFORMATION:
; APPLICANT: LU, PETER
; APPLICANT: GARMAN, JONATHAN DAVID
; APPLICANT: BELMARES, MICHAEL P.
; APPLICANT: DIAZ-SARMIENTO, CHAMORRO SOMOZA
; APPLICANT: SCHWEIZER, JOHANNES
; TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRAINS OF HPV
; TITLE OF INVENTION: AND METHODS OF THEIR USE
; FILE REFERENCE: VITA-012
; CURRENT APPLICATION NUMBER: US/11/021,949
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: 60/532,373
; PRIOR FILING DATE: 2003-12-23
; NUMBER OF SEQ ID NOS: 361
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 23
; TYPE: PRT
; ORGANISM: human papilloma virus (HPV)
; US-11-021-949-3

Query Match          14.3%; Score 119; DB 6; Length 23;
Best Local Similarity 95.7%; Pred. No. 1.6e-05;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 99 LIRICINQKPLCPPEKORHLDK 121
DB 1 LIRICINQKPLCPPEKORHLDK 23

RESULT 97
US-10-476-570-27
; Sequence 27, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
```

```

; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; TITLE OF INVENTION: papillomavirus proteins and uses thereof
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 27
; LENGTH: 23
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 44-67
; US-10-476-570-27

Query Match          13.9%; Score 115.5; DB 4; Length 23;
Best Local Similarity 95.8%; Pred. No. 3.9e-05;
Matches 23; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 37 LREYVDFAFRDLCIVYRDGNPY 60
DB 1 LREYVDFAFRDLCIVYRDGNPY 23

RESULT 98
US-10-938-249-513
; Sequence 513, Application US/10938249
; Publication No. US20050037969A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Peter S.
; APPLICANT: Rabinowitz, Joshua D.
; APPLICANT: Schweizer, Johannes
; APPLICANT: Arbor Vita Corporation
; TITLE OF INVENTION: Molecular Interactions in Hematopoietic
; TITLE OF INVENTION: Cells
; FILE REFERENCE: 020054-001130US
; CURRENT APPLICATION NUMBER: US/10/938,249
; CURRENT FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: US/09/724,553
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 60/134,114
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/134,117
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/134,118
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/160,860
; PRIOR FILING DATE: 1999-10-21
; PRIOR APPLICATION NUMBER: US 60/162,498
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 60/170,453
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: US 60/176,195
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: US 60/182,296
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: US 60/196,267
; PRIOR FILING DATE: 2000-04-11
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 543
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 513
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
```

```
; FEATURE:
; OTHER INFORMATION: HPV16 E6 C-terminal
US-10-938-249-513

Query Match      13.9%; Score 115; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.7e-05;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      132 WTGRCMSCRSSRRTRETOL 151
Db      1 WTGRCMSCRSSRRTRETOL 20

RESULT 99
US-10-476-570-41
; Sequence 41, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MATIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 20
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 121-140
US-10-476-570-41

Query Match      13.7%; Score 114; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.8e-05;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      114 EKQRHLDKQRFNIRGRWT 133
Db      1 EKQRHLDKQRFNIRGRWT 20

RESULT 100
US-10-612-818-4
; Sequence 4, Application US/10612818
; Publication No. US20040110925A1
; GENERAL INFORMATION:
; APPLICANT: Impact Diagnostics
; APPLICANT: Impact Diagnostics
; TITLE OF INVENTION: Peptides from the E2, E6 and E7 Proteins of Human Papillomavirus
; TITLE OF INVENTION: 18 for Detecting and/or Diagnosing Cervical and Other Human Pap
; FILE REFERENCE: 3352-2-2
; CURRENT APPLICATION NUMBER: US/10/612,818
; CURRENT FILING DATE: 2003-07-01
; PRIOR APPLICATION NUMBER: US 60/394,172
; PRIOR FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 09/828,645
; PRIOR FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 22
```

```
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Derived from the E6 early coding region of HPV 16
US-10-612-818-4

Query Match      13.7%; Score 114; DB 4; Length 22;
Best Local Similarity 95.5%; Pred. No. 5.4e-05;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      55 RDGNPYAVXDCKLKFYSKISEY 76
Db      1 RDGNPYAVCDCKLKFYSKISEY 22
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Search completed: May 27, 2006, 05:37:51  
Job time : 161.064 secs

GenCore version 5.1.8  
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OM protein - protein search, using bw model

Run on: May 27, 2006, 05:33:42 ; Search time 10.3092 Seconds

(without alignments)  
163.129 Million cell updates/sec

Title: US-10-530-253-13ED

Perfect score: 830  
Sequence: 1 MWDPPERRRKLPLQCTELQ.....WTGRCMSCCRSSRTRETQL 151

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 56051 seqs, 1113735 residues

Total number of hits satisfying chosen parameters: 56051

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 100 summaries

Database :

Published Applications AA New:\*

- 1: /EMC\_Celerra\_SIDS3/prodata/1/pubppaa/US09\_NEW\_PUB pep.\*
- 2: /EMC\_Celerra\_SIDS3/prodata/1/pubppaa/US06\_NEW\_PUB pep.\*
- 3: /EMC\_Celerra\_SIDS3/prodata/1/pubppaa/US07\_NEW\_PUB pep.\*
- 4: /EMC\_Celerra\_SIDS3/prodata/1/pubppaa/US08\_NEW\_PUB pep.\*
- 5: /EMC\_Celerra\_SIDS3/prodata/1/pubppaa/PC7\_NEW\_PUB pep.\*
- 6: /EMC\_Celerra\_SIDS3/prodata/1/pubppaa/US10\_NEW\_PUB pep.\*
- 7: /EMC\_Celerra\_SIDS3/prodata/1/pubppaa/US11\_NEW\_PUB pep.\*
- 8: /EMC\_Celerra\_SIDS3/prodata/1/pubppaa/US60\_NEW\_PUB pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	74.5	9.0	591	US-10-933-854-4	Sequence 4, Appl1
2	74.5	9.0	591	US-10-933-854-6	Sequence 6, Appl1
3	74.5	9.0	609	US-10-933-854-2	Sequence 2, Appl1
4	72.5	8.7	800	US-10-953-349-33871	Sequence 33871, A
5	72.5	8.7	809	US-10-953-349-33870	Sequence 33870, A
6	72.5	8.7	867	US-10-953-349-33869	Sequence 33869, A
7	71	8.6	531	US-11-293-697-2762	Sequence 2762, Ap
8	65	7.8	369	US-10-953-349-17182	Sequence 17182, Ap
9	63.5	7.7	419	US-10-953-349-6306	Sequence 6306, Ap
10	63.5	7.7	515	US-10-953-349-6305	Sequence 6305, Ap
11	63.5	7.6	540	US-10-953-349-6304	Sequence 6304, Ap
12	63	7.6	247	US-10-953-349-32521	Sequence 32521, A
13	63	7.6	276	US-10-953-349-32520	Sequence 32520, A
14	63	7.6	307	US-10-953-349-32519	Sequence 32519, A
15	62.5	7.5	278	US-11-293-697-4876	Sequence 4876, Ap
16	62.5	7.5	472	US-11-106-014-8	Sequence 8, Appl1
17	62	7.5	417	US-10-196-749-474	Sequence 474, App
18	62	7.5	1056	US-10-505-928-825	Sequence 225, App
19	61.5	7.4	176	US-10-953-349-18091	Sequence 18091, A
20	61.5	7.4	208	US-10-953-349-18090	Sequence 18090, A
21	61.5	7.4	220	US-10-953-349-18089	Sequence 18089, A
22	61.5	7.4	705	US-11-293-697-4346	Sequence 4346, Ap
23	61	7.3	259	US-10-953-349-19918	Sequence 19918, A
24	61	7.3	355	US-10-953-349-19917	Sequence 19917, A
25	60.5	7.3	267	US-10-953-349-28497	Sequence 28497, A

26	60.5	7.3	314	US-10-538-066-365	Sequence 365, App
27	60.5	7.3	706	US-11-293-697-3919	Sequence 3919, Ap
28	60.5	7.3	971	US-10-505-928-397	Sequence 397, App
29	60.5	7.3	1085	US-10-505-928-175	Sequence 175, App
30	60	7.2	867	US-11-293-697-33034	Sequence 3034, Ap
31	59	7.1	233	US-10-953-349-13389	Sequence 13389, A
32	59	7.1	258	US-10-953-349-1032	Sequence 1032, Ap
33	59	7.1	369	US-10-953-349-1031	Sequence 1031, Ap
34	59	7.1	376	US-10-953-349-1030	Sequence 1030, Ap
35	59	7.1	385	US-10-953-349-13388	Sequence 13388, A
36	59	7.1	400	US-10-953-349-13387	Sequence 13387, A
37	59	7.1	428	US-10-953-349-25008	Sequence 25008, A
38	59	7.1	433	US-10-953-349-25007	Sequence 25007, A
39	59	7.1	436	US-10-953-349-25006	Sequence 25006, A
40	58.5	7.0	204	US-10-953-349-37463	Sequence 37463, A
41	58.5	7.0	251	US-10-953-349-38140	Sequence 38140, A
42	58.5	7.0	280	US-10-953-349-38139	Sequence 38139, A
43	58.5	7.0	421	US-10-953-349-22153	Sequence 22153, A
44	58.5	7.0	471	US-10-953-349-22152	Sequence 22152, A
45	58.5	7.0	492	US-10-953-349-22151	Sequence 22151, A
46	58.5	7.0	708	US-11-170-482-16	Sequence 16, Appl
47	58	7.0	152	US-10-953-349-24130	Sequence 24130, A
48	58	7.0	177	US-10-953-349-24129	Sequence 24129, A
49	57.5	6.9	264	US-10-953-349-22949	Sequence 22949, A
50	57.5	6.9	359	US-10-953-349-22948	Sequence 22948, A
51	57.5	6.9	380	US-10-953-349-22312	Sequence 22312, A
52	57.5	6.9	393	US-10-953-349-22947	Sequence 22947, A
53	57.5	6.9	423	US-10-953-349-22311	Sequence 22311, A
54	57.5	6.9	429	US-10-953-349-21322	Sequence 21322, A
55	57.5	6.9	487	US-10-953-349-21321	Sequence 21321, A
56	57.5	6.9	495	US-10-953-349-22310	Sequence 22310, A
57	57.5	6.9	518	US-10-953-349-12540	Sequence 12540, A
58	57	6.9	320	US-10-953-349-12540	Sequence 12540, A
59	56.5	6.8	166	US-11-318-156-6	Sequence 6, Appl1
60	56.5	6.8	185	US-11-293-697-33341	Sequence 3341, Ap
61	56.5	6.8	233	US-11-318-156-2	Sequence 2, Appl1
62	56.5	6.8	516	US-10-953-349-3991	Sequence 3991, Ap
63	56.5	6.8	528	US-10-953-349-3990	Sequence 3990, Ap
64	56.5	6.8	547	US-10-953-349-3989	Sequence 3989, Ap
65	56.5	6.8	840	US-11-293-697-3121	Sequence 3121, Ap
66	56.5	6.8	938	US-11-293-697-3838	Sequence 3838, Ap
67	56	6.7	233	US-10-953-349-19251	Sequence 95, Appl
68	56	6.7	279	US-11-259-950-95	Sequence 19822, A
69	56	6.7	291	US-10-953-349-19822	Sequence 19822, A
70	56	6.7	303	US-10-953-349-19821	Sequence 19820, A
71	56	6.7	309	US-10-953-349-19820	Sequence 19820, A
72	56	6.7	335	US-10-953-349-6767	Sequence 6767, Ap
73	56	6.7	385	US-10-953-349-19249	Sequence 19249, A
74	56	6.7	410	US-10-953-349-19249	Sequence 19249, A
75	55.5	6.7	179	US-10-953-349-8916	Sequence 8916, Ap
76	55.5	6.7	274	US-10-953-349-34190	Sequence 34190, A
77	55.5	6.7	218	US-10-953-349-34189	Sequence 34189, A
78	55.5	6.7	280	US-10-953-349-34188	Sequence 34188, A
79	55.5	6.7	403	US-10-953-349-938	Sequence 938, App
80	55.5	6.7	436	US-10-953-349-937	Sequence 937, App
81	55.5	6.7	456	US-10-953-349-9369	Sequence 9639, App
82	55.5	6.7	508	US-10-953-349-936	Sequence 936, App
83	55.5	6.7	508	US-10-953-349-9368	Sequence 9688, Ap
84	55.5	6.7	538	US-10-953-349-9967	Sequence 9967, Ap
85	55.5	6.7	744	US-11-293-697-4338	Sequence 4398, Ap
86	55.5	6.7	969	US-10-505-928-94	Sequence 94, Appl
87	55	6.6	466	US-10-953-349-9685	Sequence 9685, Ap
88	55	6.6	433	US-10-953-349-9684	Sequence 9684, Ap
89	55	6.6	541	US-11-293-697-3101	Sequence 3101, Ap
90	55	6.6	560	US-10-953-349-9683	Sequence 9683, Ap
91	55	6.6	560	US-10-953-349-9683	Sequence 9683, Ap
92	54.5	6.6	167	US-10-953-349-21080	Sequence 21080, A
93	54.5	6.6	201	US-10-953-349-21079	Sequence 21079, A
94	54.5	6.6	300	US-10-953-349-21078	Sequence 21078, A
95	54.5	6.6	308	US-10-953-349-21078	Sequence 21078, A
96	54.5	6.6	337	US-10-953-349-33223	Sequence 33223, A
97	54.5	6.6	358	US-10-953-349-33222	Sequence 33222, A
98	54.5	6.6	393	US-10-953-349-36844	Sequence 36844, A



RESULT 4  
US-10-953-349-33871  
; Sequence 33871, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nikolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 33871  
; LENGTH: 800  
; TYPE: PRT  
; ORGANISM: Zea mays subsp. mays  
US-10-953-349-33871

Query Match  
Best Local Similarity 23.3%; Pred. No. 3.6;  
Matches 34; Conservative 22; Mismatches 49; Indels 41; Gaps 7;

QY 4 DPGERPRKLPQLCTELQTHDIIIECVYCKQ-----LIRREYV---DFAFRDLCIVY 54  
DB 460 DDNADPRSPKRSCHESRNTVVERNLQTPPKQSHMSTSLKAKCHPLQSTFASPVC--- 516  
QY 55 RDGNPYAVXDKCLK-----FYSKISE-----YRHYC-----YSVYGTLEQQ- 91  
DB 517 ---NPVGNKEKCADVTHTHFSSKILKLAIRINRLCERVOCVEQTERVYVVFQKIIIEQT 573  
QY 92 ---YKPLCDLLIRICINXQKPLCPPEE 114  
DB 574 TLFENRHIDQLICCLYGVAKVQCLE 599

RESULT 5  
US-10-953-349-33870  
; Sequence 33870, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nikolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 33870  
; LENGTH: 809  
; TYPE: PRT  
; ORGANISM: Zea mays subsp. mays  
US-10-953-349-33870

Query Match  
Best Local Similarity 23.3%; Pred. No. 3.6;  
Matches 34; Conservative 22; Mismatches 49; Indels 41; Gaps 7;

QY 4 DPGERPRKLPQLCTELQTHDIIIECVYCKQ-----LIRREYV---DFAFRDLCIVY 54  
DB 469 DDNADPRSPKRSCHESRNTVVERNLQTPPKQSHMSTSLKAKCHPLQSTFASPVC--- 525  
QY 55 RDGNPYAVXDKCLK-----FYSKISE-----YRHYC-----YSVYGTLEQQ- 91  
DB 526 ---NPVGNKEKCADVTHTHFSSKILKLAIRINRLCERVOCVEQTERVYVVFQKIIIEQT 582  
QY 92 ---YKPLCDLLIRICINXQKPLCPPEE 114  
DB 583 TLFENRHIDQLICCLYGVAKVQCLE 608

RESULT 6  
US-10-953-349-33869  
; Sequence 33869, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nikolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 33869  
; LENGTH: 867  
; TYPE: PRT  
; ORGANISM: Zea mays subsp. mays  
US-10-953-349-33869

Query Match  
Best Local Similarity 23.3%; Pred. No. 3.9;  
Matches 34; Conservative 22; Mismatches 49; Indels 41; Gaps 7;

QY 4 DPGERPRKLPQLCTELQTHDIIIECVYCKQ-----LIRREYV---DFAFRDLCIVY 54  
DB 527 DDNADPRSPKRSCHESRNTVVERNLQTPPKQSHMSTSLKAKCHPLQSTFASPVC--- 583  
QY 55 RDGNPYAVXDKCLK-----FYSKISE-----YRHYC-----YSVYGTLEQQ- 91  
DB 584 ---NPVGNKEKCADVTHTHFSSKILKLAIRINRLCERVOCVEQTERVYVVFQKIIIEQT 640  
QY 92 ---YKPLCDLLIRICINXQKPLCPPEE 114  
DB 641 TLFENRHIDQLICCLYGVAKVQCLE 666

RESULT 7  
US-11-293-697-2762  
; Sequence 2762, Application US/11293697  
; Publication No. US20060105376A1  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: Novel full length cDNA  
; FILE REFERENCE: H1-A0106  
; CURRENT APPLICATION NUMBER: US/11/293,697  
; PRIOR FILING DATE: 2005-12-05  
; PRIOR APPLICATION NUMBER: US/10/108,260  
; PRIOR FILING DATE: 2002-03-28  
; NUMBER OF SEQ ID NOS: 5458  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2762  
; LENGTH: 531  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-293-697-2762

Query Match  
Best Local Similarity 22.0%; Pred. No. 3.3;  
Matches 28; Conservative 16; Mismatches 55; Indels 28; Gaps 5;

QY 28 LECVYCKQ---QLIRREYVDAFRDLCIVYRDGNPYAVXDKCLKFYSKISEYRHYCVSVY 85  
DB 175 LGCFKCKSCGKILNME-----YISKDGLPYCEADYHAFGIRCDSCERY---ITG 221  
QY 86 TTLE---QGVYKPLCDLLIRICINXQKPLCPPEKORHLDKORFNNIRGWTGRCMSCRSS 143  
DB 222 RVLEAGEKHVHPSGALCVGC-----GGMFAGEEMVYLGSSIMHPARQQAARTE 270  
QY 144 RTRRETO 150  
DB 271 DRNKETR 277

## RESULT 8

US-10-953-349-17182  
; Sequence 17182, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nickolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 17182  
; LENGTH: 369  
; TYPE: PRT  
; ORGANISM: Glycine max  
US-10-953-349-17182

Query Match 7.8%; Score 65; DB 6; Length 369;  
Best Local Similarity 22.2%; Pred. No. 9.5;  
Matches 39; Conservative 24; Mismatches 59; Indels 54; Gaps 10;

QY 1 MFODPQERPRKLPOLCTELQTTIHDIILECVYCKQQLRREV-----YDFAFRD 41  
DB 62 LKSPLSRP-----LFTAESGIPETIVELLYSPDLMKVDGQNRSLFIHAIHRRQEKI 116  
QY 42 ---YDF-APRDLCTVYRDGNPVAVDKCLKFKYSKI--SEYRHVCYSVYGTLEQYN-- 93  
DB 117 FNLIYDIDGAKHDLITTSYRDNNHNI-----LHLAKGLAPSEQLHY---VSGAALQMORELL 169  
QY 94 -----KELCDLLIRCIHXQKRLCPE-----EKQRLDKQRHNRHNRGWTGRCMSCC 140  
DB 170 WPKXEVEKTIQPLFKELKIDSGRTPOMLFTBEHKELAEGE-----KWLKNTASSC 219

## RESULT 9

US-10-953-349-6306  
; Sequence 6306, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nickolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 6306  
; LENGTH: 419  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
US-10-953-349-6306

Query Match 7.7%; Score 63.5; DB 6; Length 419;  
Best Local Similarity 21.0%; Pred. No. 16;  
Matches 37; Conservative 19; Mismatches 69; Indels 51; Gaps 6;

QY 7 ERPRKLPOLCTELQTTIHDIILECVYCKQQLRREV-----YDFAFRD 49  
DB 194 ESVHKIPNVVGSITVTHIPIAPKRVHVAAYFNKRHTRERNOKTSYSITVGQVNAADGIFTD 253  
QY 50 LCTVYRDGNPVAVDKCLKFKYSKISEYRHVCYSVYGTLEQYNKPLCDLLIRCIHXQKP 109  
DB 254 VCI-----GNPGLTDDQIDLEKSSLSRQARAGMLRDSWIVGNSGFPPLTDYL----- 300  
QY 110 LCPBEKQ-----RHLDKKQ-----RFHNRIGRWTCRCMCCRSSTRRETQ 150  
DB 301 LVPTTRQNLWTQAHAFNBSIGETIGIATAFAERLKGW-----ACIQKRTVEKIQ 350

## RESULT 10

US-10-953-349-6305  
; Sequence 6305, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nickolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 6305  
; LENGTH: 515  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
US-10-953-349-6305

Query Match 7.7%; Score 63.5; DB 6; Length 515;  
Best Local Similarity 21.0%; Pred. No. 19;  
Matches 37; Conservative 19; Mismatches 69; Indels 51; Gaps 6;

QY 7 ERPRKLPOLCTELQTTIHDIILECVYCKQQLRREV-----YDFAFRD 49  
DB 290 ESVHKIPNVVGSITVTHIPIAPKRVHVAAYFNKRHTRERNOKTSYSITVGQVNAADGIFTD 349  
QY 50 LCTVYRDGNPVAVDKCLKFKYSKISEYRHVCYSVYGTLEQYNKPLCDLLIRCIHXQKP 109  
DB 350 VCI-----GNPGLTDDQIDLEKSSLSRQARAGMLRDSWIVGNSGFPPLTDYL----- 356  
QY 110 LCPBEKQ-----RHLDKKQ-----RFHNRIGRWTCRCMCCRSSTRRETQ 150  
DB 397 LVPTTRQNLWTQAHAFNBSIGETIGIATAFAERLKGW-----ACIQKRTVEKIQ 446

## RESULT 11

US-10-953-349-6304  
; Sequence 6304, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nickolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 6304  
; LENGTH: 540  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
US-10-953-349-6304

Query Match 7.7%; Score 63.5; DB 6; Length 540;  
Best Local Similarity 21.0%; Pred. No. 20;  
Matches 37; Conservative 19; Mismatches 69; Indels 51; Gaps 6;

QY 7 ERPRKLPOLCTELQTTIHDIILECVYCKQQLRREV-----YDFAFRD 49  
DB 315 ESVHKIPNVVGSITVTHIPIAPKRVHVAAYFNKRHTRERNOKTSYSITVGQVNAADGIFTD 374  
QY 50 LCTVYRDGNPVAVDKCLKFKYSKISEYRHVCYSVYGTLEQYNKPLCDLLIRCIHXQKP 109  
DB 375 VCI-----GNPGLTDDQIDLEKSSLSRQARAGMLRDSWIVGNSGFPPLTDYL----- 421  
QY 110 LCPBEKQ-----RHLDKKQ-----RFHNRIGRWTCRCMCCRSSTRRETQ 150  
DB 422 LVPTTRQNLWTQAHAFNBSIGETIGIATAFAERLKGW-----ACIQKRTVEKIQ 471

## RESULT 12

```
US-10-953-349-32521
; Sequence 32521, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 32521
; LENGTH: 247
; TYPE: PRN
; ORGANISM: Trilicium aestivum
US-10-953-349-32521

Query Match      7.6%; Score 63; DB 6; Length 247;
Best Local Similarity 25.7%; Pred. No. 9.9;
Matches 19; Conservative 11; Mismatches 10; Indels 34; Gaps 4;

QY 60 YAVXDKLKFYSKISEYRHC-----YSYVG-----TTLQO----- 90
DB 63 YGFYDECLRRKYSVNWVR-YCTEIFDYLISALIENTKIFSVHGLSPATITLQDIRIVDR 121
QY 91 ----QYKNPLCDLL 100
DB 122 KQEVPHDGMCDLL 135

RESULT 13
US-10-953-349-32520
; Sequence 32520, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 32520
; LENGTH: 276
; TYPE: PRN
; ORGANISM: Trilicium aestivum
US-10-953-349-32520

Query Match      7.6%; Score 63; DB 6; Length 276;
Best Local Similarity 25.7%; Pred. No. 11;
Matches 19; Conservative 11; Mismatches 10; Indels 34; Gaps 4;

QY 60 YAVXDKLKFYSKISEYRHC-----YSYVG-----TTLQO----- 90
DB 92 YGFYDECLRRKYSVNWVR-YCTEIFDYLISALIENTKIFSVHGLSPATITLQDIRIVDR 150
QY 91 ----QYKNPLCDLL 100
DB 151 KQEVPHDGMCDLL 164

RESULT 14
US-10-953-349-32519
; Sequence 32519, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
```

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; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 32519
; LENGTH: 307
; TYPE: PRN
; ORGANISM: Trilicium aestivum
US-10-953-349-32519

Query Match      7.6%; Score 63; DB 6; Length 307;
Best Local Similarity 25.7%; Pred. No. 13;
Matches 19; Conservative 11; Mismatches 10; Indels 34; Gaps 4;

QY 60 YAVXDKLKFYSKISEYRHC-----YSYVG-----TTLQO----- 90
DB 123 YGFYDECLRRKYSVNWVR-YCTEIFDYLISALIENTKIFSVHGLSPATITLQDIRIVDR 181
QY 91 ----QYKNPLCDLL 100
DB 182 KQEVPHDGMCDLL 195

RESULT 15
US-11-293-697-4876
; Sequence 4876, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4876
; LENGTH: 278
; TYPE: PRN
; ORGANISM: Homo sapiens
US-11-293-697-4876

Query Match      7.5%; Score 62.5; DB 7; Length 278;
Best Local Similarity 22.3%; Pred. No. 13;
Matches 33; Conservative 18; Mismatches 56; Indels 41; Gaps 8;

QY 30 CVYCKOQLRREYVDFAF-----RDLCIVYRDGNPYAVXDKLKFYSKISEYRHC--- 80
DB 7 CTCKHQK-----PFPEALSGOQQLCKECLRIAPVVKCTYCRTEYQDSKWTICKC 58
QY 81 ---YSYVGTTLQOYKNPLCDLL-----RCINXQPLCPB-----EKORHLDKQ 123
DB 59 AQNVQLYGTGPKQCY-----CNIIAFLGNKCGRCSTSEKKGYPYSCGCKQCCAFDRKD 114
QY 124 RFINIRGRMTGRGMSCCRS-SRTRRERQ 150
DB 115 DRKKVQDKLL-CWLCTLSYKRVLQKTK 140

RESULT 16
US-11-106-014-8
; Sequence 8, Application US/11106014
; Publication No. US20060088846A1
; GENERAL INFORMATION:
; APPLICANT: Pagano, Michele
; APPLICANT: Chianur, Dah Sharim
; APPLICANT: Latres, Esther
; APPLICANT: Stivaestava, Promod
; APPLICANT: Chandawarkar, Rajiv
; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT
; FILE REFERENCE: 5914-106-999
; CURRENT APPLICATION NUMBER: US/11/106,014
```

CURRENT FILING DATE: 2005-04-13  
PRIOR APPLICATION NUMBER: 10/633,150  
PRIOR FILING DATE: 2003-07-30  
PRIOR APPLICATION NUMBER: 10/042,417  
PRIOR FILING DATE: 2002-01-07  
PRIOR APPLICATION NUMBER: 09/385,219  
PRIOR FILING DATE: 1999-08-27  
PRIOR APPLICATION NUMBER: 60/118,568  
PRIOR FILING DATE: 1999-02-03  
PRIOR APPLICATION NUMBER: 60/098,355  
PRIOR FILING DATE: 1998-08-28  
PRIOR APPLICATION NUMBER: 60/124,449  
PRIOR FILING DATE: 1997-03-15  
NUMBER OF SEQ ID NOS: 96  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 8  
LENGTH: 472  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-106-014-8

Query Match 7.5%; Score 62.5; DB 7; Length 472;  
Best Local Similarity 26.3%; Pred. No. 22;  
Matches 26; Conservative 14; Mismatches 40; Indels 19; Gaps 5;

QY 36 QLRB---EYVDFAPRDLCTVYRDNPNYA--VXDKCLKFYSISEYRHYC-----YSV 83  
DB 122 QILKRPISVSDGAFPDYMAVYLMCCPYTRASSSRPMYAVTSFLHSILIEPPRAL 181  
QY 84 YGTTLEQYNNKPLCDLLIRCNXKQPLCPPE--KORHLD 120  
DB 182 FGPRLEQ-----LNTSLVLSLSSEELCPFTAGLPQRQD 215

RESULT 17  
US-10-196-749-474  
Sequence 474, Application US/10196749  
Publication No. US2006094864A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Chen, Jian  
APPLICANT: Deenoyers, Luc  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Pan, James  
APPLICANT: Smith, Victoria  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
TITLE OF INVENTION: ACTIS ENCODING THE SAME  
FILE REFERENCE: P3430R1C340  
CURRENT APPLICATION NUMBER: US/10/196, 749  
CURRENT FILING DATE: 2002-07-16  
PRIOR APPLICATION NUMBER: 10/052586  
PRIOR FILING DATE: 2002-01-15  
PRIOR APPLICATION NUMBER: 60/059263  
PRIOR FILING DATE: 1997-09-18  
PRIOR APPLICATION NUMBER: 60/059266  
PRIOR FILING DATE: 1997-09-18  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/063120  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/063121  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/063486  
PRIOR FILING DATE: 1997-10-21  
PRIOR APPLICATION NUMBER: 60/063540  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/063541  
PRIOR FILING DATE: 1997-10-28

PRIOR APPLICATION NUMBER: 60/063544  
PRIOR FILING DATE: 1997-10-28  
PRIOR Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 612  
SEQ ID NO 474  
LENGTH: 417  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-196-749-474

Query Match 7.5%; Score 62; DB 6; Length 417;  
Best Local Similarity 26.2%; Pred. No. 22;  
Matches 17; Conservative 18; Mismatches 22; Indels 8; Gaps 4;

QY 15 LCTELQTTIHDIILECY-YKQQLRREYVDFAPRDLCTVYRDNPNYA-VXDKCLKFYSKI 73  
DB 174 ICSALATVLLALILLCVYCKRFMEKRP-SWSLRSDIOY-NGSELSCFDR-----POL 226  
QY 74 SEYRH 78  
DB 227 HEYAH 231

RESULT 18  
US-10-505-928-225  
Sequence 225, Application US/10505928  
Publication No. US20060080532A1  
GENERAL INFORMATION:  
APPLICANT: Ludwig, Institute for Cancer Research et al.  
TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES  
FILE REFERENCE: 28967/39178  
CURRENT APPLICATION NUMBER: US/10/505,928  
CURRENT FILING DATE: 2004-08-27  
PRIOR APPLICATION NUMBER: US 60/363,019  
PRIOR FILING DATE: 2002-03-07  
NUMBER OF SEQ ID NOS: 866  
SOFTWARE: PatentIn 3.2  
SEQ ID NO 225  
LENGTH: 1056  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-505-928-225

Query Match 7.5%; Score 62; DB 6; Length 1056;  
Best Local Similarity 26.3%; Pred. No. 60;  
Matches 15; Conservative 12; Mismatches 14; Indels 16; Gaps 2;

QY 87 TLEQYNNKPLCDLL-----IRCNXKQPLCP---BEKORHLDKORFHN 127  
DB 713 TIKQTHSQELCKLMNLTWTERFCALBEKCEINIQKPLSSQGENIOOKSKDIOVNMKTFHS 769

RESULT 19  
US-10-953-349-18091  
Sequence 18091, Application US/10953349  
Publication No. US20060107345A1  
GENERAL INFORMATION:  
APPLICANT: ALEXANDROV, Nicholas et al.  
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
FILE REFERENCE: 2750-1579PUS2  
CURRENT APPLICATION NUMBER: US/10/953,349  
CURRENT FILING DATE: 2004-09-30  
NUMBER OF SEQ ID NOS: 40252  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 18091  
LENGTH: 176  
TYPE: PRT  
ORGANISM: Glycine max  
US-10-953-349-18091

Query Match 7.4%; Score 61.5; DB 6; Length 176;  
Best Local Similarity 21.6%; Pred. No. 9.9;





Db 381 PHSPPKDNNAVYKVCVKCNKSTPEALEHNLQTATNN--PSPCHQKVFPCERYLRRLHP 438  
Qy 43 -YFAFRLDLCIVYRDGNPVAVXOKLKF-----YSKISEYRH-----YCVSYG-- 85  
Db 439 THSGGGKFKQV-----CKKFFREHRLKJLHAHISGEKPKYKSCVCSAFNRK 486  
Qy 86 -----TTLEQYNNKPLCDLLIRCIYNKQK-----PLCPE-- 113  
Db 487 DKLKRNHLIHEPFRKVKYKCPSTHTGCKEKNRP--DLKXAHILSHSGMKLHKALCKSKSF 544  
Qy 114 EKQRLDKQRFNINRGWTRGRCMSCCR 141  
Db 545 SRAHLAEHQRAHT--GNYKFRCCAGCAK 570

RESULT 28  
US-10-505-928-397  
; Sequence 397, Application US/10505928  
; Publication No. US20060088532A1  
; GENERAL INFORMATION:  
; APPLICANT: Ludwig Institute for Cancer Research et al.  
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES  
; FILE REFERENCE: 28967/39178  
; CURRENT APPLICATION NUMBER: US/10/505,928  
; CURRENT FILING DATE: 2004-08-27  
; PRIOR APPLICATION NUMBER: US 60/363,019  
; PRIOR FILING DATE: 2002-03-07  
; NUMBER OF SEQ ID NOS: 866  
; SOFTWARE: PatentIn 3.2  
; SEQ ID NO 397  
; LENGTH: 971  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-505-928-397

Query Match 7.3%; Score 60.5; DB 6; Length 971;  
Best Local Similarity 18.2%; Pred. No. 79;  
Matches 30; Conservative 22; Mismatches 56; Indels 57; Gaps 8;  
Qy 16 CTEPLQTTIHDIIEC-VYCKQ-----QLLRREYVDFAFRDLCIVYRDGNPVAVXDKC 66  
Db 104 CCELA-----IALECRQACKQASSKNDISKVCRKEYNALFS--CISRNE-----MGSVC 151  
Qy 67 LKPYSKISEYRYHYGYVGTLE-----QOYNKPLCDLLIRCI-----X 106  
Db 152 CSYAGHTNCREYCOALFRIDSSPGSQIKAVENYCASISPOLHCVNNYTOGYPMKNPT 211  
Qy 107 OKPLCPEKORHLDKQRFNINRGWTRGRCMSCCRSRTRETOI 151  
Db 212 DSLYCCDRAEDH-----ACONACKRIILMSKTIEM 240

RESULT 29  
US-10-505-928-175  
; Sequence 175, Application US/10505928  
; Publication No. US20060088532A1  
; GENERAL INFORMATION:  
; APPLICANT: Ludwig Institute for Cancer Research et al.  
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES  
; FILE REFERENCE: 28967/39178  
; CURRENT APPLICATION NUMBER: US/10/505,928  
; CURRENT FILING DATE: 2004-08-27  
; PRIOR APPLICATION NUMBER: US 60/363,019  
; PRIOR FILING DATE: 2002-03-07  
; NUMBER OF SEQ ID NOS: 866  
; SOFTWARE: PatentIn 3.2  
; SEQ ID NO 175  
; LENGTH: 1085  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-505-928-175

Query Match 7.3%; Score 60.5; DB 6; Length 1085;

Best Local Similarity 24.4%; Pred. No. 89;  
Matches 20; Conservative 14; Mismatches 27; Indels 21; Gaps 3;  
Qy 25 DILIECYCKQQLLRREYVDFAFRDLCIVYRDGNPVAVXOKLKFYSK-----ISRYRH 78  
Db 230 DVEQVWYCKEKIRIG-SEFSFEEL-----RAQKYNGRRHQGVNEDRH 274  
Qy 79 YCVSYVGTLEQOYNNKPLCDLL 100  
Db 275 YMKRKNAAFEEQLKQKXDEL 296

RESULT 30  
US-11-293-697-3034  
; Sequence 3034, Application US/11293697  
; Publication No. US20060105376A1  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: Novel full length cDNA  
; FILE REFERENCE: H1-A0106  
; CURRENT APPLICATION NUMBER: US/11/293,697  
; CURRENT FILING DATE: 2005-12-05  
; PRIOR APPLICATION NUMBER: US/10/108,260  
; PRIOR FILING DATE: 2002-03-28  
; NUMBER OF SEQ ID NOS: 5458  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3034  
; LENGTH: 867  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-293-697-3034

Query Match 7.2%; Score 60; DB 7; Length 867;  
Best Local Similarity 20.9%; Pred. No. 79;  
Matches 29; Conservative 18; Mismatches 34; Indels 58; Gaps 7;  
Qy 12 LPQLCTELQTTIHDIIECYCKQQLLRREYVDFAFRDLCIVYRDGNPVAVXDKLFEYS 71  
Db 474 LPQLCTAMEQYKGD-----KQVC-----TNIAKIFS 499  
Qy 72 KISEYR-----HYCVSYVGTLEQOYNNKPLCDLLIRCI-----NXQKPLCP 112  
Db 500 KLTSYRDCCTALASYSYCALF--LNLINKYQKQ-DLVAVVVFILGULTAKNNQARQFS 557  
Qy 113 EEK---QRHLDKQRFNIN 128  
Db 558 KEKGSIQTLISLFTFPHQL 576

RESULT 31  
US-10-953-349-13389  
; Sequence 13389, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nicholas et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 13389  
; LENGTH: 233  
; TYPE: PRT  
; ORGANISM: Glycine max  
US-10-953-349-13389

Query Match 7.1%; Score 59; DB 6; Length 233;  
Best Local Similarity 23.9%; Pred. No. 24;  
Matches 37; Conservative 21; Mismatches 53; Indels 44; Gaps 9;  
Qy 11 KLPQLCTELQTTIHDIIECYCKQQLLRREYVDFAFRDLCIVY 54

```
Db      26 KLVQIGSNLELKH--TLQFVEVLQNGTRADALKARTYLAAPFASLNGEFPKLMGCILY 83
Qy      55 R---DGNPYAVXDKLKFYSKISEY-RHYCYSVYGTTLQOYNKPL-----CDLL 100
Db      84 AGRLESSPYSLLSPIHWMETTELARQFC-----TLIGQSYENPLSYAAGVGEGLPIL 138
Qy      101 IRCIN---XOKPLCPSEKOR---HLDKQRFHNI 128
Db      139 LKLANVMAAKQWQEMKQLPVPVELGKEFQFHSI 173

RESULT 32
US-10-953-349-1032
; Sequence 1032, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1032
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-1032

Query Match      7.1%; Score 59; DB 6; Length 258;
Best Local Similarity 29.7%; Pred. No. 27;
Matches 27; Conservative 14; Mismatches 32; Indels 18; Gaps 7;

Qy      1 MFODPQERPRKLPOLCTELQTTIHDIILECYCCKQQLLRREYVDFARFDLCIVYRDGNPY 60
Db      52 MAPDPPE-PQDLPEIC-----RDVME--YSKQVMILGE---FLF-ELLSAALGLNPN 97
Qy      61 AVXD-KCLKFYSKISEYRHYCYs---VYGT 87
Db      98 HLKDMCKLGLRLCHYFPPEPDLTFGTs 128

RESULT 33
US-10-953-349-1031
; Sequence 1031, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1031
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-1031

Query Match      7.1%; Score 59; DB 6; Length 369;
Best Local Similarity 29.7%; Pred. No. 40;
Matches 27; Conservative 14; Mismatches 32; Indels 18; Gaps 7;

Qy      1 MFODPQERPRKLPOLCTELQTTIHDIILECYCCKQQLLRREYVDFARFDLCIVYRDGNPY 60
Db      163 MAPDPPE-PQDLPEIC-----RDVME--YSKQVMILGE---FLF-ELLSAALGLNPN 208
Qy      61 AVXD-KCLKFYSKISEYRHYCYs---VYGT 87
```

```
Db      209 HLKDMCKLGLRLCHYFPPEPDLTFGTs 239

RESULT 34
US-10-953-349-1030
; Sequence 1030, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1030
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-1030

Query Match      7.1%; Score 59; DB 6; Length 376;
Best Local Similarity 29.7%; Pred. No. 41;
Matches 27; Conservative 14; Mismatches 32; Indels 18; Gaps 7;

Qy      1 MFODPQERPRKLPOLCTELQTTIHDIILECYCCKQQLLRREYVDFARFDLCIVYRDGNPY 60
Db      170 MAPDPPE-PQDLPEIC-----RDVME--YSKQVMILGE---FLF-ELLSAALGLNPN 215
Qy      61 AVXD-KCLKFYSKISEYRHYCYs---VYGT 87
Db      216 HLKDMCKLGLRLCHYFPPEPDLTFGTs 246

RESULT 35
US-10-953-349-13388
; Sequence 13388, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13388
; LENGTH: 385
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-13388

Query Match      7.1%; Score 59; DB 6; Length 385;
Best Local Similarity 23.9%; Pred. No. 42;
Matches 37; Conservative 21; Mismatches 53; Indels 44; Gaps 9;

Qy      11 KLPLCTELQTTIHDIILECYCCKQQLLRREYVDFARFDLCIVYRDGNPY 54
Db      178 KLVQIGSNLELKH--TLQFVEVLQNGTRADALKARTYLAAPFASLNGEFPKLMGCILY 235
Qy      55 R---DGNPYAVXDKLKFYSKISEY-RHYCYSVYGTTLQOYNKPL-----CDLL 100
Db      236 AGRLESSPYSLLSPIHWMETTELARQFC-----TLIGQSYENPLSYAAGVGEGLPIL 290
Qy      101 IRCIN---XOKPLCPSEKOR---HLDKQRFHNI 128
Db      291 LKLANVMAAKQWQEMKQLPVPVELGKEFQFHSI 325

RESULT 36
US-10-953-349-13387
```

```

; Sequence 13387, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13387
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Glycine max
; US-10-953-349-13387

```

```

Query Match          7.1%; Score 59; DB 6; Length 400;
Best Local Similarity 23.9%; Pred. No. 44;
Matches 37; Conservative 21; Mismatches 53; Indels 44; Gaps 9;

```

```

Qy      11 KLPOLCTELQTTIHDIIECVCYCKQQLRREYVDFP-----FRDL-----CIVY 54
      193 KLVQIGSNELKIH--TLQFVYVLQNGTRADALKVARTYLAFASLKGEFPLMGCLTY 250
Db
Qy      55 R---DGNPVAVXDKCLKFYKISFY-RHYCYSVYGTTLQOYNKPL-----CDLL 100
      251 AGRLESPYSBELSPHMENTTEBLAQFC-----TLGQSYENPLSVAAVAGVGPIL 305
Db
Qy      101 IRCIN---XOKPLCPREKOR---HLKKORPHNI 128
      306 LKLANVMAKKQKQEMKQLPVPELGEKGFPHSI 340
Db

```

```

RESULT 37
US-10-953-349-25008
; Sequence 25008, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 25008
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Glycine max
; US-10-953-349-25008

```

```

Query Match          7.1%; Score 59; DB 6; Length 428;
Best Local Similarity 28.9%; Pred. No. 47;
Matches 13; Conservative 9; Mismatches 13; Indels 10; Gaps 2;

```

```

Qy      16 CTBLQTTIHDIIEC-----VYCKQQLRREYVDFAPRDL 51
      171 CT-LKQTVKPVLLPCYDLVTRAAVFSRADALVVDGDFGMRDVC 214
Db

```

```

; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 25007
; LENGTH: 433
; TYPE: PRT
; ORGANISM: Glycine max
; US-10-953-349-25007

```

```

Query Match          7.1%; Score 59; DB 6; Length 433;
Best Local Similarity 28.9%; Pred. No. 47;
Matches 13; Conservative 9; Mismatches 13; Indels 10; Gaps 2;

```

```

Qy      16 CTBLQTTIHDIIEC-----VYCKQQLRREYVDFAPRDL 51
      176 CT-LKQTVKPVLLPCYDLVTRAAVFSRADALVVDGDFGMRDVC 219
Db

```

```

RESULT 39
US-10-953-349-25006
; Sequence 25006, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 25006
; LENGTH: 436
; TYPE: PRT
; ORGANISM: Glycine max
; US-10-953-349-25006

```

```

Query Match          7.1%; Score 59; DB 6; Length 436;
Best Local Similarity 28.9%; Pred. No. 48;
Matches 13; Conservative 9; Mismatches 13; Indels 10; Gaps 2;

```

```

Qy      16 CTBLQTTIHDIIEC-----VYCKQQLRREYVDFAPRDL 51
      179 CT-LKQTVKPVLLPCYDLVTRAAVFSRADALVVDGDFGMRDVC 222
Db

```

```

RESULT 40
US-10-953-349-37463
; Sequence 37463, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 37463
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; US-10-953-349-37463

```

```

Query Match          7.0%; Score 58.5; DB 6; Length 204;
Best Local Similarity 34.9%; Pred. No. 24;
Matches 15; Conservative 4; Mismatches 7; Indels 17; Gaps 2;

```

```

Qy      121 KQRFNIRKRWGR-----CNSCRSSSTR 147
      94 QROGRGH-RARGTSRGWRRCSPSPRCSCISCCRCHRR 135
Db

```



QY 104 INXKPLCEPKORHLDKORFNINRGRTGRCMSC 139  
DB 250 QKEREPACPHHCPR-----RCH-----PDCPCPC 273

## RESULT 46

US-11-170-482-16  
; Sequence 16, Application US/11170482  
; Publication No. US2006094037A1  
; GENERAL INFORMATION:  
; APPLICANT: St. George-Hyslop, Peter H.  
; APPLICANT: Fraser, Paul E.  
; APPLICANT: University of Toronto  
; TITLE OF INVENTION: PROTEINS RELATED TO SCHIZOPHRENIA AND USES THEREOF  
; FILE REFERENCE: 1034/1H570  
; CURRENT APPLICATION NUMBER: US/11/170,482  
; CURRENT FILING DATE: 2005-06-28  
; PRIOR APPLICATION NUMBER: US/09/945,258  
; PRIOR FILING DATE: 2001-08-31  
; PRIOR APPLICATION NUMBER: US 60/229,889  
; PRIOR FILING DATE: 2000-09-01  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 16  
; LENGTH: 708  
; TYPE: PRT  
; ORGANISM: mouse  
US-11-170-482-16

Query Match 7.0%; Score 58.5; DB 7; Length 708;

Best Local Similarity 21.2%; Pred. No. 91; Indels 33; Gaps 8;  
Matches 35; Conservative 26; Mismatches 71;

QY 2 PDPOE-----RPRKLPLCTELQTTIHDI-----ILECVYCKQQLRREYVDFAFRD 49  
DB 469 WQSPBEDLNFVTPTAKLANVATVLAVALYELAGTWFSSIQADPQTVTRLLYGFLVRA 528

QY 50 -----LCIVYRDGNPNVAVXKCLFKFSKISEYRHYCSVGTTLLEQYNNKPLCDLIRCI 104  
DB 529 NNSWFOISLKHGDIKRSY-LIDRPLQHYTAVS-----SPNTTYVYQY--ALANLTGKAT 578

QY 105 NXQKPLCEPKORHLDKORFNH--IRGRV-----TGRCMSCRSS 143  
DB 579 NLTRQCCQDPSKVPNESKDIYYSWQGPNNRNTERLPOCVAST 623

## RESULT 47

US-10-953-349-24130  
; Sequence 24130, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nikolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 24130  
; LENGTH: 152  
; TYPE: PRT  
; ORGANISM: Glycine max  
US-10-953-349-24130

Query Match 7.0%; Score 58; DB 6; Length 152;

Best Local Similarity 26.8%; Pred. No. 20; Indels 8; Gaps 3;  
Matches 19; Conservative 15; Mismatches 29;

QY 88 LEOQYNNKPLCDLIRICINXKPLCE---EKORHLDKORFNINRGRTGRC---MSCC 140  
DB 62 LNEBNNKGLLTMISEELNOKIVANETMEHTKQILMDARKTFSHYQ-KEAEKCNIGVETC 120

QY 141 RSRTRRETOL 151  
DB 121 EEARERAEAE 131

## RESULT 48

US-10-953-349-24129  
; Sequence 24129, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nikolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 24129  
; LENGTH: 177  
; TYPE: PRT  
; ORGANISM: Glycine max  
US-10-953-349-24129

Query Match 7.0%; Score 58; DB 6; Length 177;

Best Local Similarity 26.8%; Pred. No. 23; Indels 8; Gaps 3;  
Matches 19; Conservative 15; Mismatches 29;

QY 88 LEOQYNNKPLCDLIRICINXKPLCE---EKORHLDKORFNINRGRTGRC---MSCC 140  
DB 87 LNEBNNKGLLTMISEELNOKIVANETMEHTKQILMDARKTFSHYQ-KEAEKCNIGVETC 145

QY 141 RSRTRRETOL 151  
DB 146 EEARERAEAE 156

## RESULT 49

US-10-953-349-22948  
; Sequence 22948, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nikolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 22948  
; LENGTH: 264  
; TYPE: PRT  
; ORGANISM: Glycine max  
US-10-953-349-22948

Query Match 6.9%; Score 57.5; DB 6; Length 264;

Best Local Similarity 26.7%; Pred. No. 40; Indels 29; Gaps 8;  
Matches 32; Conservative 20; Mismatches 39;

QY 6 QERPRKLPLCTELQTTIHDIILECVYCKQQL---LRREYVDFAFRDLCIVYDGNPYAV 62  
DB 39 QYNNKTLPLQ--TTLKTSVVELDLAALAEHLVKNKEAAD-----RGEKTI-- 83

QY 63 XDKCLFKFSKISEYRHYCSVGTTLLEQYNNKPLCDLIRICINXKPL-CP-EKORHL 120  
DB 84 --KITTLARNV-EMDEYDVMHRSFEER-----EALTRDISCRALGLPLEEPGRYMD 134

RESULT 50  
US-10-953-349-22948  
; Sequence 22948, Application US/10953349

```
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; CURRENT APPLICATION NUMBER: US/10/953,349
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22948
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-22948
```

```
Query Match      6.9%; Score 57.5; DB 6; Length 359;
Best Local Similarity 26.7%; Pred. No. 56;
Matches 32; Conservative 20; Mismatches 39; Indels 29; Gaps 8;
```

```
Oy      6 QERRKLPOLCTELQTHIHILIECVYCKQOL---LRREYVDFAFRDLCTVYRDGNPYAV 62
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      134 QYKNTTLPQ--TTLKTSVKELDEALALAEHLVAKRKEAD-----RGEKY-- 178

Oy      63 XDKCLKFEYSKISEYRHYCVSYGTTLLEQYNNKPLCDLLIRICINXOKPL-CP-EKKORHLD 120
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      179 --KITKLRRNV-EMDEVYMHMRRSPFER-----EALTRDISCKKALGLPEEPGRYMD 229
```

```
RESULT 51
US-10-953-349-22312
; Sequence 22312, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22312
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-22312
```

```
Query Match      6.9%; Score 57.5; DB 6; Length 390;
Best Local Similarity 23.1%; Pred. No. 61;
Matches 30; Conservative 19; Mismatches 60; Indels 21; Gaps 6;
```

```
Oy      17 TELQTHIHILIECVYCKQOLLRREYDFAFRDL--CTVYRDGNPYAVXDKCLKFSKIS 74
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      13 TKMQAEIOKIDDE---VNEMKLKNEBEKLAIDLEMLIKRRK---AECCRLEAQS 65

Oy      75 EYRHYCVSYGTTLLEQ-----QYNNKPLCDLLIRICINXOKPL-PEEKORHLDKKOR- 124
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      66 SYRTMLEKMRDSDHOSVIYKEOYRLNOASNALMARLEAQREICDAAEKDLHKYKORD 125
```

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Oy      125 --FHNIRGRW 132
      | | | | |
Db      126 DIEKQIRPEW 135
```

```
RESULT 52
US-10-953-349-22947
; Sequence 22947, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
```

```
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22947
; LENGTH: 393
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-22947
```

```
Query Match      6.9%; Score 57.5; DB 6; Length 393;
Best Local Similarity 26.7%; Pred. No. 61;
Matches 32; Conservative 20; Mismatches 39; Indels 29; Gaps 8;
```

```
Oy      6 QERRKLPOLCTELQTHIHILIECVYCKQOL---LRREYVDFAFRDLCTVYRDGNPYAV 62
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      168 QYKNTTLPQ--TTLKTSVKELDEALALAEHLVAKRKEAD-----RGEKY-- 212

Oy      63 XDKCLKFEYSKISEYRHYCVSYGTTLLEQYNNKPLCDLLIRICINXOKPL-CP-EKKORHLD 120
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      213 --KITKLRRNV-EMDEVYMHMRRSPFER-----EALTRDISCKKALGLPEEPGRYMD 263
```

```
RESULT 53
US-10-953-349-22311
; Sequence 22311, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22311
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-22311
```

```
Query Match      6.9%; Score 57.5; DB 6; Length 423;
Best Local Similarity 23.1%; Pred. No. 66;
Matches 30; Conservative 19; Mismatches 60; Indels 21; Gaps 6;
```

```
Oy      17 TELQTHIHILIECVYCKQOLLRREYDFAFRDL--CTVYRDGNPYAVXDKCLKFSKIS 74
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      46 TKMQAEIOKIDDE---VNEMKLKNEBEKLAIDLEMLIKRRK---AECCRLEAQS 98

Oy      75 EYRHYCVSYGTTLLEQ-----QYNNKPLCDLLIRICINXOKPL-PEEKORHLDKKOR- 124
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      99 SYRTMLEKMRDSDHOSVIYKEOYRLNOASNALMARLEAQREICDAAEKDLHKYKORD 158
```

```
Oy      125 --FHNIRGRW 132
      | | | | |
Db      159 DIEKQIRPEW 168
```

```
RESULT 54
US-10-953-349-21332
; Sequence 21332, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
```

SEQ ID NO 21322  
LENGTH: 429  
TYPE: PRT  
ORGANISM: Glycine max  
US-10-530-349-21322

Query Match 6.9%; Score 57.5; DB 6; Length 429;  
Best Local Similarity 22.6%; Pred. No. 67;  
Matches 31; Conservative 13; Mismatches 54; Indels 39; Gaps 4;

QY 24 HDIIIECVYCKQQLRREYVDFAFRDLCIYVRDGNPYAVXDKCLKFYSKISEYRHVCYSV 83  
DB 116 HLIITLSRC---LLGREVADKLFDDVSALFHDLDNGMLPISVLPFLPIPAHKK----- 167  
QY 84 YGTTLEQYNNKPLCDLLIRICINXQKPLCPBEK---QRHLDKK----- 122  
DB 168 ---RDQARKKLAEIFASIIITSRSKASKEEDMLQCFIDSKYKDGSTTEAVTGLLIA 222  
QY 123 ---ORFHNIIRGRWTG 134  
DB 223 ALFAGQHTSITSTWTG 239

RESULT 55  
US-10-530-349-21321

Sequence 21321, Application US/10953349  
Publication No. US20060107345A1  
GENERAL INFORMATION:  
APPLICANT: ALEXANDROV, Nickolai et al.  
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
FILE REFERENCE: 2750-1579PUS2  
CURRENT APPLICATION NUMBER: US/10/953,349  
CURRENT FILING DATE: 2004-09-30  
NUMBER OF SEQ ID NOS: 40252  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 21321  
LENGTH: 487  
TYPE: PRT  
ORGANISM: Glycine max  
US-10-530-349-21321

Query Match 6.9%; Score 57.5; DB 6; Length 487;  
Best Local Similarity 22.6%; Pred. No. 77;  
Matches 31; Conservative 13; Mismatches 54; Indels 39; Gaps 4;

QY 24 HDIIIECVYCKQQLRREYVDFAFRDLCIYVRDGNPYAVXDKCLKFYSKISEYRHVCYSV 83  
DB 174 HLIITLSRC---LLGREVADKLFDDVSALFHDLDNGMLPISVLPFLPIPAHKK----- 225  
QY 84 YGTTLEQYNNKPLCDLLIRICINXQKPLCPBEK---QRHLDKK----- 122  
DB 226 ---RDQARKKLAEIFASIIITSRSKASKEEDMLQCFIDSKYKDGSTTEAVTGLLIA 280  
QY 123 ---ORFHNIIRGRWTG 134  
DB 281 ALFAGQHTSITSTWTG 297

RESULT 56  
US-10-530-349-22310

Sequence 22310, Application US/10953349  
Publication No. US20060107345A1  
GENERAL INFORMATION:  
APPLICANT: ALEXANDROV, Nickolai et al.  
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
FILE REFERENCE: 2750-1579PUS2  
CURRENT APPLICATION NUMBER: US/10/953,349  
CURRENT FILING DATE: 2004-09-30  
NUMBER OF SEQ ID NOS: 40252  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 22310

LENGTH: 495  
TYPE: PRT  
ORGANISM: Glycine max  
US-10-530-349-22310

Query Match 6.9%; Score 57.5; DB 6; Length 495;  
Best Local Similarity 23.1%; Pred. No. 79;  
Matches 30; Conservative 19; Mismatches 60; Indels 21; Gaps 6;

QY 17 TELQTIHDIIECVYCKQQLRREYVDFAFRDL--CIYVRDGNPYAVXDKCLKFYSKIS 74  
DB 118 TKWQAEIQKIDDE---VNEKTLKNEBEKLAIQLEMLIRRRK---AEKCRRLAEAGS 170  
QY 75 EYRHVCYSYGTTLLEQ-----QYNNKPLCDLLIRICINXQKPLC-PBEKQRHLDKKQR- 124  
DB 171 SYRTMLEKMRDMSHQSIVYKEQVRLNQASNALMARLEAQREICDAAEKDLHKRYKQRD 230  
QY 125 ---FHNIRGRW 132  
DB 231 DIEKQIRPEW 240

RESULT 57  
US-10-530-349-21320

Sequence 21320, Application US/10953349  
Publication No. US20060107345A1  
GENERAL INFORMATION:  
APPLICANT: ALEXANDROV, Nickolai et al.  
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
FILE REFERENCE: 2750-1579PUS2  
CURRENT APPLICATION NUMBER: US/10/953,349  
CURRENT FILING DATE: 2004-09-30  
NUMBER OF SEQ ID NOS: 40252  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 21320  
LENGTH: 518  
TYPE: PRT  
ORGANISM: Glycine max  
US-10-530-349-21320

Query Match 6.9%; Score 57.5; DB 6; Length 518;  
Best Local Similarity 22.6%; Pred. No. 82;  
Matches 31; Conservative 13; Mismatches 54; Indels 39; Gaps 4;

QY 24 HDIIIECVYCKQQLRREYVDFAFRDLCIYVRDGNPYAVXDKCLKFYSKISEYRHVCYSV 83  
DB 205 HLIITLSRC---LLGREVADKLFDDVSALFHDLDNGMLPISVLPFLPIPAHKK----- 256  
QY 84 YGTTLEQYNNKPLCDLLIRICINXQKPLCPBEK---QRHLDKK----- 122  
DB 257 ---RDQARKKLAEIFASIIITSRSKASKEEDMLQCFIDSKYKDGSTTEAVTGLLIA 311  
QY 123 ---ORFHNIIRGRWTG 134  
DB 312 ALFAGQHTSITSTWTG 328

RESULT 58  
US-10-530-349-12540

Sequence 12540, Application US/10953349  
Publication No. US20060107345A1  
GENERAL INFORMATION:  
APPLICANT: ALEXANDROV, Nickolai et al.  
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
FILE REFERENCE: 2750-1579PUS2  
CURRENT APPLICATION NUMBER: US/10/953,349  
CURRENT FILING DATE: 2004-09-30  
NUMBER OF SEQ ID NOS: 40252  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 12540  
LENGTH: 320

TYPE: PRT  
ORGANISM: Glycine max  
US-10-953-349-12540

Query Match 6.8%; Score 57; DB 6; Length 320;  
Best Local Similarity 35.8%; Pred. No. 55;  
Matches 19; Conservative 5; Mismatches 13; Indels 16; Gaps 4;

QY 80 CV-SVYGTTEQYQNK-----PLCDLLIRICINXQKRLCEPEKQRLDKQR 124  
DB 209 CYNLYGNTLEQDIKCGNDLESILMTVICID----CPE---KRPKAVR 253

## RESULT 59

US-11-318-156-6  
Sequence 6, Application US/11318156  
Publication No. US20060101529A1  
GENERAL INFORMATION:  
APPLICANT: Bram, Richard J.  
APPLICANT: Von Bulow, Richard J.  
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS  
FILE REFERENCE: 44158/254623  
CURRENT APPLICATION NUMBER: US/11/318,156  
CURRENT FILING DATE: 2005-12-23  
PRIOR APPLICATION NUMBER: US/10/293,816  
PRIOR FILING DATE: 2002-11-12  
PRIOR APPLICATION NUMBER: US 09/782,857  
PRIOR FILING DATE: 2001-02-14  
PRIOR APPLICATION NUMBER: US 09/290,333  
PRIOR FILING DATE: 1999-04-12  
PRIOR APPLICATION NUMBER: US 08/810,572  
PRIOR FILING DATE: 1997-03-03  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 6  
LENGTH: 166  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-318-156-6

Query Match 6.8%; Score 56.5; DB 7; Length 166;  
Best Local Similarity 26.7%; Pred. No. 31;  
Matches 16; Conservative 6; Mismatches 17; Indels 21; Gaps 2;  
QY 89 EEOYNKRLCDLLIRICINXQKRLCEPEKQRLDKQRHINIRGRTGRCMCCSSRRRE 148  
DB 36 EEOYMDPLGTQMSC---KTICNHQSOR-----TCAAFCRSLSCRKE 74

## RESULT 60

US-11-293-697-3341  
Sequence 3341, Application US/11293697  
Publication No. US20060105376A1  
GENERAL INFORMATION:  
APPLICANT: HELIX RESEARCH INSTITUTE  
TITLE OF INVENTION: Novel full length cDNA  
FILE REFERENCE: H1-A0106  
CURRENT APPLICATION NUMBER: US/11/293,697  
CURRENT FILING DATE: 2005-12-05  
PRIOR APPLICATION NUMBER: US/10/108,260  
PRIOR FILING DATE: 2002-03-28  
NUMBER OF SEQ ID NOS: 5458  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 3341  
LENGTH: 185  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-293-697-3341

Query Match 6.8%; Score 56.5; DB 7; Length 185;  
Best Local Similarity 23.8%; Pred. No. 35;  
Matches 29; Conservative 17; Mismatches 51; Indels 25; Gaps 5;

QY 16 CTELQTTIHDIIECVCKQOQLRREYVDFAFRLDCLIV--YRD-----GNPYAV 62  
DB 46 CCGLOEKGYSLILKPT--NQLTR--VNKALKVLCETIGAYRPELOVFASFKNPTFFLY 100  
QY 63 XDKCKEYKISEYRHYC-----YSVGTTEEQYQNKPLCDLLIRICINXQKRLCEPEK 115  
DB 101 LVAAIKSHYTLASSRANCHGLWSHSLRMWTNNSQINMKAAAFIPRPMLTITAPCEVE 160  
QY 116 QR 117  
DB 161 LR 162

## RESULT 61

US-11-318-156-2  
Sequence 2, Application US/11318156  
Publication No. US20060101529A1  
GENERAL INFORMATION:  
APPLICANT: Bram, Richard J.  
APPLICANT: Von Bulow, Richard J.  
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS  
FILE REFERENCE: 44158/254623  
CURRENT APPLICATION NUMBER: US/11/318,156  
CURRENT FILING DATE: 2005-12-23  
PRIOR APPLICATION NUMBER: US/10/293,816  
PRIOR FILING DATE: 2002-11-12  
PRIOR APPLICATION NUMBER: US 09/782,857  
PRIOR FILING DATE: 2001-02-14  
PRIOR APPLICATION NUMBER: US 09/290,333  
PRIOR FILING DATE: 1999-04-12  
PRIOR APPLICATION NUMBER: US 08/810,572  
PRIOR FILING DATE: 1997-03-03  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 293  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-318-156-2

Query Match 6.8%; Score 56.5; DB 7; Length 293;  
Best Local Similarity 26.7%; Pred. No. 57;  
Matches 16; Conservative 6; Mismatches 17; Indels 21; Gaps 2;  
QY 89 EEOYNKRLCDLLIRICINXQKRLCEPEKQRLDKQRHINIRGRTGRCMCCSSRRRE 148  
DB 36 EEOYMDPLGTQMSC---KTICNHQSOR-----TCAAFCRSLSCRKE 74

## RESULT 62

US-10-953-349-3991  
Sequence 3991, Application US/10953349  
Publication No. US20060107345A1  
GENERAL INFORMATION:  
APPLICANT: ALEXANDROV, Nikolai et al.  
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
FILE REFERENCE: 2750-1579PUS2  
CURRENT APPLICATION NUMBER: US/10/953,349  
CURRENT FILING DATE: 2004-09-30  
NUMBER OF SEQ ID NOS: 40252  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 3991  
LENGTH: 516  
TYPE: PRT  
ORGANISM: Arabidopsis thaliana  
US-10-953-349-3991

Query Match 6.8%; Score 56.5; DB 6; Length 516;  
Best Local Similarity 27.5%; Pred. No. 1e+02;  
Matches 19; Conservative 10; Mismatches 21; Indels 19; Gaps 4;



## RESULT 71

## RESULT 71



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; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953.349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8916
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-8916

Query Match      6.7%; Score 55.5; DB 6; Length 179;
Best Local Similarity 19.7%; Pred. No. 43;
Matches 31; Conservative 23; Mismatches 40; Indels 63; Gaps 7;

Qy      1 MFODPGRPRRLPOLCT-----ELQTTIHDLLEC----- 30
Db      24 LLOLPSCPKMPKRYKTRVYPRGWELEPTLRELDAKKEAEFTSDSHGKRKCELTLP 83
Qy      31 -----YYCKQQLRREYVDFAFRDLCTVYRDGNPYAVXDKLKFYSKISEYR 77
Db      84 FKVSHQRSRYVDYDYYRREISKELYE-----CL-----DQGYA--DRSLAKWKKSQYE 132
Qy      78 HYCY-----SYVGTLEEQYKPLC-DLIRICIN 105
Db      133 RLCCRLCIQPRDHNYGTTTCVGRVFKHLREKVCVH 169

RESULT 76
US-10-953-349-34190
; Sequence 34190, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953.349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 34190
; LENGTH: 274
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-34190

Query Match      6.7%; Score 55.5; DB 6; Length 274;
Best Local Similarity 23.5%; Pred. No. 67;
Matches 16; Conservative 8; Mismatches 21; Indels 23; Gaps 2;

Qy      36 QLRREYDFAFRDLCTVYRDGNPYAVXDKLKFY-----SKISEYRHVCYSV 83
Db      209 ELARRAIFYGATFRD-----AASGGCVSYHVGPDPGWTKLSDGDVGEIHHYHPV 257
Qy      84 YGTTLEEQ 91
Db      258 QKTPEOE 265

RESULT 77
US-10-953-349-34189
; Sequence 34189, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
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; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953.349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 34189
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-34189

Query Match      6.7%; Score 55.5; DB 6; Length 278;
Best Local Similarity 23.5%; Pred. No. 68;
Matches 16; Conservative 8; Mismatches 21; Indels 23; Gaps 2;

Qy      36 QLRREYDFAFRDLCTVYRDGNPYAVXDKLKFY-----SKISEYRHVCYSV 83
Db      213 ELARRAIFYGATFRD-----AASGGCVSYHVGPDPGWTKLSDGDVGEIHHYHPV 261
Qy      84 YGTTLEEQ 91
Db      262 QKTPEOE 269

RESULT 78
US-10-953-349-34188
; Sequence 34188, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953.349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 34188
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-34188

Query Match      6.7%; Score 55.5; DB 6; Length 280;
Best Local Similarity 23.5%; Pred. No. 69;
Matches 16; Conservative 8; Mismatches 21; Indels 23; Gaps 2;

Qy      36 QLRREYDFAFRDLCTVYRDGNPYAVXDKLKFY-----SKISEYRHVCYSV 83
Db      215 ELARRAIFYGATFRD-----AASGGCVSYHVGPDPGWTKLSDGDVGEIHHYHPV 263
Qy      84 YGTTLEEQ 91
Db      264 QKTPEOE 271

RESULT 79
US-10-953-349-938
; Sequence 938, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953.349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 938
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
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RESULT 89  
US-11-293-697-3101  
; Sequence 3101, Application US/11293697  
; Publication No. US20060105376A1  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: Novel full length cDNA  
; FILE REFERENCE: H1-A0106  
; CURRENT APPLICATION NUMBER: US/11/293,697  
; CURRENT FILING DATE: 2005-12-05  
; PRIOR APPLICATION NUMBER: US/10/108,260  
; PRIOR FILING DATE: 2002-03-28  
; NUMBER OF SEQ ID NOS: 5458  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3101  
; LENGTH: 541  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-293-697-3101

Query Match 6.6%; Score 55; DB 7; Length 541;  
Best Local Similarity 22.9%; Pred. No. 1.6e+02;  
Matches 33; Conservative 16; Mismatches 53; Indels 42; Gaps 10;

QY 13 POLCTELQTTIHDIIECVYCKQQLRREYVDFAPRDLCTIYRDGNPYAVXDKCLKFYSK 72  
DB 398 PYECKEGCKT---FIESAY---LIRHQ-----RHTGKPKYGC-NOCCKLFRN 438  
QY 73 ISE-YRHYCVSVGTTLEGOYNKPLCDLLIR---CINXQKPL-----CPE-----EK 115  
DB 439 IAGLIRHQ---RHTGKPKYECNOCGAFRDSCLTHQRIHYKETYQCPECKSKFKQ 494  
QY 116 QRHLDKQRFNIRGRWTCMASC 139  
DB 495 NSHLAVHQRLHSREG--PSRCPCQ 516

RESULT 90  
US-11-293-697-3790  
; Sequence 3790, Application US/11293697  
; Publication No. US20060105376A1  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: Novel full length cDNA  
; FILE REFERENCE: H1-A0106  
; CURRENT APPLICATION NUMBER: US/11/293,697  
; CURRENT FILING DATE: 2005-12-05  
; PRIOR APPLICATION NUMBER: US/10/108,260  
; PRIOR FILING DATE: 2002-03-28  
; NUMBER OF SEQ ID NOS: 5458  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3790  
; LENGTH: 541  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-293-697-3790

Query Match 6.6%; Score 55; DB 7; Length 541;  
Best Local Similarity 22.9%; Pred. No. 1.6e+02;  
Matches 33; Conservative 16; Mismatches 53; Indels 42; Gaps 10;

QY 13 POLCTELQTTIHDIIECVYCKQQLRREYVDFAPRDLCTIYRDGNPYAVXDKCLKFYSK 72  
DB 398 PYECKEGCKT---FIESAY---LIRHQ-----RHTGKPKYGC-NOCCKLFRN 438  
QY 73 ISE-YRHYCVSVGTTLEGOYNKPLCDLLIR---CINXQKPL-----CPE-----EK 115  
DB 439 IAGLIRHQ---RHTGKPKYECNOCGAFRDSCLTHQRIHYKETYQCPECKSKFKQ 494  
QY 116 QRHLDKQRFNIRGRWTCMASC 139  
DB 495 NSHLAVHQRLHSREG--PSRCPCQ 516

RESULT 91  
US-10-953-349-9683  
; Sequence 9683, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nickolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 9683  
; LENGTH: 560  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
US-10-953-349-9683

Query Match 6.6%; Score 55; DB 6; Length 560;  
Best Local Similarity 21.8%; Pred. No. 1.6e+02;  
Matches 34; Conservative 16; Mismatches 56; Indels 50; Gaps 9;

QY 2 FQDPQERPKLPOLCTELQTTIHDIIECVYCKQQLRREYVDFAPRDLCTIYRD 56  
DB 177 FKDPVEDGNLPRVDLWVNH-PSI---CDGCKSAIEGSHVAGVNMHPECFCCRYCD 232  
QY 57 GNPYAVXDKCLKFYSKISEYRHYCVSVGTTLEGOYNKPLCDLLIRGINXQKPLCPEEKQ 116  
DB 233 -KPIAMHE-----FSNKGKRGCH-----ITYESHFNCHYCKK 264  
QY 117 RHLDKQRFNIRGRWTCMASC 141  
DB 265 KFGKRYKEHPFWKEKXCPHEVDG--TPKCCSCER 298

RESULT 92  
US-10-953-349-21080  
; Sequence 21080, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nickolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 21080  
; LENGTH: 167  
; TYPE: PRT  
; ORGANISM: Glycine max  
US-10-953-349-21080

Query Match 6.6%; Score 54.5; DB 6; Length 167;  
Best Local Similarity 20.2%; Pred. No. 50;  
Matches 24; Conservative 24; Mismatches 44; Indels 27; Gaps 5;

QY 14 QCTELQTTIHDIIECVYCKQQLR-----REYVDFAPRDLCTIYRDGNPYAVXDK 65  
DB 47 QLC-----H--LMISVYRNNMLQDLVXLFKGLFAFDRKPRDKSIQKVAAYEVLG- 96  
QY 66 CLKFYSKISEYRHYCVSVGTTLEGOYNKPLCDLLIRGINXQKPLCPEEKQRLDKKOR 124  
DB 97 LVKEKEVLEKINHLFTETGPTKHKHNS-----FAKKGVHFTYKEKGRHOKQSKR 146

RESULT 93  
US-11-293-697-3380  
; Sequence 3380, Application US/11293697

```

; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: HL-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3380
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-3380

Query Match
Best Local Similarity 21.2%; Pred. No. 88;
Matches 18; Conservative 15; Mismatches 31; Indels 21; Gaps 4;

Oy 59 PYAVXDKLKFYSKSEYRHVCYSYGTTLLEQVYNNKPLCDLLIRGINXOKPLCPB--EKQ 116
Db 80 PFSHTTSGCKEPNRDPDKLKAHLSSHGKMLR-----KC-----ALCKSFSSR 122

Oy 117 RHLDKQRFHNI RGHMTRCSCCR 141
Db 123 AHLAEHQRAHT--GNYKFRCCAGCAK 145

RESULT 94
US-10-953-349-21079
; Sequence 21079, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 21079
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-21079

Query Match
Best Local Similarity 20.2%; Pred. No. 94;
Matches 24; Conservative 24; Mismatches 44; Indels 27; Gaps 5;

Oy 14 QLCTELQTTIHDIIECYCKQQLR-----REYVDFAPRDLCTIYRDGNPYAVXDK 65
Db 180 QLC-----H--LMISVYRNMLQDVLKFLGLEAFDRKRDKSIIOKVANAWEVLG- 229

Oy 66 CLKFYKISEYRHVCYSYGTTLLEQVYNNKPLCDLLIRGINXOKPLCPBEKORHLDKOR 124
Db 230 LVKKEKRVLEKYNHLFTETGPTKHKRNS-----FEAKGHVPTKEKHOKQSKR 279

RESULT 95
US-10-953-349-21078
; Sequence 21078, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
```

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; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 21078
; LENGTH: 308
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-21078

Query Match
Best Local Similarity 20.2%; Pred. No. 97;
Matches 24; Conservative 24; Mismatches 44; Indels 27; Gaps 5;

Oy 14 QLCTELQTTIHDIIECYCKQQLR-----REYVDFAPRDLCTIYRDGNPYAVXDK 65
Db 188 QLC-----H--LMISVYRNMLQDVLKFLGLEAFDRKRDKSIIOKVANAWEVLG- 237

Oy 66 CLKFYKISEYRHVCYSYGTTLLEQVYNNKPLCDLLIRGINXOKPLCPBEKORHLDKOR 124
Db 238 LVKKEKRVLEKYNHLFTETGPTKHKRNS-----FEAKGHVPTKEKHOKQSKR 287

RESULT 96
US-10-953-349-33223
; Sequence 33223, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 33223
; LENGTH: 337
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-33223

Query Match
Best Local Similarity 21.6%; Pred. No. 11e+02;
Matches 19; Conservative 15; Mismatches 17; Indels 37; Gaps 4;

Oy 12 LPOLCTELQ-----TTIHDIIECY-----CKQQLRREYVDF 45
Db 179 LPTICSPLRKACTGMDLSAVAHIDILKKTGYKDBGAENELSPQEWNTQVQENLTKKRGDI 238

Oy 46 AFRDLCTIYRDGNPYAVXDKCLKFYSKI 73
Db 239 AFRD-----KD-----FKTAIDVYSKL 255

RESULT 97
US-10-953-349-33222
; Sequence 33222, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 33222
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-33222

Query Match
Best Local Similarity 21.6%; Pred. No. 11e+02;
Matches 19; Conservative 15; Mismatches 17; Indels 37; Gaps 4;
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GenCore version 5.1.8  
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OM protein - protein search, using sw model

Run on: May 27, 2006, 05:10:28 ; Search time 18.8916 Seconds  
(without alignments)  
499.124 Million cell updates/sec

Title: US-10-530-253-14ED

Perfect score: 517  
Sequence: 1 MNGDPTTHRYMLDLPETT.....LEDLMGTGIVXPTCSQXP 98

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 100 summaries

Database : PIR 80:\*  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	512	99.0	98	1	E7 protein - human
2	381.5	73.8	99	1	E7 protein - human
3	372	72.0	98	1	E7 protein - human
4	295	57.1	97	1	E7 protein - human
5	294	56.9	99	2	E7 protein - human
6	289.5	56.0	98	1	E7 protein - human
7	245	47.4	98	1	E7 protein - human
8	243	47.0	98	1	E7 protein - human
9	222.5	43.0	97	2	E7 protein - human
10	218.5	42.3	113	1	E7 protein - human
11	213	41.2	106	2	E7 protein - human
12	209.5	40.5	105	2	E7 protein - human
13	208.5	40.3	105	2	E7 protein - human
14	200.5	38.8	101	1	E7 protein - human
15	200.5	38.8	105	1	E7 protein - human
16	194	37.5	98	1	E7 protein - human
17	183.5	35.5	93	1	E7 protein - human
18	183.5	35.5	105	2	E7 protein - human
19	178.5	34.5	92	1	E7 protein - human
20	178.5	34.5	105	2	E7 protein - human
21	178.5	34.5	111	2	E7 protein - human
22	178	34.4	101	1	E7 protein - human
23	175.5	33.9	92	1	E7 protein - human
24	173.5	33.6	86	2	E7 protein - human
25	170	32.9	95	2	E7 protein - human
26	170	32.9	109	1	E7 protein - human
27	169	32.7	104	2	E7 protein - human
28	166.5	32.2	92	2	E7 protein - human
29	157.5	30.5	110	1	E7 protein - human

30	150.5	29.1	111	2	S36556	E7 protein - human
31	148	28.6	93	2	S36474	E7 protein - human
32	140.5	27.2	104	2	S36545	E7 protein - human
33	138	26.7	93	1	W7ML	E7 protein - human
34	122	23.6	93	2	S36591	E7 protein - human
35	120.5	23.3	102	2	S36492	E7 protein - human
36	119	22.5	103	2	S36539	E7 protein - human
37	116.5	22.0	102	2	S36486	E7 protein - human
38	113	21.9	103	1	W7ML47	E7 protein - human
39	112	21.7	103	1	W7ML5	E7 protein - human
40	109	21.1	103	1	W7MLB5	E7 protein - human
41	105	20.3	103	1	W7MLB	E7 protein - human
42	87	16.8	94	1	W7MLRB	E7 protein - human
43	83.5	16.2	98	2	B61399	early protein E7 -
44	80	15.5	55	2	S19907	early protein E7 -
45	79.5	15.4	98	2	A61399	E7 protein - deer
46	77.5	15.0	102	1	W7MLDP	E7 protein - human
47	76	14.7	114	1	W7ML41	E7 protein - human
48	75	14.5	103	2	S36568	E7 protein - cotto
49	73.5	14.2	102	1	W7MLP	early protein E7 -
50	70.5	13.6	1273	2	C96767	unknown protein F2
51	68	13.2	622	2	I48733	protein kinase rck
52	68	13.2	3924	2	S37431	ankyrin 2, neuron
53	66	12.8	261	2	T38157	short-chain dehydr
54	65.5	12.7	455	2	AD0782	probable L-serine
55	65	12.6	99	1	M6MLB4	E6 protein - bovin
56	65	12.6	770	2	A90880	hypothetical prote
57	65	12.6	770	2	H85738	hypothetical prote
58	64.5	12.5	100	2	C61399	early protein E7 -
59	64.5	12.5	614	2	D86342	hypothetical prote
60	64	12.4	138	1	PSRSAT	phospholipase A2 h
61	63.5	12.3	391	1	T14580	STEPL protein pre
62	63	12.2	138	1	I51380	phospholipase A2 h
63	63	12.2	855	2	S56948	HLA5 protein - yea
64	63	12.2	1250	2	T40062	probable nuclear e
65	62.5	12.1	1490	2	T20513	hypothetical prote
66	62	12.0	675	2	T00198	VP80 protein - leu
67	61.5	11.9	433	2	T04509	hypothetical prote
68	61.5	11.9	508	2	F86458	unknown protein, 7
69	61.5	11.9	823	2	T21104	hypothetical prote
70	61.5	11.9	1964	2	A59282	nonmuscle myosin I
71	61	11.8	338	2	JC7867	endo-1,3(4)-beta-g
72	61	11.8	635	2	T09648	nucleolin homolog
73	61	11.8	815	2	T40524	hypothetical prote
74	60.5	11.7	222	2	AB0007	probable DNA repai
75	60.5	11.7	411	2	S40936	hypothetical prote
76	60.5	11.7	551	2	C89134	protein F2566.6 (i
77	60.5	11.7	1269	2	T14476	p61A protein - sli
78	60.5	11.7	1287	2	A41685	SIL protein - huma
79	60.5	11.7	1389	2	I50090	carboxypeptidase g
80	60.5	11.7	1826	2	H86502	excinuclease ABC s
81	60.5	11.7	1826	2	D72120	excinuclease ABC,
82	60	11.6	172	2	T03396	invertease inhibit
83	60	11.6	370	1	E70341	conserved hypotet
84	60	11.6	465	2	H86352	protein F282.2 (im
85	60	11.6	562	2	S46281	P element - fruit
86	60	11.6	1175	2	T37192	nebulin-related pr
87	60	11.6	1634	1	JC5500	phosphoinositide 3
88	59.5	11.5	333	2	T39642	conserved hypotet
89	59.5	11.5	389	1	A48355	coat protein - pel
90	59.5	11.5	404	2	C96640	hypothetical prote
91	59.5	11.5	438	2	C69455	tungsten formylmet
92	59.5	11.5	512	2	E71474	probable hep60 cha
93	59.5	11.5	596	2	A85438	hypothetical prote
94	59.5	11.5	617	2	T10102	diphosphate-fructo
95	59.5	11.5	617	2	E96793	hypothetical prote
96	59.5	11.5	822	2	T01622	probable salt-indu
97	59.5	11.5	1708	2	F69189	protoporphyryn IX
98	59.5	11.5	1959	1	A33977	myosin heavy chain
99	59.5	11.5	4572	2	S57908	hypothetical 527k
100	59	11.4	214	2	AF1164	hypothetical prote

## ALIGNMENTS

## RESULT 1

E7 protein - human papillomavirus type 16

C/Species: human papillomavirus type 16

C/Date: 28-May-1986 #sequence revision 28-May-1986 #text\_change 09-Jul-2004

C/Accession: A03688; S12367; T10428

R/Seedorf, K.; Krammer, G.; Dürst, M.; Suhai, S.; Roweckamp, W.G.

Virology 145, 181-185, 1985

A/Title: Human papillomavirus type 16 DNA sequence.

A/Reference number: A22355; MUID:85246220; PMID:2990099

A/Accession: A03688

A/Molecule type: DNA

A/Residues: 1-98 &lt;SEB&gt;

A/Cross-references: UNIPROT:P03129; UNIPARC:UPI000000034E; GB:K02718; NID:G333031; PIDN:

R/Barbosa, M.S.; Edmonde, C.; Fisher, C.; Schiller, J.T.; Lowy, D.R.; Youaden, K.H.

EMBO J. 9, 153-160, 1990

A/Title: The region of the HPV E7 oncoprotein homologous to adenovirus E1a and SV40 large

A/Reference number: S12367; MUID:90107938; PMID:2153075

A/Accession: S12367

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-98 &lt;BAR&gt;

A/Cross-references: UNIPARC:UPI000000034E

R/Kennedy, I.M.; Haddow, J.K.; Clements, J.B.

J. Virol. 65, 2093-2097, 1991

A/Title: A negative element in the human poapillomavirus type 16 genome acts at the level

A/Reference number: Z17014; MUID:91162763; PMID:1848319

A/Accession: T10428

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-98 &lt;KEN&gt;

A/Cross-references: UNIPARC:UPI000000034E; EMBL:K02718; NID:G333031; PIDN:AAA6940.1; PI

C/Genetics:

A/Gene: E7

C/Superfamily: Papillomavirus E7 protein

C/Keywords: DNA binding; early protein; transcription regulation; zinc finger

F:58-94/Region: zinc finger CCCC motif

## Query Match

Best Local Similarity 99.0%; Score 512; DB 1; Length 98;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEMYMDLOPETTDLYXXQUNDSSEDEIDGPAQAEPRAHYNIVTFCC 60

Db 1 MHGDTPLHEMYMDLOPETTDLYCYEQUNDSSEDEIDGPAQAEPRAHYNIVTFCC 60

Qy 61 CDSTLRVCVOSTHVDIRTELDLMGTGIVXPICSO 98

Db 61 CDSTLRVCVOSTHVDIRTELDLMGTGIVPICSO 98

## RESULT 2

E7 protein - human papillomavirus type 35

C/Species: human papillomavirus type 35

A/Note: host Homo sapiens (man)

C/Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 09-Jul-2004

C/Accession: F40824; S36522

R/Marlich, J.E.; Pontleier, A.V.; Rice, S.M.; McGraw, K.A.; Dubensky, T.W.

Virology 186, 770-776, 1992

A/Title: The phylogenetic relationship and complete nucleotide sequence of human papillid

A/Reference number: A40824; MUID:92124753; PMID:1310198

A/Accession: F40824

A/Status: translation not shown

A/Molecule type: DNA

A/Residues: 1-99 &lt;MAR&gt;

A/Cross-references: UNIPROT:P27230; UNIPARC:UPI000000035E; GB:M74117; NID:G333050; PIDN:

R/Delius, H.; Hofmann, B.  
submitted to the EMBL Data Library, August 1993  
A/Description: Primer-directed sequencing of human papillomavirus types.

A/Reference number: S36469

A/Accession: S36522

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-99 &lt;DEL&gt;

A/Cross-references: UNIPARC:UPI000000035E; EMBL:X74477; NID:G396997; PIDN:CAA52562.1; PI

A/Experimental source: strain 35H

C/Superfamily: papillomavirus E7 protein

C/Keywords: DNA binding; early protein; transcription regulation; zinc finger

F:59-95/Region: zinc finger CCCC motif

Query Match 73.8%; Score 381.5; DB 1; Length 99;  
Best Local Similarity 73.5%; Pred. No. 2.2e-35;  
Matches 72; Conservative 11; Mismatches 14; Indels 1; Gaps 1;

Qy 1 MHGDTPLHEMYMDLOPETTDLYXXQUNDS-REDEIDGPAQAEPRAHYNIVTFCC 59

Db 1 MHGDTPLQYVDLDEPAVDLYCYEQUNDSSEDEIDGPAQAEPRAHYNIVTFCC 60

Qy 60 KCSTLRVCVOSTHVDIRTELDLMGTGIVXPICSO 97

Db 61 KCSTLRVCVOSTHVDIRTELDLMGTGIVPCSO 98

## RESULT 3

E7 protein - human papillomavirus type 31

C/Species: human papillomavirus type 31

A/Note: host Homo sapiens (man)

C/Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 09-Jul-2004

C/Accession: B32444

R/Goldsbrough, M.D.; Disilvestre, D.; Temple, G.F.; Lorincz, A.T.

Virology 171, 306-311, 1989

A/Title: Nucleotide sequence of human papillomavirus type 31: a cervical neoplasia-associ

A/Reference number: A94398; MUID:89299478; PMID:2545036

A/Accession: B32444

A/Status: translation not shown

A/Molecule type: DNA

A/Residues: 1-98 &lt;COL&gt;

A/Cross-references: UNIPROT:P17387; UNIPARC:UPI000013840A; GB:J04353; NID:G333048; PIDN:

C/Comment: This protein may be involved in the oncogenic potential of this virus.

C/Superfamily: papillomavirus E7 protein

C/Keywords: DNA binding; early protein; transcription regulation; zinc finger

F:58-94/Region: zinc finger CCCC motif

Query Match 72.0%; Score 372; DB 1; Length 98;  
Best Local Similarity 71.1%; Pred. No. 2.5e-34;  
Matches 69; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEMYMDLOPETTDLYXXQUNDSSEDEIDGPAQAEPRAHYNIVTFCC 60

Db 1 MHGDTPLQYVDLDEPAVDLYCYEQUNDSSEDEIDGPAQAEPRAHYNIVTFCC 60

Qy 61 CDSTLRVCVOSTHVDIRTELDLMGTGIVXPICSO 97

Db 61 CKSTLRVCVOSTGVDIRTELDLMGSRGIVCPNCSTR 97

## RESULT 4

E7 protein - human papillomavirus type 33

C/Species: human papillomavirus type 33

C/Date: 30-Jun-1987 #sequence revision 30-Jun-1987 #text\_change 09-Jul-2004

C/Accession: A03689; S23831; S23827

R/Cole, S.T.; Strebeck, R.E.

J. Virol. 58, 991-995, 1986

A/Title: Genome organization and nucleotide sequence of human papillomavirus type 33, whi

A/Reference number: A93020; MUID:86200464; PMID:3009902

A/Accession: A03689

A/Molecule type: DNA

A/Residues: 1-97 &lt;COL&gt;

A/Cross-references: UNIPROT:P06429; UNIPARC:UPI000013840C; GB:M12732; NID:G333049; PIDN:

R/Shijfers, P.J.F.; van den Brule, A.J.C.; Schrijnemakers, H.F.J.; Raaphorst, P.M.C.; Meij

submitted to the EMBL Data Library, January 1992

A;Description: HPV type 33 in a consillar carcinoma generates its putative E7 mRNA via c

A;Reference number: S19906

A;Accession: S23831

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-97 <SN1>

A;Cross-references: UNIPARC:UPI000013840C; EMBL:X64085; NID:g60278; PIDN:CA45434.1; PII

C;Superfamily: papillomavirus E7 protein

C;Keywords: DNA binding; early protein; transcription regulation; zinc finger

F;58-94/Region: zinc finger CCCC motif

Query Match 57.1%; Score 295; DB 1; Length 97;  
Best Local Similarity 57.7%; Pred. No. 9.4e-26;  
Matches 56; Conservative 16; Mismatches 25; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEVMDLOPETTDLYXXQOLNDSSEED--IDGPAGQAEPPRAHNYITFCCK 60  
1 MRGHKPTLKEYVDLYPEPTDLYCYEQLSDBSDEBGLDRPDGAQAPATADYIVTCCHT 60  
C;Species: human papillomavirus type 52  
C;Date: 08-May-1995 #sequence\_revision 26-Jul-1996 #text\_change 09-Jul-2004  
C;Accession: S36574

Qy 61 CDSITRLCVQSTHVDIRLTEDLLMGTGIVXPICSQK 97  
61 CMTTTRLCVNSTASDTRITQQLMGTVINIVCPFCACQ 97  
Db

#### RESULT 5

S36574  
E7 protein - human papillomavirus type 52

C;Species: human papillomavirus type 52

C;Date: 08-May-1995 #sequence\_revision 26-Jul-1996 #text\_change 09-Jul-2004

C;Accession: S36574

R;Belius, H.; Hofmann, B.

submitted to the EMBL Data Library, August 1993

A;Description: Primer-directed sequencing of human papillomavirus types.

A;Reference number: S36469

A;Accession: S36574

A;Molecule type: DNA

A;Residues: 1-99 <DEL>

A;Cross-references: UNIPROT:P36831; UNIPARC:UPI000013841C; EMBL:X74481; NID:g397038; PID

C;Superfamily: papillomavirus E7 protein

C;Keywords: DNA binding; early protein; transcription regulation

Query Match 56.9%; Score 294; DB 2; Length 99;  
Best Local Similarity 57.1%; Pred. No. 1.2e-25;  
Matches 56; Conservative 17; Mismatches 23; Indels 2; Gaps 1;

Qy 1 MHGDTPLHEVMDLOPETTDLYXXQOLNDSSEED--IDGPAGQAEPPRAHNYITFC 58  
1 MRGHKPTLKEYVDLYPEPTDLYCYEQLSDBSDEBGLDRPDGAQAPATADYIVTCC 60  
Db

Qy 59 CKCDSTRLCVQSTHVDIRLTEDLLMGTGIVXPICSQ 96  
61 HSCDSTRLCVQSTHVDIRLTEDLLMGTGIVXPICSQ 98  
Db

#### RESULT 6

W7ML58  
E7 protein - human papillomavirus type 58

C;Species: human papillomavirus type 58

A;Note: host Homo sapiens (man)

C;Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 09-Jul-2004

C;Accession: F36779

R;Kitil, Y.; Iwamoto, S.; Matsukura, T.

Virology 185, 424-427, 1991

A;Title: Human papillomavirus type 58 DNA sequence.

A;Reference number: A36779; MUID:92024102; PMID:1656594

A;Accession: F36779

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-98 <KIR>

A;Cross-references: UNIPROT:P26557; UNIPARC:UPI000000348B; GB:D90400; NID:g222386; PIDN:

C;Superfamily: papillomavirus E7 protein  
C;Keywords: DNA binding; early protein; transcription regulation; zinc finger

F;59-95/Region: zinc finger CCCC motif

Query Match 56.0%; Score 289.5; DB 1; Length 98;  
Best Local Similarity 57.1%; Pred. No. 3.3e-25;  
Matches 56; Conservative 16; Mismatches 25; Indels 1; Gaps 1;

Qy 1 MHGDTPLHEVMDLOPETTDLYXXQOLNDSSEED--EIDGPAGQAEPPRAHNYITFCCK 59  
1 MRGHKPTLKEYVDLYPEPTDLYCYEQLSDBSDEBGLDRPDGAQAPATADYIVTCCY 60  
Db

Qy 60 KCDSTRLCVQSTHVDIRLTEDLLMGTGIVXPICSQK 97  
61 TCGTTRLCVNSTASDTRITQQLMGTCTIVCPFCACQ 98  
Db

#### RESULT 7

W7ML11  
E7 protein - human papillomavirus type 11

C;Species: human papillomavirus type 11

C;Date: 13-Aug-1986 #sequence\_revision 13-Aug-1986 #text\_change 09-Jul-2004

C;Accession: A03690

R;Dartmann, K.; Schwarz, E.; Gissmann, L.; zur Hausen, H.

Virology 151, 124-130, 1986

A;Title: The nucleotide sequence and genome organization of human papilloma virus type 1

A;Reference number: A94338; MUID:86181601; PMID:3008427

A;Accession: A03690

A;Molecule type: DNA

A;Residues: 1-98 <DAR>

A;Cross-references: UNIPROT:P04020; UNIPARC:UPI00001383F7; GB:M14119; NID:g333026; PIDN:

C;Superfamily: papillomavirus E7 protein

C;Keywords: DNA binding; early protein; transcription regulation; zinc finger

F;58-94/Region: zinc finger CCCC motif

Query Match 47.4%; Score 245; DB 1; Length 98;  
Best Local Similarity 53.0%; Pred. No. 3.5e-20;  
Matches 53; Conservative 14; Mismatches 29; Indels 4; Gaps 3;

Qy 1 MHGDTPLHEVMDLOPETTDLYXXQOLNDSSEED--DEIDGPAGQAEPPRAHNYITFC 58  
1 MRGHKPTLKEYVDLYPEPTDLYCYEQLSDBSDEBGLDRPDGAQAPATADYIVTCC 58  
Db

Qy 59 CKCDSTRLCVQSTHVDIRLTEDLLMGTGIVXPICSQK 98  
59 CGCDSTRLCVQSTHVDIRLTEDLLMGTGIVXPICSQK 98  
Db

#### RESULT 8

W7ML6  
E7 protein - human papillomavirus type 6b

C;Species: human papillomavirus type 6b

C;Date: 30-Sep-1987 #sequence\_revision 30-Sep-1987 #text\_change 09-Jul-2004

C;Accession: D20558

R;Schwarz, E.; Dürst, M.; Demankowski, C.; Lattemann, O.; Zech, R.; Wolfspurger, E.; Su

EMBO J. 2, 2341-2348, 1983

A;Title: DNA sequence and genome organization of genital human papillomavirus type 6b.

A;Reference number: A90975; MUID:84131949; PMID:6321162

A;Accession: D20558

A;Molecule type: DNA

A;Residues: 1-98 <SCA>

A;Cross-references: UNIPROT:P06464; UNIPARC:UPI0000138429; GB:X00203; NID:g60955; PIDN:C

C;Superfamily: papillomavirus E7 protein

C;Keywords: DNA binding; early protein; transcription regulation; zinc finger

F;58-94/Region: zinc finger CCCC motif

Query Match 47.0%; Score 243; DB 1; Length 98;  
Best Local Similarity 52.5%; Pred. No. 5.9e-20;  
Matches 52; Conservative 15; Mismatches 28; Indels 4; Gaps 3;

Qy 1 MHGDTPLHEVMDLOPETTDLYXXQOLNDSSEED--DEIDGPAGQAEPPRAHNYITFC 58  
1 MRGHKPTLKEYVDLYPEPTDLYCYEQLSDBSDEBGLDRPDGAQAPATADYIVTCC 58  
Db

Qy 59 CKCDSTRLCVQSTHVDIRLTEDLLMGTGIVXPICSQK 97

Db 59 CGCDSNRLVVOCTETDIRVQOLLGTLNVCPICAK 97

## RESULT 9

S36516 E7 protein - human papillomavirus type 34

C:Species: human papillomavirus type 34  
C>Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004

C:Accession: S36516  
R:Delius, H.; Hofmann, B.

A:Description: Primer-directed sequencing of human papillomavirus types.  
A:Reference number: S36469

A:Accession: S36516

A:Molecule type: DNA

A:Residues: 1-97 <DEL>  
A:Cross-references: UNIPROT:P36828; UNIPARC:UPI000013840D; EMBL:X74476; NID:g396989; PID

C:Superfamily: papillomavirus E7 protein  
C:Keywords: DNA binding; early protein; transcription regulation

Query Match 43.0%; Score 222.5; DB 2; Length 97;  
Best Local Similarity 49.0%; Pred. No. 1.1e-17;  
Matches 48; Conservative 18; Mismatches 29; Indels 3; Gaps 3;

Qy 1 MHGDPPLHEMYMLDLOPET--TDLYXXYQXNDSSSEEDIDGPAGQAEPRAHNYVFC 59

Db 1 MHGKPSYQDVLVLDKPTETEDLCTYESL-DNSEBEDTDSHL-BRQAEQMYRIIVDCS 58

Qy 60 KCDSTLRVCVOSTHVDIRTLIEDLIMGTIGIYXPICSOK 97

Db 59 RCSTVCTLTETSTADLVLEDLMLGALIKVICPNCSSR 96

## RESULT 10

M7WLR1 E7 protein - rhesus papillomavirus (type 1)

C:Species: rhesus papillomavirus  
C>Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 09-Jul-2004

C:Accession: B38503  
R:Ostrow, R.S.; Labresh, K.V.; Paras, A.J.

A:Title: Characterization of the complete RHPV 1 genomic sequence and an integration loc

A:Reference number: A38503; MUID:9135018; PMID:1847267

A:Accession: B38503  
A:Status: translation not shown

A:Molecule type: DNA  
A:Residues: 1-113 <OST>

A:Cross-references: UNIPROT:P22161; UNIPARC:UPI000013842F; EMBL:M37717

C:Superfamily: papillomavirus E7 protein  
C:Keywords: DNA binding; early protein; transcription regulation

Query Match 42.3%; Score 218.5; DB 1; Length 113;  
Best Local Similarity 43.8%; Pred. No. 3.7e-17;  
Matches 49; Conservative 13; Mismatches 35; Indels 15; Gaps 2;

Qy 1 MHGDPPLHEMYMLD---OPEETDLYXXYQXNDSSSEEDIDGPAGQAEPRAH----- 51

Db 1 MIGKPTLEDVLVLDQPPQPVYDLMCTEQLSSSEDEDDVHNHNNQOQHARPEV 60

Qy 52 -----YNIYVFCCKDSTLRVCVOSTHVDIRTLIEDLIMGTIGIYXPICSOK 97

Db 61 PEDGDCRIYSDCYSCGKRLRLVYVSSHELRVLEDLIMGTLDIVCPGCAAR 112

## RESULT 11

S36562 E7 protein - human papillomavirus type 45

C:Species: human papillomavirus type 45  
C>Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004

C:Accession: S36562  
R:Delius, H.; Hofmann, B.

A:Description: Primer-directed sequencing of human papillomavirus types.  
A:Reference number: S36469

A:Description: Primer-directed sequencing of human papillomavirus types.  
A:Reference number: S36469

A:Accession: S36562

A:Molecule type: DNA

A:Residues: 1-106 <DEL>  
A:Cross-references: UNIPROT:P21736; UNIPARC:UPI0000138416; EMBL:X74479; NID:g397022; PID

C:Superfamily: papillomavirus E7 protein  
C:Keywords: DNA binding; early protein; transcription regulation

Query Match 41.2%; Score 213; DB 2; Length 106;  
Best Local Similarity 43.8%; Pred. No. 1.4e-16;  
Matches 46; Conservative 15; Mismatches 32; Indels 12; Gaps 3;

Qy 1 MHGDPPLHEMYMLDLOPET--TDLYXXYQXNDSSSEEDIDG-----PAGQAEPRDA 50

Db 1 MHGPRETLQETVLHLEQONELDPVDLCTEQLSSSEEDBDAVSHQAQPARAEFOR- 59

Qy 51 HNYIVFCCKDSTLRVCVOSTHVDIRTLIEDLIMGTIGIYXPICS 95

Db 60 -HKLVCCKDGRIELTVSSAEDLRTIQQLFLSTISFVCPWCA 103

## RESULT 12

S36504 E7 protein - human papillomavirus type 30

C:Species: human papillomavirus type 30  
C>Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004

C:Accession: S36504  
R:Delius, H.; Hofmann, B.

A:Description: Primer-directed sequencing of human papillomavirus types.  
A:Reference number: S36469

A:Accession: S36504

A:Molecule type: DNA

A:Residues: 1-105 <DEL>  
A:Cross-references: UNIPROT:P36826; UNIPARC:UPI0000138409; EMBL:X74474; NID:g396973; PID

C:Superfamily: papillomavirus E7 protein  
C:Keywords: DNA binding; early protein; transcription regulation

Query Match 40.5%; Score 209.5; DB 2; Length 105;  
Best Local Similarity 45.2%; Pred. No. 3.5e-16;  
Matches 47; Conservative 17; Mismatches 33; Indels 7; Gaps 4;

Qy 1 MHGDPPLHEMYMLDLOPET--TDLYXXYQXNDSSSEEDIDG---PAGQAEPRDAH--YN 53

Db 1 MHGKVTIIPAYIIDLVPQTEIDHCTEQLSSSEEDDEVDNLOKQOQARQEHQHCYL 60

Qy 54 IVTFCKCDSTLRVCVOSTHVDIRTLIEDLIMGTIGIYXPICSOK 97

Db 61 INTGCCRCAVQVLAQVSPKELRALQWMLGALVELVCPICATR 104

## RESULT 13

S36528 E7 protein - human papillomavirus type 53

C:Species: human papillomavirus type 53  
C>Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004

C:Accession: S36528  
R:Delius, H.; Hofmann, B.

A:Description: Primer-directed sequencing of human papillomavirus types.  
A:Reference number: S36469

A:Accession: S36528

A:Molecule type: DNA

A:Residues: 1-105 <DEL>  
A:Cross-references: UNIPROT:P36832; UNIPARC:UPI000013841D; EMBL:X74482; NID:g397046; PID

C:Superfamily: papillomavirus E7 protein  
C:Keywords: DNA binding; early protein; transcription regulation

Query Match 40.3%; Score 208.5; DB 2; Length 105;  
Best Local Similarity 43.3%; Pred. No. 4.5e-16;  
Matches 45; Conservative 23; Mismatches 29; Indels 7; Gaps 4;

Qy 1 MHGDTPTLHEMYMDLOPER-TDLYXXYQXQNDSSSEDEDEID---GPAGQAEPPRAH--YN 53  
 Db 1 MGNVNTPLQYIIELEPQTEIDIQCHQNLSSSEDEDEIDLOEOPQQAARDEQHPCYL 60

Qy 54 IYTPCCCKDSTLRCLVOSTHVDIRTLBDMGLTGLIYXPCISQK 97  
 Db 61 IETGCCRCESIVQLANVQSSTKERILIQQMLMGTVELVCPICATR 104

RESULT 14  
 W7ML13  
 E7 protein - human papillomavirus type 13  
 C/Species: human papillomavirus type 13  
 A/Note: host Homo sapiens (man)  
 C/Date: 30-Jun-1993 #sequence\_revision 30-Jun-1993 #text\_change 09-Jul-2004  
 C/Accession: B42955  
 R:van Ranst, M.; Fuse, A.; Fiten, P.; Beuken, E.; Pfeister, H.; Burk, R.D.; Odenakker, G.  
 Virology 190, 587-596, 1992  
 A/Title: Human papillomavirus type 13 and pygmy chimpanzee papillomavirus type 1: Comparison of the DNA sequences and the protein sequences  
 A/Reference number: A42955; PMID:92391075; PMID:1325697  
 A/Accession: B42955  
 A/Molecule type: DNA  
 A/Residues: 1-101 <VAN>  
 A/Cross-references: UNIPROT:Q02271; UNIPARC:UPI00001383F9; EMBL:X62843; NID:G60295; PIDN:C/Superfamily: papillomavirus E7 protein  
 C/Keywords: DNA binding; early protein; transcription regulation; zinc finger  
 F/61-97/Region: zinc finger CCCC motif

Query Match 38.8%; Score 200.5; DB 1; Length 101;  
 Best Local Similarity 44.7%; Pred. No. 3.3e-15;  
 Matches 46; Conservative 13; Mismatches 35; Indels 9; Gaps 2;

Qy 1 MHGDTPTLHEMYMDLOPETTDLYXXYQXQNDSSSEDEIDGPAGQAEPPRAH-----YNT 54  
 Db 1 MHGKTYTLKQIVLDFPDVGLHCHNEQLDSS---EDEVDQATQATQATGHTLLGCTCYQI 57

Qy 55 VTFCCCKDSTLRCLVOSTHVDIRTLBDMGLTGLIYXPCISQK 97  
 Db 58 LITSCKSCSNVRLVVECTGPDHDLHDLGLTINIVCPICAPK 100

RESULT 15  
 W7ML18  
 E7 protein - human papillomavirus type 18  
 C/Species: human papillomavirus type 18  
 C/Date: 30-Sep-1987 #sequence\_revision 30-Sep-1987 #text\_change 09-Jul-2004  
 C/Accession: B26165; H26251  
 R:Seedorf, K.; Oltersdorf, T.; Kraemer, G.; Roewekamp, W.  
 EMBO J. 6, 139-144, 1987  
 A/Title: Identification of early proteins of the human papilloma viruses type 16 (HPV 16) and type 18 (HPV 18)  
 A/Reference number: A91068; PMID:87218459; PMID:3034571  
 A/Accession: B26165  
 A/Molecule type: DNA  
 A/Residues: 1-105 <SEE>  
 A/Cross-references: UNIPROT:P06788; UNIPARC:UPI00000000DB5; GB:X04773; NID:G60876; PIDN:C/Superfamily: papillomavirus E7 protein  
 C/Keywords: DNA binding; early protein; transcription regulation

Query Match 38.8%; Score 200.5; DB 1; Length 105;  
 Best Local Similarity 39.6%; Pred. No. 3.5e-15;  
 Matches 42; Conservative 20; Mismatches 33; Indels 11; Gaps 3;

Qy 1 MHGDTPTLHEMYMDLOPET--TDLYXXYQXQNDSSSEDEIDG-----PAGQAEPPRAH 51  
 Db 1 MHGKATLQIVLHLEPQNEIPVDLCHQQLSDSEENDEIDGYNHGLPARRARAFPR-- 58

Qy 52 YNIVTFCCCKDSTLRCLVOSTHVDIRTLBDMGLTGLIYXPCISQK 97  
 Db 59 HTMLCMCKCKEARIELVESSADDLRAFOQLFIMTLSPFCPCWCAQ 104

RESULT 16  
 W7MLC1  
 E7 protein - pygmy chimpanzee papillomavirus (type 1)  
 C/Species: pygmy chimpanzee papillomavirus  
 C/Date: 30-Jun-1993 #sequence\_revision 30-Jun-1993 #text\_change 16-Jul-1999  
 C/Accession: B36818  
 R:van Ranst, M.; Fuse, A.; Fiten, P.; Beuken, E.; Pfeister, H.; Burk, R.D.; Odenakker, G.  
 Virology 190, 587-596, 1992  
 A/Title: Human papillomavirus type 13 and pygmy chimpanzee papillomavirus type 1: Comparison of the DNA sequences and the protein sequences  
 A/Reference number: A42955; PMID:92391075; PMID:1325697  
 A/Accession: B36818  
 A/Molecule type: DNA  
 A/Residues: 1-98 <VAN>  
 A/Cross-references: UNIPARC:UPI000013842E; EMBL:X62844; NID:G61010; PIDN:CAA44656.1; PIDN:C/Superfamily: papillomavirus E7 protein  
 C/Keywords: DNA binding; early protein; transcription regulation; transforming protein; zinc finger CCCC motif  
 F/58-94/Region: zinc finger CCCC motif

Query Match 37.5%; Score 194; DB 1; Length 98;  
 Best Local Similarity 46.4%; Pred. No. 1.7e-14;  
 Matches 45; Conservative 13; Mismatches 35; Indels 4; Gaps 2;

Qy 1 MHGDTPTLHEMYMDLOPETTDLYXXYQXQNDSSSEDEIDGPAGQAEPPRAHYNIVTFC 58  
 Db 1 MHGKTYTLKQIVLDFPDVGLHCHNEQLD--SSEDEVDQATQATQATGHTQHYVTCC 58

Qy 59 CKCDSTLRCLVOSTHVDIRTLBDMGLTGLIYXPCISQK 95  
 Db 59 GQCDSNVRLVVECTGSDIQLHRLGLSLINIVCPICLA 95

RESULT 17  
 W7ML42  
 E7 protein - human papillomavirus type 42  
 C/Species: human papillomavirus type 42  
 A/Note: host Homo sapiens (man)  
 C/Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 09-Jul-2004  
 C/Accession: F39451  
 R:Phillips, W.; Honore, N.; Sapp, M.; Cole, S.T.; Strecek, R.E.  
 Virology 186, 331-334, 1992  
 A/Title: Human papillomavirus type 42: new sequence, conserved genome organization.  
 A/Reference number: A39451; PMID:92087479; PMID:1309278  
 A/Accession: F39451  
 A/Status: translation not shown  
 A/Molecule type: DNA  
 A/Residues: 1-93 <PHA>  
 A/Cross-references: UNIPROT:P27231; UNIPARC:UPI0000138414; GB:M73236  
 C/Superfamily: papillomavirus E7 protein  
 C/Keywords: DNA binding; early protein; transcription regulation

Query Match 35.5%; Score 183.5; DB 1; Length 93;  
 Best Local Similarity 44.4%; Pred. No. 2.4e-13;  
 Matches 44; Conservative 17; Mismatches 27; Indels 11; Gaps 4;

Qy 1 MHGDTPTLHEMYMDLOP--ET--TDLYXXYQXQNDSSSEDEIDGPAGQAEPPRAHYNIVTF 57  
 Db 1 MHGKTYTLKQIVLDFPDVGLHCHNEQLDSSDEDD-----QAKQDIQRITLCV 52

Qy 58 CKCDSTLRCLVOSTHVDIRTLBDMGLTGLIYXPCISQK 96  
 Db 53 CTGCVKSVKLWQCTEADIRNLQQMLGLTIDVCPICAR 91

RESULT 18  
 B44890  
 E7 protein - human papillomavirus type 66  
 C/Species: human papillomavirus type 66

C>Date: 31-Mar-1993 #sequence\_revision 31-Mar-1993 #text\_change 09-Jul-2004  
C/Accession: B44890  
C/Reviewed, A.R.; Beaudenon, S.; Favre, M.; Orth, G.  
J. Clin. Microbiol. 29, 2656-2660, 1991  
A>Title: Characterization of human papillomavirus type 66 from an invasive carcinoma of  
A/Reference number: A44890; MUID:92129556; PMID:1663515  
A/Accession: B44890  
A/Molecule type: DNA  
A/Residues: 1-105 <TAM>  
A/Cross-references: UNIPROT:Q80956; UNIPARC:UPI0000138426  
A/Note: Sequence extracted from NCBI backbone (NCBI:78637, NCBI:78639)  
C/Superfamily: papillomavirus E7 protein  
C/Keywords: DNA binding; early protein; transcription regulation

Query Match 35.5%; Score 183.5; DB 2; Length 105;  
Best Local Similarity 42.7%; Pred. No. 2.7e-13;  
Matches 44; Conservative 17; Mismatches 33; Indels 9; Gaps 4;

Oy 1 MHGDTPTLHEWMLDQET-TDLYXXQLNDS-SEEDSID-----GPAGQAEPPRAHY 52  
Db 1 MHGKVPPTLGEVLEAPTEITDLOCNEQDSDSEDEDEIDHLLERPGQAQAQGHNC-Y 59  
Oy 53 NITPCKKCDSTLRLCVOSTHVDIRTEEDLLMGTLGIYPICS 95  
Db 60 LIHVPCCKCELVQDIOSTKEBELRVVQQLMGALTVCPLCA 102

RESULT 19  
E7 protein - human papillomavirus type 57  
C/Species: human papillomavirus type 57  
A/Note: host Homo sapiens (man)  
C/Date: 17-Feb-1994 #sequence\_revision 17-Feb-1994 #text\_change 09-Jul-2004  
C/Accession: S15622  
R:Hirsch-Behnam, A.; Delius, H.; de Villiers, E.M.  
Virus Res. 18, 81-98, 1990  
A>Title: A comparative sequence analysis of two human papillomavirus (HPV) types 2a and  
A/Reference number: S15614; MUID:91188699; PMID:1964523  
A/Accession: S15622  
A/Molecule type: DNA  
A/Residues: 1-92 <HIR>  
A/Cross-references: UNIPROT:P22160; UNIPARC:UPI0000138421; EMBL:X55965; NID:g60882; PIDN  
C/Superfamily: papillomavirus E7 protein  
C/Keywords: DNA binding; early protein; transcription regulation; zinc finger  
F:55-91/Region: zinc finger CCCC motif

Query Match 34.5%; Score 178.5; DB 1; Length 92;  
Best Local Similarity 43.3%; Pred. No. 8.6e-13;  
Matches 42; Conservative 15; Mismatches 31; Indels 9; Gaps 3;

Oy 1 MHGDTPTLHEWMLDQ-PEFTDLYXXQLNDSSEED-EIDGPAQAEPPRAHYNTVF 57  
Db 1 MHGKRPSTLIEDITLLLEIPRIYDLHCDFQNSESDITVQLTEPAVQA-----YGVVTT 54  
Oy 58 CCKCDSTLRLCVOSTHVDIRTEEDLLMGTLGIYPIIC 94  
Db 55 CCKCHSTVRLVYEGCADIRHLEQLFNTLTITVCPRC 91

RESULT 20  
S36580  
E7 protein - human papillomavirus type 56  
C/Species: human papillomavirus type 56  
C/Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
C/Accession: S36580  
R:Delius, H.; Hofmann, B.  
submitted to the EMBL Data Library, August 1993  
A/Description: Primer-directed sequencing of human papillomavirus types.  
A/Reference number: S36469  
A/Accession: S36580  
A/Molecule type: DNA  
A/Residues: 1-105 <DEL>  
A/Cross-references: UNIPROT:P36633; UNIPARC:UPI0000138420; EMBL:X74483; NID:g397053; PMID:

```

C:Superfamily: papillomavirus E7 protein
C:Keywords: DNA binding; early protein; transcription regulation

Query Match          34.5%; Score 178.5; DB 2; Length 105;
Best Local Similarity 40.8%; Pred. No. 9..9e-13;
Matches 42; Conservative 17; Mismatches 35; Indels 9; Gaps 3;

QY 1 MHGDPPTLHEWMLDQPER-TDLVYXXQLNDSEEDDEIDGPAQOAPDRH-----Y 52
DB 1 MHGKVPITLDDVLELTPQTEIDLCNEQL-DSEEDDEBVDHLQERPGARQAKHTCY 59
53 NIVTECKCKDSTLRLCVOSTHVDIRTLBDLMLGTGLIAYPIC 95
60 LIHVPCKECKFVQDIDISTKEDIRVQQLMGALVTTCPLCA 102

RESULT 21
S36585
E7 protein - human papillomavirus type 7
C:Species: human papillomavirus type 7
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S36585
R:Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36469
A:Accession: S36585
A:Molecule type: DNA
A:Residues: 1-111 <DEL>
A:Cross-references: UNIPROT:P36816; UNIPARC:UPI00001383F3; EMBL:X74463; NID:g397060; PIDD
C:Superfamily: papillomavirus E7 protein
C:Keywords: DNA binding; early protein; transcription regulation

Query Match          34.5%; Score 178.5; DB 2; Length 111;
Best Local Similarity 39.8%; Pred. No. 1e-12;
Matches 45; Conservative 12; Mismatches 33; Indels 23; Gaps 3;

QY 1 MHGDPPTLHEWMLDQPERTTDLVYXXQLNDSEEDDEIDGPAQOAPDRH----- 51
DB 1 MHGEPPTLGDIVLDIQPEVSLSCNEQL-DSSPSEDDH-----QDOLDSHNRQEQPTQ 55
52 -----YNIVTECKCKDSTLRLCVOSTHVDIRTLBDLMLGTGLIAYPIC 95
56 ODLVNLOSFKIVTHCVFCHCLRVLWACLTADIRQVHQLMGTLLNIVCPNCA 108

RESULT 22
W7ML51
E7 protein - human papillomavirus type 51
C:Species: human papillomavirus type 51
A>Note: host Homo sapiens (man)
C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C:Accession: F40415
R:lungu, O.; Crum, C.P.; Silverstein, S.J.
J. Virol. 65: 4216-4225, 1991
A:Title: Biologic properties and nucleotide sequence analysis of human papillomavirus type
A:Reference number: A40415; MUID:91303675; PMID:1649326
A:Accession: F40415
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-101 <LUN>
A:Cross-references: UNIPROT:P26558; UNIPARC:UPI000013841B; GB:M62877
C:Superfamily: papillomavirus E7 protein
C:Keywords: DNA binding; early protein; transcription regulation

Query Match          34.4%; Score 178; DB 1; Length 101;
Best Local Similarity 41.0%; Pred. No. 1.1e-12;
Matches 41; Conservative 16; Mismatches 37; Indels 6; Gaps 3;

QY 1 MHGDPPTLHEWMLDQPER-TDLVYXXQLNDSEEDDEIDGPAQOAPDRH-----YNIV 55
DB 1 MGNVNPQLKDVVLLHTPQTEIDLQCYEQF-DSESEEDVDNMRDQLPERRPAGQATCYRIE 59

```

QY 56 TPCKCDSTLRKLCVOSTHVDIRTLDELMLGTLGIYXPIC 95  
DB 60 APCRCSSVVOQLAVASSGDTLRVQOMLWGLSELVCPCCA 99

## RESULT 23

S15615  
E7 protein - human papillomavirus type 2a  
C/Species: human papillomavirus type 2a  
A/Note: host Homo sapiens (man)  
C/Date: 17-Feb-1994 #sequence\_rev150117-Feb-1994 #text\_change 09-Jul-2004  
R/Accession: S15615  
R/Author: Behnam, A.; Delius, H.; de Villiers, E.M.  
Virus Res. 18, 81-98, 1990  
A/Title: A comparative sequence analysis of two human papillomavirus (HPV) types 2a and  
A/Reference number: S15614, PMID:9118669; PMID:1964523  
A/Accession: S15615  
A/Molecule type: DNA  
A/Residues: 192 <HR>  
A/Cross-references: UNIPROT:P25485; UNIPARC:UPI0000138408; EMBL:X55964  
C/Superfamily: papillomavirus E7 protein  
C/Keywords: DNA binding; early protein; transcription regulation; zinc finger  
F:55-91/Region: zinc finger CCCC motif

Query Match 33.9%; Score 175.5; DB 1; Length 92;  
Best Local Similarity 43.3%; Pred. No. 1.8e-12;  
Matches 42; Conservative 13; Mismatches 35; Indels 7; Gaps 3;

QY 1 MHGDTPTLHE--YMLDQPETDLYXXQLNDSSEEDIDPAGQAEPPRAHYNTVFC 58  
DB 1 MGNRRSLNDITLIDELIPVLDHCEQF-DSEENNHQ---LTFPVOAYGVVTTTC 55  
QY 59 CKCDSTLRKLCVOSTHVDIRTLDELMLGTLGIYXPIC 95  
DB 56 CKCGRTVRLVVECGQADRLRELQLEFKTLTVCPHCA 92

## RESULT 24

S36533  
E7 protein - human papillomavirus type 10  
C/Species: human papillomavirus type 10  
C/Date: 20-Feb-1995 #sequence\_rev15020-Feb-1995 #text\_change 09-Jul-2004  
C/Accession: S36533  
R/Author: H.; Hofmann, B.  
submitted to the EMBL Data Library, August 1993  
A/Description: Primer-directed sequencing of human papillomavirus types.  
A/Reference number: S36469  
A/Accession: S36533  
A/Molecule type: DNA  
A/Residues: 1-86 <DEL>  
A/Cross-references: UNIPROT:P36818; UNIPARC:UPI00001383F6; EMBL:X74465; NID:G396901; PID  
C/Superfamily: papillomavirus E7 protein  
C/Keywords: DNA binding; early protein; transcription regulation

Query Match 33.6%; Score 173.5; DB 2; Length 86;  
Best Local Similarity 42.6%; Pred. No. 2.9e-12;  
Matches 40; Conservative 10; Mismatches 35; Indels 9; Gaps 2;

QY 1 MHGDTPTLHEYMLDQPETDLYXXQLNDSSEEDIDPAGQAEPPRAHYNTVFC 60  
DB 1 MGNRRSLNDITLIDELIPVLDHCEQF-DSEENNHQ---LTFPVOAYGVVTTTC 51  
QY 61 CDSTLRKLCVOSTHVDIRTLDELMLGTLGIYXPIC 94  
DB 52 CSLPLRLVVECSHADIRALQQLGLTGLKLVCPRC 85

## RESULT 25

S36480  
E7 protein - human papillomavirus type 17  
C/Species: human papillomavirus type 17  
C/Date: 20-Feb-1995 #sequence\_rev15020-Feb-1995 #text\_change 09-Jul-2004  
C/Accession: S36480

R/Author: H.; Hofmann, B.  
submitted to the EMBL Data Library, August 1993  
A/Description: Primer-directed sequencing of human papillomavirus types.  
A/Reference number: S36469  
A/Accession: S36480  
A/Molecule type: DNA  
A/Residues: 1-95 <DEL>  
A/Cross-references: UNIPROT:P36821; UNIPARC:UPI00001383F6; EMBL:X74469; NID:G396932; PID  
C/Superfamily: papillomavirus E7 protein  
C/Keywords: DNA binding; early protein; transcription regulation

Query Match 32.9%; Score 170; DB 2; Length 95;  
Best Local Similarity 42.4%; Pred. No. 7.8e-12;  
Matches 42; Conservative 15; Mismatches 32; Indels 10; Gaps 3;

QY 1 MHGDTPTLHEYMLDQPETDLYXXQLNDSSEEDIDPAGQAEPPRAHYNTVFC 58  
DB 1 MGNRRSLNDITLIDELIPVLDHCEQF-DSEENNHQ---LTFPVOAYGVVTTTC 52  
QY 59 CKCDSTLRKLCVOSTHVDIRTLDELMLGTLGIYXPIC 97  
DB 53 CFCGSLRLVLAIVTAHGRSQBELLEGEVQLVCPNCREK 91

## RESULT 26

W7MLJ3  
E7 protein - human papillomavirus type 39  
C/Species: human papillomavirus type 39  
A/Note: host Homo sapiens (man)  
C/Date: 31-Dec-1991 #sequence\_rev15031-Dec-1991 #text\_change 09-Jul-2004  
C/Accession: B38502  
R/Author: C.; Srecek, R.R.  
Virology 181, 419-423, 1991  
A/Title: Genome organization and nucleotide sequence of human papillomavirus type 39.  
A/Reference number: A38502; PMID:1847266  
A/Accession: B38502  
A/Status: translation not shown  
A/Molecule type: DNA  
A/Residues: 1-109 <VOL>  
A/Cross-references: UNIPROT:P24837; UNIPARC:UPI0000138411; GB:M62849; EMBL:M8185; NID:G  
C/Superfamily: papillomavirus E7 protein  
C/Keywords: DNA binding; early protein; transcription regulation

Query Match 32.9%; Score 170; DB 1; Length 109;  
Best Local Similarity 39.1%; Pred. No. 9.1e-12;  
Matches 43; Conservative 16; Mismatches 31; Indels 20; Gaps 4;

QY 1 MHGDTPTLHEYMLDQPETDLYXXQLNDSSEEDIDPAGQAEPPRAHYNTVFC 45  
DB 1 MGNRRSLNDITLIDELIPVLDHCEQF-DSEENNHQ---LTFPVOAYGVVTTTC 57  
QY 46 EPDRAHYNTVFCCKCDSTLRKLCVOSTHVDIRTLDELMLGTLGIYXPIC 95  
DB 58 EPDR--HTICSCCKCNTLQLVVEASRDTRLQQLFMDSLGFCWCA 105

## RESULT 27

S36510  
E7 protein - human papillomavirus type 32  
C/Species: human papillomavirus type 32  
C/Date: 20-Feb-1995 #sequence\_rev15020-Feb-1995 #text\_change 09-Jul-2004  
C/Accession: S36510  
R/Author: H.; Hofmann, B.  
submitted to the EMBL Data Library, August 1993  
A/Description: Primer-directed sequencing of human papillomavirus types.  
A/Reference number: S36469  
A/Accession: S36510  
A/Molecule type: DNA  
A/Residues: 1-104 <DEL>  
A/Cross-references: UNIPROT:P36827; UNIPARC:UPI0000138408; EMBL:X74475; NID:G396981; PID  
C/Superfamily: papillomavirus E7 protein  
C/Keywords: DNA binding; early protein; transcription regulation





E7 protein - human papillomavirus type 19  
 C:Species: human papillomavirus type 19  
 C>Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
 C:Accession: S36486  
 R:Delius, H.; Hofmann, B.  
 Submitted to the EMBL Data Library, August 1993  
 A:Description: Primer-directed sequencing of human papillomavirus types.  
 A:Reference number: S36469  
 A:Accession: S36486  
 A:Molecule type: DNA  
 A:Residues: 1-102 <DEL>  
 A:Cross-references: UNIPROT:P36822; UNIPARC:UPI00001383FC; EMBL:X74470; NID:G396940; PIR  
 A:Superfamily: papillomavirus E7 protein  
 C:Keywords: DNA binding; early protein; transcription regulation

Query Match 22.5%; Score 116.5; DB 1; Length 102;  
 Best Local Similarity 32.7%; Pred. No. 7.8e-06;  
 Matches 33; Conservative 18; Mismatches 35; Indels 15; Gaps 4;

OY 1 MHGDTPTLHEMYL---DLOPET--TDLYXXYQLNDSSEEDDEIDGPAGQAEPPRAHYNIY 53  
 DB 1 MIGKEVTVQDIIELSEVQPEVLPVDFCEBELPNEGTEBPN-----ERATERSAYK 52  
 OY 54 IYFPCCKCDSTLRLCVOSTHVDIRTLBDMGLMTGLIYXPIC 94  
 DB 53 VVVLGCGCKVLRIFVNAATNRGIRTFQGLTGDQLLCPDC 93

RESULT 38  
 W7WLB  
 E7 protein - human papillomavirus type 47  
 C:Species: human papillomavirus type 47  
 A:Note: host Homo sapiens (man)  
 C>Date: 31-Mar-1991 #sequence\_revision 31-Mar-1991 #text\_change 09-Jul-2004  
 C:Accession: B35324  
 R:Kiyono, T.; Adachi, A.; Ishibashi, M.  
 Virology 177, 401-405, 1990  
 A:Title: Genome organization and taxonomic position of human papillomavirus type 47 infe  
 A:Reference number: A35324; MUID:90281611; PMID:2162112  
 A:Accession: B35324  
 A:Status: translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-103 <KTY>  
 A:Cross-references: UNIPROT:P22423; UNIPARC:UPI0000138417; GB:M33305; NID:G333062; PIDN:  
 C:Superfamily: papillomavirus E7 protein  
 C:Keywords: DNA binding; early protein; transcription regulation

Query Match 21.9%; Score 113; DB 1; Length 103;  
 Best Local Similarity 31.7%; Pred. No. 1.9e-05;  
 Matches 32; Conservative 21; Mismatches 34; Indels 14; Gaps 5;

OY 1 MHGDTPTLHEMYL---DLOPET--TDLYXXYQLNDSSEEDDEIDGPAGQAEPPRAHYNIY 55  
 DB 1 MIGKEVTVQDIIELSEVQPEVLPVDFCEBELPNEGTEBPN-----IDRVYKVI 53

OY 56 TFC-CK-CDSTLRLCVOSTHVDIRTLBDMGLMTGLIYXPIC 94  
 DB 54 APCGSCCEVLRIFVNAATNRGIRTFQGLTGDQLLCPDC 94

RESULT 39  
 W7WLB  
 E7 protein - human papillomavirus type 5  
 C:Species: human papillomavirus type 5  
 C>Date: 30-Sep-1987 #sequence\_revision 30-Sep-1987 #text\_change 09-Jul-2004  
 C:Accession: G26277  
 R:Zachow, K.R.; Oeltow, R.S.; Faras, A.J.  
 Virology 158, 251-254, 1987  
 A:Title: Nucleotide sequence and genome organization of human papillomavirus type 5.  
 A:Reference number: A94360; MUID:87207670; PMID:3033892  
 A:Accession: G26277  
 A:Molecule type: DNA  
 A:Residues: 1-103 <ZAC>

A:Cross-references: UNIPROT:P06932; UNIPARC:UPI00000013C6; GB:M17463; NID:G333071; PIDN:  
 C:Superfamily: papillomavirus E7 protein  
 C:Keywords: DNA binding; early protein; transcription regulation

Query Match 21.7%; Score 112; DB 1; Length 103;  
 Best Local Similarity 31.7%; Pred. No. 2.5e-05;  
 Matches 32; Conservative 18; Mismatches 37; Indels 14; Gaps 5;

OY 1 MHGDTPTLHEMYL---DLOPET--TDLYXXYQLNDSSEEDDEIDGPAGQAEPPRAHYNIY 55  
 DB 1 MIGKEVTVQDIIELSEVQPEVLPVDFCEBELPNEGTEBPN-----ERATERSAYK 53

OY 56 TFC-CK-CDSTLRLCVOSTHVDIRTLBDMGLMTGLIYXPIC 94  
 DB 54 APCGSCCEVLRIFVNAATNRGIRTFQGLTGDQLLCPDC 94

RESULT 40  
 W7WLB  
 E7 protein - human papillomavirus type 5b  
 C:Species: human papillomavirus type 5b  
 A:Note: host Homo sapiens (man)  
 C>Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 09-Jul-2004  
 C:Accession: F40480  
 R:Yabe, Y.; Sakai, A.; Hishimoto, T.; Kato, H.; Ogura, H.  
 Virology 183, 793-798, 1991  
 A:Title: A subtype of human papillomavirus 5 (HPV-5b) and its subgenomic segment amplifica  
 A:Reference number: A40480; MUID:91306467; PMID:1649510  
 A:Accession: F40480  
 A:Status: translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-103 <YAB>  
 A:Cross-references: UNIPROT:P26559; UNIPARC:UPI0000006C7; GB:D90252; NID:G222395; PIDN:  
 C:Superfamily: papillomavirus E7 protein  
 C:Keywords: DNA binding; early protein; transcription regulation

Query Match 21.1%; Score 109; DB 1; Length 103;  
 Best Local Similarity 31.7%; Pred. No. 5.4e-05;  
 Matches 32; Conservative 18; Mismatches 37; Indels 14; Gaps 5;

OY 1 MHGDTPTLHEMYL---DLOPET--TDLYXXYQLNDSSEEDDEIDGPAGQAEPPRAHYNIY 55  
 DB 1 MIGKEVTVQDIIELSEVQPEVLPVDFCEBELPNEGTEBPN-----IERISYKVI 53

OY 56 TFC-CK-CDSTLRLCVOSTHVDIRTLBDMGLMTGLIYXPIC 94  
 DB 54 APCGSCCEVLRIFVNAATNRGIRTFQGLTGDQLLCPDC 94

RESULT 41  
 W7WLB  
 E7 protein - human papillomavirus type 8  
 C:Species: human papillomavirus type 8  
 C>Date: 30-Jun-1987 #sequence\_revision 30-Jun-1987 #text\_change 09-Jul-2004  
 C:Accession: A03691  
 R:Finch, P.G.; Ifener, T.; Weninger, J.; Pfister, H.  
 J. Virol. 58, 626-634, 1986  
 A:Title: Epidermodysplasia verruciformis-associated human papillomavirus 8: genomic sequ  
 A:Reference number: A93019; MUID:66200410; PMID:3009874  
 A:Accession: A03691  
 A:Molecule type: DNA  
 A:Residues: 1-103 <FUC>  
 A:Cross-references: UNIPROT:P06430; UNIPARC:UPI00001383F4; GB:M12737; NID:G333074  
 A:Note: this ORF is not annotated in Genbank entry PP88CG  
 C:Superfamily: papillomavirus E7 protein  
 C:Keywords: DNA binding; early protein; transcription regulation

Query Match 20.3%; Score 105; DB 1; Length 103;  
 Best Local Similarity 32.7%; Pred. No. 0.00015;  
 Matches 33; Conservative 17; Mismatches 37; Indels 14; Gaps 5;

OY 1 MHGDTPTLHEMYL---DLOPET--TDLYXXYQLNDSSEEDDEIDGPAGQAEPPRAHYNIY 55

Db 1 MICKETVADPVLKLSRIQPEVLVFDLCEBELPNEQTEBELD-----IERTVKIV 53  
 QY 56 TFC-CK-CDSTLRKCVOSTHVDIRTELDLMGTGIVXPIC 94  
 Db 54 APCGCCCCQVKLRIFVATDSGIRTFQELLFRDLQLCPCC 94

RESULT 42  
 W7WLRB  
 E7 protein - cottontail rabbit papillomavirus  
 C:Species: cottontail rabbit papillomavirus  
 C>Date: 28-Aug-1985 #sequence\_revision 28-Aug-1985 #text\_change 16-Feb-1997  
 C:Accession: A03692  
 R:Giri, I.; Danos, O.; Yaniv, M.  
 Proc. Natl. Acad. Sci. U.S.A. 82, 1580-1584, 1985  
 A:Title: Genomic structure of the cottontail rabbit (Shope) papillomavirus.  
 A:Reference number: A94027; MUID:85166175; PMID:2984661  
 A:Accession: A03692  
 A:Molecule type: DNA  
 A:Residues: 1-94 <GIR>  
 A:Cross-references: UNIPARC:UPI0000000954  
 C:Superfamily: papillomavirus E7 protein  
 C:Keywords: DNA binding; early protein; transcription regulation

Query Match 16.8%; Score 87; DB 1; Length 94;  
 Best Local Similarity 32.6%; Pred. No. 0.014;  
 Matches 31; Conservative 15; Mismatches 45; Indels 4; Gaps 4;

QY 1 MHGDTPLHEMYLDLOPETTDLYXXYXQUNDSEEEDEIDGPAGAPDRAHNIYVFCCK 60  
 Db 1 MGRTPPLSLSELVGETMELSLHCDEALENLSDDDEE-DHDDQVFIERR-YANVSVCCK 58

QY 61 CDSTLR-LCVOSTHVDIRTELDLMGTGIVXPIC 94  
 Db 59 CROTFSEVCAPKA-IRTLNRLISASLSIVCPCC 92

RESULT 43  
 B61399  
 early protein E7 - bovine papillomavirus type 4  
 C:Species: bovine papillomavirus type 4  
 C>Date: 09-Sep-1994 #sequence\_revision 09-Sep-1994 #text\_change 09-Jul-2004  
 C:Accession: B61399  
 R:Jackson, M.E.; Pennie, W.D.; McCaffery, R.E.; Smith, K.T.; Grindley, G.J.; Campo, M.S.  
 Mol. Carcinog. 4, 382-387, 1991  
 A:Title: The B subgroup bovine papillomaviruses lack an identifiable E6 open reading fra  
 A:Reference number: A61399; MUID:92000191; PMID:1654923  
 A:Accession: B61399  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-98 <JAC>  
 A:Cross-references: UNIPROT:Q7L2V7; UNIPARC:UPI000002F8BF; GB:X59063  
 C:Superfamily: bovine papillomavirus type 4 E6 protein

Query Match 16.2%; Score 83.5; DB 2; Length 98;  
 Best Local Similarity 27.0%; Pred. No. 0.036;  
 Matches 27; Conservative 16; Mismatches 40; Indels 17; Gaps 4;

QY 1 MHGDTPLHEMYLDLOPETTDLYXXYXQUNDSEEE--DEIDGPAGAPDRAHNIYVFC 57  
 Db 1 MKGNVTLQDAILED-----TISPINLHCEBIEIEBVDTP-----NPFATAT 46

QY 58 CCKCDSTLRKCVOSTHVDIRTELDLMGTGIVXPIC 97  
 Db 47 CYACEQVRLALVNSTEGIHQLQLLPDNLFLCAACSKQ 86

RESULT 44  
 S19907  
 E7-C protein - human papillomavirus type 33  
 C:Species: human papillomavirus type 33  
 C>Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 09-Jul-2004  
 C:Accession: S19907

R:Snijders, P.J.F.; van den Brule, A.J.C.; Schrijnemakers, H.F.J.; Raaphorst, P.M.C.; Me  
 submitted to the EMBL Data Library, January 1992  
 A:Description: HPV type 33 in a tonsillar carcinoma generates its putative E7 mRNA via tr  
 A:Reference number: S19906  
 A:Accession: S19907  
 A:Molecule type: mRNA  
 A:Residues: 1-55 <SNI>  
 A:Cross-references: UNIPROT:Q81866; UNIPARC:UPI00000F593F; EMBL:X64086; NID:g60282; PIDN  
 C:Superfamily: papillomavirus E7 protein  
 C:Keywords: early protein

Query Match 15.5%; Score 80; DB 2; Length 55;  
 Best Local Similarity 55.6%; Pred. No. 0.047;  
 Matches 15; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 71 SHVDIRTELDLMGTGIVXPIC 97  
 Db 29 STASDLRTIQQLMGTVNIVCPCTCAQ 55

RESULT 45  
 A61399  
 early protein E7 - bovine papillomavirus type 3  
 C:Species: bovine papillomavirus type 3  
 C>Date: 09-Sep-1994 #sequence\_revision 09-Sep-1994 #text\_change 09-Jul-2004  
 C:Accession: A61399  
 R:Jackson, M.E.; Pennie, W.D.; McCaffery, R.E.; Smith, K.T.; Grindley, G.J.; Campo, M.S.  
 Mol. Carcinog. 4, 382-387, 1991  
 A:Title: The B subgroup bovine papillomaviruses lack an identifiable E6 open reading fra  
 A:Reference number: A61399; MUID:92000191; PMID:1654923  
 A:Accession: A61399  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-98 <JAC>  
 A:Cross-references: UNIPROT:Q8BD8; UNIPARC:UPI00000FA386; GB:X59062  
 C:Superfamily: bovine papillomavirus type 4 E6 protein

Query Match 15.4%; Score 79.5; DB 2; Length 98;  
 Best Local Similarity 25.3%; Pred. No. 0.099;  
 Matches 25; Conservative 19; Mismatches 40; Indels 15; Gaps 3;

QY 1 MHGDTPLHEMYLDLOPETTDLYXXYXQUNDSE--EEDIDGPAGAPDRAHNIYVFC 58  
 Db 1 MKGQDTLKNVAVALEVVSPI-----ILCEBIEIEBVDTP-----APAVAVVC 47

QY 59 CCKCDSTLRKCVOSTHVDIRTELDLMGTGIVXPIC 97  
 Db 48 YVCENPLRLALVSPDGIHQHLQQLDPCISILCANCSRE 86

RESULT 46  
 W7WLRB  
 E7 protein - deer papillomavirus  
 C:Species: deer papillomavirus  
 C>Date: 28-May-1986 #sequence\_revision 28-May-1986 #text\_change 16-Feb-1997  
 C:Accession: A03693  
 R:Groff, D.B.; Lancaster, W.D.  
 J. Virol. 56, 85-91, 1985  
 A:Title: Molecular cloning and nucleotide sequence of deer papillomavirus.  
 A:Reference number: A93013; MUID:85293253; PMID:2993669  
 A:Accession: A03693  
 A:Molecule type: DNA  
 A:Residues: 1-102 <GRO>  
 A:Cross-references: UNIPARC:UPI00001749SD  
 C:Superfamily: papillomavirus E7 protein  
 C:Keywords: DNA binding; early protein; transcription regulation

Query Match 15.0%; Score 77.5; DB 1; Length 102;  
 Best Local Similarity 32.3%; Pred. No. 0.17;  
 Matches 20; Conservative 8; Mismatches 31; Indels 3; Gaps 2;

QY 38 IDGPAGAP--DRAHNIYVFCCKCDSTLRKCVOSTHVDIRTELDLMGTGIVXPIC 95

Db 40 VKDE-GKPPKRRHROYVTVSCNDCKRNNFSVTTCTITLTLOQLTLEDDJLCSFCE 98  
Oy 96 QK 97  
Db 99 AK 100

RESULT 47  
W7ML41  
E7 protein - human papillomavirus type 41  
C:Species: human papillomavirus type 41  
C:Accession: B294499; G94457; G94506  
A:Note: host Homo sapiens (man)  
C:Date: 30-Jun-1993 #sequence\_revision 30-Jun-1993 #text\_change 09-Jul-2004  
C:Accession: B43550  
R:Hirt, L.; Hirtsch-Behnam, A.; De Villiers, E.M.  
Virus Res. 18, 179-190, 1990  
A:Title: Nucleotide sequence of human papillomavirus (HPV) type 41: an unusual HPV type  
A:Reference number: A43550  
A:Accession: B43550  
A:Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-114 <H1R>  
A:Cross-references: UNIPROT:P27556; UNIPARC:UPI0000138413; EMBL:X56147; NID:g60942; PIDN:C;Superfamily: papillomavirus E7 protein  
C:Keywords: DNA binding; early protein; transcription regulation; transforming protein;  
F:62-99/Region: zinc finger CCCC motif

Query Match 14.7%; Score 76; DB 1; Length 114;  
Best Local Similarity 26.7%; Pred. No. 0.29; Mismatches 45; Indels 4; Gaps 2;  
Matches 24; Conservative 17; Mismatches 45; Indels 4; Gaps 2;

Oy 1 MHGDTPLHEYMLDQ--PETTDLYXXYQLNDSSEEDIDGPAGQA-EPPRAHYNIIVT 56  
Db 1 MRGNSVDLQELIVQQGGEVFENAAVHSGEHSDDGESESEEREQVQVPTPRRTLYLVES 60  
Oy 57 FCCCKDSTLRICVQSTHVDIRTELDLMGT 86  
Db 61 QCPCFOAIRFVCVANSNTGIRNLQALLVNS 90

RESULT 48  
S36568  
E7 protein - human papillomavirus type 49  
C:Species: human papillomavirus type 49  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
C:Accession: S36568  
R:Delius, H.; Hofmann, B.  
Submitted to the EMBL Data Library, August 1993  
A:Description: Primer-directed sequencing of human papillomavirus types.  
A:Reference number: S36469  
A:Accession: S36568  
A:Molecule type: DNA  
A:Residues: 1-103 <DEL>  
A:Cross-references: UNIPROT:P36830; UNIPARC:UPI0000138419; EMBL:X74480; NID:g397030; PIDN:C;Superfamily: papillomavirus E7 protein  
C:Keywords: DNA binding; early protein; transcription regulation

Query Match 14.5%; Score 75; DB 2; Length 103;  
Best Local Similarity 25.5%; Pred. No. 0.33; Mismatches 45; Indels 10; Gaps 4;  
Matches 26; Conservative 21; Mismatches 45; Indels 10; Gaps 4;

Oy 1 MHGDTPLHEYMLDQ--PETTDLYXXYQLNDSSEEDIDGPAGQAEPBRAH---YNIIVT 56  
Db 1 MIGKEVITPDIILQEFKQPIDLOCYENVLTAEAPAEDEL-----EAEBELIQGIPIYKIVA 55  
Oy 57 FC-CKCDSTLRICVQSTHVDIRTELDLMGTGLVXPICSQK 97  
Db 56 TCGGCGARLRVFLATDAIRSFQELLEELQFLCPQCRRE 97

RESULT 49  
W7HLEP  
E7 protein - European elk papillomavirus

C:Species: European elk papillomavirus  
C:Date: 31-Mar-1989 #sequence\_revision 31-Mar-1989 #text\_change 09-Jul-2004  
C:Accession: B294499; G94457; G94506  
R:Abola, H.; Bergman, P.; Stroem, A.C.; Moreno-Lopez, J.; Petersson, U.  
Gene 50, 195-205, 1986  
A:Title: Organization and expression of the transforming region from the European elk papillomavirus  
A:Reference number: A91567; MUID:87219878; PMID:3034730  
A:Accession: B29499  
A:Molecule type: DNA  
A:Residues: 1-102 <AHO>  
A:Cross-references: UNIPROT:P11332; UNIPARC:UPI000013842D; GB:M15953; NID:g333025; PIDN:C;Superfamily: papillomavirus E7 protein  
R:Petersson, U.  
submitted to GenBank, August 1987  
A:Reference number: A94506  
A:Accession: G94506  
A:Molecule type: DNA  
A:Residues: 1-102 <BRI>  
A:Cross-references: UNIPARC:UPI000013842D; GB:M15953; NID:g333025; PIDN:C;Superfamily: papillomavirus E7 protein  
A:Reference number: A94506  
A:Accession: G94506  
A:Molecule type: DNA  
A:Residues: 1-102 <PBT>  
A:Cross-references: UNIPARC:UPI000013842D; GB:M15953; NID:g333025; PIDN:AAA66850.1; PID:C;Superfamily: papillomavirus E7 protein  
C:Keywords: DNA binding; early protein; transcription regulation

Query Match 14.2%; Score 73.5; DB 1; Length 102;  
Best Local Similarity 28.1%; Pred. No. 0.48; Mismatches 28; Indels 3; Gaps 1;  
Matches 16; Conservative 10; Mismatches 28; Indels 3; Gaps 1;

Oy 41 PACQAEPBRAH---YNIIVFCCKDSTLRICVQSTHVDIRTELDLMGTGLVXPI 94  
Db 41 PPSQKHKKHKKVSYTVPCNGCDKYLFCARTSNTITLQNLKDLCLSTC 97

RESULT 50  
C96767  
unknown protein P2P9.17 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C:Accession: C96767  
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Hutzar, L.  
Nature 408, 816-820, 2000  
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luoro, J.S.; Maizel, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Iker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: A86141; MUID:21016719; PMID:11130712  
A:Accession: C96767  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1273 <STO>  
A:Cross-references: UNIPROT:Q9C9B7; UNIPARC:UPI000004AAB; GB:AE005173; NID:g7109476; PIDN:C;Genetics  
A:Gene: P2P9.17  
A:Map position: 1

Query Match 13.6%; Score 70.5; DB 2; Length 1273;  
Best Local Similarity 20.9%; Pred. No. 16; Mismatches 39; Indels 15; Gaps 2;  
Matches 19; Conservative 18; Mismatches 39; Indels 15; Gaps 2;

Oy 1 MHGDTPLHEYMLDQ--PETTDLYXXYQLNDSSEEDIDGPAGQAEPBRAHY----- 52  
Db 59 LHAENLGIESVLDGSEPTVEYRPHQNSSETSNMNSVSPASADAAAEYGVLRKD 118  
Oy 53 --NIIVFCCKDSTLRICVQSTHVDIRTELD 81

Db 119 TANLINCKPKMDL-----SEQLDSTVLEN 144

RESULT 51  
148733  
protein kinase rck (EC 2.7.1.-) - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 05-Oct-2004  
C:Accession: I48733; S24241  
R:Bladt, P.; Birchmeier, C.  
Differentiation 53, 115-122, 1993  
A>Title: Characterization and expression analysis of the murine rck gene: a protein kinase  
A:Reference number: I48733; PMID:9336030; PMID:8359591  
A:Accession: I48733  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-622 <RES>  
A:Cross-references: UNIPROT:Q04859; UNIPARC:UPI000002747F; EMBL:X66983; NID:G53913; PIDD:R.Bladt, P.; Birchmeier, C.  
Submitted to the EMBL Data Library, June 1992  
A:Description: The murine rck gene encodes a protein kinase with a potential function in  
A:Reference number: S24241  
A:Accession: S24241  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-622 <BLA>  
A:Cross-references: UNIPARC:UPI000002747F; EMBL:X66983; NID:G53913; PIDD:CAA47392.1; PIDD:Genetics:  
A:Gene: rck  
C:Keywords: ATP; phosphotransferase  
F:2-260/Domain: protein kinase homology <KIN>  
F:10-18/Region: protein kinase ATP-binding motif

Query Match 13.2%; Score 68; DB 2; Length 622;  
Best Local Similarity 32.3%; Pred. No. 14;  
Matches 20; Conservative 8; Mismatches 16; Indels 18; Gaps 3;

QY 2 HGDT-PTLHEHYMDLQPERTTLDYXKQKQNDSEBDE-----IDGACGAEPPRAHYNI 54  
Db 296 HLDTKQTLHKQLDPLRPK-----PSSSRDPKPLPNTLDPAQGPQPKQGIQL 344

QY 55 VT 56  
Db 345 QT 346

RESULT 52  
S37431  
ankyrin 2, neuronal long splice form - human  
N:Alternate names: ankyrin B, 440K splice form; ankyrin-B; brain ankyrin; non-erythroid  
N:Contains: ankyrin 2, short form  
C:Species: Homo sapiens (man)  
C>Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004  
C:Accession: S37431; A39643; B39643; A40334; A49462; S14533; S14569  
R:Chan, W.  
Submitted to the EMBL Data Library, September 1993  
A:Reference number: S37431  
A:Accession: S37431  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-3924 <CHA>  
A:Cross-references: UNIPROT:Q01484; UNIPARC:UPI0000125B19; EMBL:Z26634; NID:G406287; PIDD:R:Octo, E.; Kunitomo, M.; McLaughlin, T.; Bennett, V.  
J. Cell Biol. 114, 241-253, 1991  
A>Title: Isolation and characterization of cDNAs encoding human brain ankyrins reveal a  
A:Reference number: A39643; PMID:91302466; PMID:1830053  
A:Accession: A39643  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-2077 <OTI>  
A:Cross-references: UNIPARC:UPI0000177547; GB:X56957  
A:Accession: B39643  
A:Status: preliminary

A:Molecule type: mRNA  
A:Residues: 1-1443, 3585-3924 <OTT>  
A:Cross-references: UNIPARC:UPI0000177548; EMBL:X56958  
R:Tse, W.T.; Menninger, J.C.; Yang-Feng, T.L.; Francke, U.; Sahr, K.E.; Lux, S.E.; Ward, G.  
Genomics 10, 858-866, 1991  
A>Title: Isolation and chromosomal localization of a novel nonerythroid ankyrin gene.  
A:Reference number: A40334; PMID:92009921; PMID:1833308  
A:Accession: A40334  
A:Molecule type: DNA  
A:Residues: 463-474, 'PE', 477-495 <TSE>  
A:Cross-references: UNIPARC:UPI000016A5B5; GB:M37123; NID:G178647; PIDD:AAA62828.1; PIDD:R:Chan, W.; Kordeli, E.; Bennett, V.  
J. Cell Biol. 123, 1463-1473, 1993  
A>Title: 440-kD ankyrinB: structure of the major developmentally regulated domain and seq  
A:Reference number: A49462; PMID:94075409; PMID:8253844  
A:Accession: A49462  
A:Status: preliminary; nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-3924 <RES>  
A:Cross-references: UNIPARC:UPI0000125B19; EMBL:Z26634; NID:G406287; PIDD:CAA81387.1; PIDD:Genetics:  
A:Gene: GDB:ANK2  
A:Cross-references: GDB:127607; OMIM:106410  
A:Map position: 4q25-4q27  
C:Superfamily: ankyrin; ankyrin repeat homology  
C:Keywords: alternative splicing  
F:2-3924/Product: ankyrin 2, long form #status predicted <MA1>  
F:2-1443, 3585-3924/Product: ankyrin 2, short form #status predicted <MA2>  
F:63-95/Domain: ankyrin repeat homology <AN01>  
F:96-128/Domain: ankyrin repeat homology <AN02>  
F:129-161/Domain: ankyrin repeat homology <AN03>  
F:162-190/Domain: ankyrin repeat homology <AN04>  
F:191-223/Domain: ankyrin repeat homology <AN05>  
F:232-264/Domain: ankyrin repeat homology <AN06>  
F:265-297/Domain: ankyrin repeat homology <AN07>  
F:298-330/Domain: ankyrin repeat homology <AN08>  
F:331-363/Domain: ankyrin repeat homology <AN09>  
F:364-396/Domain: ankyrin repeat homology <AN10>  
F:397-429/Domain: ankyrin repeat homology <AN11>  
F:430-462/Domain: ankyrin repeat homology <AN12>  
F:463-495/Domain: ankyrin repeat homology <AN13>  
F:496-528/Domain: ankyrin repeat homology <AN14>  
F:529-561/Domain: ankyrin repeat homology <AN15>  
F:562-594/Domain: ankyrin repeat homology <AN16>  
F:595-627/Domain: ankyrin repeat homology <AN17>  
F:628-660/Domain: ankyrin repeat homology <AN18>  
F:661-693/Domain: ankyrin repeat homology <AN19>  
F:694-726/Domain: ankyrin repeat homology <AN20>  
F:727-759/Domain: ankyrin repeat homology <AN21>  
F:760-792/Domain: ankyrin repeat homology <AN22>  
F:793-825/Domain: ankyrin repeat homology <AN23>

Query Match 13.2%; Score 68; DB 2; Length 3924;  
Best Local Similarity 27.3%; Pred. No. 1e+02;  
Matches 15; Conservative 15; Mismatches 23; Indels 2; Gaps 1;

QY 4 DPTLHEHYMDLQPERTTLDYX--YKQKNDSEBDEIDGACGAEPPRAHYNI 56  
Db 2506 DTPSSEVSYEVYPPKTTDVSTPRPAVHBCAEHDSNGSKKFTPEEMFKWVT 2560

RESULT 53  
T38157  
short-chain dehydrogenase/reductase (EC 1.-.-.-) SPAC22A12.17c [similarity] - fission yeast  
C:Species: Schizosaccharomyces pombe  
C>Date: 20-Oct-2000 #sequence\_revision 20-Oct-2000 #text\_change 05-Oct-2004  
C:Accession: T38157  
R:Pearson, D.; Churcher, C.M.; Barrett, B.G.; Rajandream, M.A.; Wood, V.  
Submitted to the EMBL Data Library, September 1997  
A:Reference number: T38157  
A:Accession: T38157  
A:Molecule type: DNA  
A:Residues: 1-261 <PEA>



Db 446 HGDLKMTTPESKXIAVLYQKR-----ENDDDLGLALFLALPDNLQFVKKREKSPAY 501

Qy 57 FCCCK 60  
Db 502 FCCCK 505

## RESULT 58

early protein E7 - bovine papillomavirus type 6  
C/Species: bovine papillomavirus type 6  
C/Date: 09-Sep-1994 #sequence\_revision 09-Sep-1994 #text\_change 09-Jul-2004  
C/Accession: C61399  
R/Jackson, M.B.; Pennie, W.D.; McCaffery, R.E.; Smith, K.T.; Grindlay, G.J.; Campo, M.S.  
Mol. Carcinog. 4, 382-387, 1991  
A/Title: The B subgroup bovine papillomaviruses lack an identifiable E6 open reading frame  
A/Reference number: A61399; MUID:92000191; PMID:1654923  
A/Accession: C61399  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-100 <3AC>  
A/Cross-references: UNIPROT:Q7LZV6; UNIPARC:UPI0000178418; GB:X59064  
C/Superfamily: bovine papillomavirus type 4 E6 protein

Query Match 12.5%; Score 64.5; DB 2; Length 100;  
Best Local Similarity 26.2%; Pred. No. 4.8;

Matches 28; Conservative 17; Mismatches 33; Indels 29; Gaps 6;

Qy 1 MHGDTPLHEVMDLQPETTDLYXXYQLNDSSEB---DEIDGPAQAEPDRAHYNIVTF 57  
Db 1 MKQSMILKRLAELAEVVS-----PINDCBEELNEVDCE-----VTF 41

Qy 58 C-----CK-CDSTRLCVOGSTHVDIRTELDLM-GLGIVXPICSQK 97  
Db 42 CLVEAVCHVCEQVRLAVVSPDIIQLQQLLTDSISFLCTSCSR 88

## RESULT 59

hypochemical protein F9H16.6 - Arabidopsis thaliana  
C/Species: Arabidopsis thaliana (mouse-ear cress)  
C/Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 05-Oct-2004  
C/Accession: D86342  
R/Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.; Chiu, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Jensen, N.F.; Hughes, B.; Huzar, L.  
Nature 408, 816-820, 2000  
A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani, R.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, K.; M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A/Reference number: A86141; MUID:21016719; PMID:11130712  
A/Accession: D86342  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-614 <STO>  
A/Cross-references: UNIPARC:UPI000004829A; GB:AE005172; NID:94836893; PTDN:AMD30596.1; C  
C/Genetic: 1  
A/Map position: 1  
C/Superfamily: pyrophosphate-dependent phosphofructokinase, PfFB type, 6-phosphofructoki

Query Match 12.5%; Score 64.5; DB 2; Length 614;  
Best Local Similarity 25.0%; Pred. No. 34;  
Matches 26; Conservative 15; Mismatches 28; Indels 35; Gaps 5;

Qy 6 PTLHEVMDLQPETTDLYXXYQLNDSSEB---ED-----EIDGPAQAEPDRAHYNIVTF 54  
Db 507 PALHPAVVDDIKGKAYD-----LRQNAQKFLMEDLYNNPGLQYDGGADAK----- 553  
Qy 55 VTFCCKCDSTRLCVOGSTHV--DIRTELDLMGLTGLVXPICSQ 96

Db 554 -----AVSLCVEDDDPMERIKKQLQEVLDQVRIIVKGCSSG 588

## RESULT 60

phospholipase A2 homolog crotoxin acidic subunit precursor - tropical rattlesnake  
C/Species: Crotalus durissus terrificus (tropical rattlesnake, cascade)  
C/Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 16-Aug-2004  
C/Accession: S01392; A23861; S11382; B23861; C23861  
R/Bouchier, C.; Ducancel, F.; Guignery-Frelat, G.; Bon, C.; Boulain, J.C.; Menez, A.  
Nucleic Acids Res. 16, 9050, 1988  
A/Title: Cloning and sequencing of cDNAs encoding the two subunits of crotoxin.  
A/Reference number: S01392; MUID:89016587; PMID:3174444  
A/Accession: S01392  
A/Molecule type: mRNA  
A/Residues: 1-138 <BDU>  
A/Cross-references: UNIPROT:P08878; UNIPARC:UPI0000131108; EMBL:X12606; NID:952685; PTDN  
Biochemistry 24, 7054-7058, 1985  
R/Aird, S.D.; Kaiser, I.I.; Lewis, R.V.; Kruggel, W.G.

A/Title: Rattlesnake presynaptic neurotoxins: primary structure and evolutionary origin  
A/Reference number: A90500; MUID:86104201; PMID:4084559  
A/Accession: A23861  
A/Molecule type: protein  
A/Residues: 39-73; 'N', 75-76; 'XXXXXXX', 95-102; 'G', 104-118; 125-138 <AIR1>  
A/Cross-references: UNIPARC:UPI0000172777; UNIPARC:UPI0000172778; UNIPARC:UPI0000172779  
R/Aird, S.D.; Yates III, J.R.; Martino, P.A.; Shabnohitz, J.; Hunt, D.F.; Kaiser, I.I.  
Biochim. Biophys. Acta 1040, 217-224, 1990

A/Title: The amino acid sequence of the acidic subunit B-chain of crotoxin.  
A/Reference number: S11382; MUID:90381276; PMID:2400773  
A/Accession: S11382  
A/Molecule type: protein  
A/Residues: 7, 85-118 <AIR2>  
A/Cross-references: UNIPARC:UPI000017277A  
C/Comment: This subunit has no enzymatic or toxin activity. It helps target crotoxin base  
C/Complex: heterodimer of acidic and basic subunits; mature acidic subunit has 3 chains,  
C/Superfamily: Phospholipase A2

C/Keywords: calcium; heterodimer; metalloprotein; pyroglutamic acid; venom  
F/1-16/Domain: signal sequence #status predicted <SIG>  
F/17-38/Domain: propeptide #status predicted <PRO>  
F/39-76/Domain: crotoxin acidic subunit chain A #status experimental <CHA>  
F/79-118/Domain: crotoxin acidic subunit chain B #status experimental <CHB>  
F/125-138/Domain: crotoxin acidic subunit chain C #status experimental <CHC>  
F/44-131/Domain: crotoxin acidic subunit chain A #status predicted  
F/43,45,47,64/Binding site: calcium (Tyr, Gly, Asp) #status predicted  
F/84/Modified site: pyroglutamic acid (Gln) (in mature form) #status experimental  
F/125/Modified site: pyroglutamic acid (Gln) (in mature form) #status experimental

Query Match 12.4%; Score 64; DB 1; Length 138;  
Best Local Similarity 29.3%; Pred. No. 7.7;  
Matches 17; Conservative 7; Mismatches 12; Indels 22; Gaps 3;

Qy 19 TTDLYXXYQLNDSSEBDEI-----DGPAGQAEPDRAHYNIVTFCCCKDSTRLCVOGST 72  
Db 76 TTDVYTRQ-----EDGEIVCGEDPCG-----TQCECDKXAATCFRNS 115

## RESULT 61

TI14580  
C/Species: Beta vulgaris (beet)  
C/Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 31-Dec-2004  
C/Accession: T14580  
R/Alexandrova, R.; Barkla, B.; Blumwald, E.  
submitted to the EMBL Data Library, June 1995  
A/Reference number: Z18149  
A/Accession: T14580  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-391 <ALE>  
A/Cross-references: UNIPROT:Q39436; UNIPARC:UPI00000AD016; EMBL:X87931; NID:g1107525  
A/Experimental source: storage tissue

Query Match 12.4%; Score 64; DB 1; Length 138;  
Best Local Similarity 29.3%; Pred. No. 7.7;  
Matches 17; Conservative 7; Mismatches 12; Indels 22; Gaps 3;



QY 57 FCCKDSTLRACVQSTHYDIRTLEDILMGTLG 88  
 DB 183 LAIQFNSTLPKTYQYSHVDLETKEETLEVSG 214

## RESULT 65

T20513  
 hypothetical protein F02E9.4 - Caenorhabditis elegans  
 C/Species: Caenorhabditis elegans  
 C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
 C/Accession: T20513

R/Gray, I.  
 submitted to the EMBL Data Library, November 1996

A/Reference number: Z19285  
 A/Accession: T20513  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 1-1490 <WIL>  
 A/Cross-references: UNIPROT:O01319; UNIPARC:UPI000007CA61; EMBL:Z81494; PIDD:CA804052.1;  
 A/Experimental source: clone F02E9  
 C/Genetics:  
 A/Map position: 1  
 A/Map position: 1  
 A/Intons: 225/3; 321/2; 373/3; 474/3; 619/3; 664/3; 697/3; 828/3; 868/3; 902/2; 965/2;

Query Match 12.1%; Score 62.5; DB 2; Length 1490;  
 Best Local Similarity 37.1%; Pred. No. 1.5e+02;  
 Matches 13; Conservative 5; Mismatches 8; Indels 9; Gaps 1;

QY 29 NDSSEDEIDGPAGQAPDRA-----HNYI 54  
 DB 1385 DDEDEDEDEPDSGADEPESTSGSNVPMDLNI 1419

## RESULT 66

T00198  
 vtp0 protein - Leucania separata nuclear polyhedrosis virus  
 C/Species: Leucania separata nuclear polyhedrosis virus  
 C/Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004  
 C/Accession: T00198  
 R/Jin, T.; Qi, B.; Qi, Y.  
 submitted to the EMBL Data Library, December 1997

A/Description: Leucania separata multiple nuclear polyhedrosis virus genome DNA 5118bp  
 A/Reference number: Z14120  
 A/Accession: T00198  
 A/Status: translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 1-675 <JIN>  
 A/Cross-references: UNIPROT:O55574; UNIPARC:UPI00000FOF12; EMBL:AB009613; NID:d1177438;  
 C/Genetics:  
 A/Map position: 1  
 A/Map position: 1  
 A/Intons: 225/3; 321/2; 373/3; 474/3; 619/3; 664/3; 697/3; 828/3; 868/3; 902/2; 965/2;

Query Match 12.0%; Score 62; DB 2; Length 675;  
 Best Local Similarity 25.6%; Pred. No. 71;  
 Matches 22; Conservative 12; Mismatches 34; Indels 18; Gaps 3;

QY 1 MNGDPTLHEHYMLDOPETDLYXXYXNDSSSEEDIDGPAQAEPRRAHYIVTFCK 60  
 DB 436 VEGNEPTLG-----RPMRQRYIDTQLG-----DGSFEPRPDQOHVVEALLN 481

QY 61 -----CSTLRACVQSTHYDIRTLEDL 82  
 DB 482 VIPAPSRMAFCELRKHVDIKRPENL 507

## RESULT 67

T04509  
 hypothetical protein F8F16.240 - Arabidopsis thaliana  
 C/Species: Arabidopsis thaliana (mouse-ear cress)  
 C/Date: 30-Apr-1999 #sequence\_revision 30-Apr-1999 #text\_change 09-Jul-2004  
 C/Accession: T04509  
 R/Bevan, M.; Brandt, P.; Dose, S.; Jarke, D.; Scharfe, M.; Schon, O.; Hohnsbeil, J.; Mewe  
 submitted to the Protein Sequence Database, April 1998

A/Reference number: Z15375

A/Accession: T04509  
 A/Molecule type: DNA  
 A/Residues: 1-433 <BEV>  
 A/Cross-references: UNIPROT:O49591; UNIPARC:UPI00000AB12F; EMBL:AL021633  
 A/Experimental source: cultivar Columbia; BAC clone F8F16  
 C/Genetics:  
 A/Map position: 4  
 A/Intons: 14/1; 57/3; 246/3; 303/2; 394/3  
 A/Note: F8F16.240

Query Match 11.9%; Score 61.5; DB 2; Length 433;  
 Best Local Similarity 30.7%; Pred. No. 50;  
 Matches 23; Conservative 7; Mismatches 28; Indels 17; Gaps 4;

QY 18 ETTDLYXXYXNDSSSEED-EIDGPAQAEPRRAHYIVTFCKCD---STLRACVQSTH 73  
 DB 167 EASDSLKLVNNSGASBMDDDGDADKYELD-----PTCLMCDKHKHTLSGMLHMH 220

QY 74 -----VDIRTEED 81  
 DB 221 KHHGFPIPIEYKLD 235

## RESULT 68

F86458  
 unknown protein, 73879-71181 [imported] - Arabidopsis thaliana  
 C/Species: Arabidopsis thaliana (mouse-ear cress)  
 C/Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
 C/Accession: F86458

A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;  
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani,  
 ansen, N.F.; Hughes, B.; Huizar, L.  
 Nature 408, 816-820, 2000  
 A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;  
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani,  
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
 A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon, I  
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
 A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
 A/Reference number: A86141; MUID:21016719; PMID:11130712  
 A/Accession: F86458  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-508 <STO>  
 A/Cross-references: UNIPROT:Q9C804; UNIPARC:UPI00000A876C; GB:AE005172; NID:g10645505; P1  
 C/Genetics:  
 A/Map position: 1

Query Match 11.9%; Score 61.5; DB 2; Length 508;  
 Best Local Similarity 22.7%; Pred. No. 59;  
 Matches 15; Conservative 15; Mismatches 31; Indels 5; Gaps 2;

QY 6 PTLHEHYMLDOPETDLYXXYXNDSSSE--EIDGPAQAEPRRAHYIVTFCKCDS 63  
 DB 204 PVVNHGVSQPSQPV--NHTNDGHQCCDDVBFKEMEDERNVIGTSSACSCRT 260

QY 64 TLRACV 69  
 DB 261 VHYCCV 266

## RESULT 69

T21104  
 hypothetical protein F19B2.6 - Caenorhabditis elegans  
 C/Species: Caenorhabditis elegans  
 C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
 C/Accession: T21104  
 R/Mortimore, B.  
 submitted to the EMBL Data Library, January 1998  
 A/Reference number: Z19374  
 A/Accession: T21104  
 A/Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA  
 A:Residues: 1-823 <WLI>  
 A:Cross-references: UNIPROT:Q9YXS6; UNIPARC:UPI0000060FA9; EMBL:AL021447; NID:e1519050;  
 A:Experimental source: clone F19B2  
 C:Genetics:  
 A:Gene: CESP.F19B2.6  
 A:Map position: 5  
 A:Insertions: 176/3; 369/3; 449/3; 495/1; 528/1; 552/3; 751/3

Query Match 11.9%; Score 61.5; DB 2; Length 823;  
 Best Local Similarity 27.2%; Pred. No. 1e+02;  
 Matches 22; Conservative 11; Mismatches 33; Indels 15; Gaps 4;

Qy 6 PTHHEVMDLOPETTDLYXXYXQLNDSSEEDIDGPAGQAEPPRAHYNIYTFCKCSTL 65  
 Db 127 PTRHSQVYDAAPQ---YGSQALPENORPE-----SAPDR-YQIMVGVGNPS-- 173  
 Qy 66 RLCVQSTHVDIRTELLMGT 86  
 Db 174 --AQQHAQMEIPTWSHQLIGT 192

RESULT 70  
 A59282  
 nonmuscle myosin II heavy chain A - African clawed frog  
 C:Species: Xenopus laevis (African clawed frog)  
 C>Date: 09-Jun-2000 #sequence\_revision 09-Jun-2000 #text\_change 09-Jul-2004  
 C:Accession: A59282  
 R:Bhacti.Dey, N.; Talra, M.; Conci, M.A.; Nooruddin, H.; Melstein, R.S.  
 Mech. Dev. 78, 33-36, 1998  
 A:Title: Differential expression of non-muscle myosin heavy chain genes during Xenopus e  
 A:Reference number: A59282; MUID:99077683; PMID:9858676  
 A:Accession: A59282  
 A:Status: preliminary; not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 1-1964 <BHA>  
 A:Cross-references: UNIPROT:O93522; UNIPARC:UPI00000FB8F7; GB:AF055895; NID:g3660671; P  
 A:Experimental source: cell line XC  
 C:Superfamily: myosin heavy chain; myosin motor domain homology  
 F:84-764/Domain: myosin motor domain homology <MMO>

Query Match 11.9%; Score 61.5; DB 2; Length 1964;  
 Best Local Similarity 27.8%; Pred. No. 2.5e+02;  
 Matches 15; Conservative 15; Mismatches 19; Indels 5; Gaps 2;  
 Qy 1 MHGPTLHEVMDLOPETTDLYXXYXQLNDSSEEDIDGPAGQAEPPRAHYNI 54  
 Db 1053 LEGDSTLDHDIQLAELQAQIAEL--KLQD--AKKEELQALALABEBAQKXL 1101

RESULT 71  
 JC7867  
 endo-1,3(4)-beta-glucanase (EC 3.2.1.6) 1, Osg1 - rice  
 N:Alternate names: endo-1,3(4)-beta-glucanase; endo-1,3-beta-glucanase; Osg1 protein  
 C:Species: Oryza sativa (rice)  
 C>Date: 09-Dec-2002 #sequence\_revision 09-Dec-2002 #text\_change 09-Jul-2004  
 C:Accession: JC7867  
 R:Yamaguchi, T.; Nakayama, K.; Hayashi, T.; Tanaka, Y.; Koike, S.  
 Biosci. Biotechnol. Biochem. 66, 1403-1406, 2002  
 A:Title: Molecular cloning and characterization of a novel beta-1,3-glucanase gene from  
 A:Reference number: JC7867; MUID:22152203; PMID:12162569  
 A:Accession: JC7867  
 A:Molecule type: DNA  
 A:Residues: 1-338 <YAM>  
 A:Cross-references: UNIPROT:Q8LP99; UNIPARC:UPI00000A0PDD; DDBJ:AB070742  
 C:Comment: This enzyme, a hydrolytic enzyme, which belongs to monooxygenous endo-beta  
 glucanase, synergistically acts with chitinase to inhibit fungal growth in vitro. It is a  
 C:Genetics:  
 A:Gene: osg1  
 A:Insertions: 26/1  
 C:Keywords: glycoisidase; hydrolase

Query Match 11.8%; Score 61; DB 2; Length 338;  
 Best Local Similarity 28.6%; Pred. No. 43;  
 Matches 12; Conservative 10; Mismatches 20; Indels 0; Gaps 0;  
 Qy 16 QPETTDLYXXYXQLNDSSEEDIDGPAGQAEPPRAHYNIYTF 57  
 Db 296 RPYPIETRYIFAMFENEMKTDIERNFGLEPDPKSPVPIYTF 337

RESULT 72  
 T09648  
 nucleolin homolog num1 - alfalfa  
 N:Alternate names: num1 protein  
 C:Species: Medicago sativa (alfalfa)  
 C>Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004  
 C:Accession: T09648  
 R:Boegre, U.; Jonak, C.; Mink, M.; Mesikene, I.; Traas, J.; Ha, D.T.C.; Svoboda, I.; Plar  
 Plant Cell 8, 417-428, 1996  
 A:Title: Developmental and cell cycle regulation of Alfalfa nuclel a plant homolog of the  
 A:Reference number: 216796; MUID:96361876; PMID:8721748  
 A:Accession: T09648  
 A:Status: preliminary; translated from GB/EMBL/DDBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-635 <BOE>  
 A:Cross-references: UNIPROT:Q40363; UNIPARC:UPI00000AA67F; EMBL:X88845; NID:g1279562; PII  
 C:Genetics:  
 A:Gene: num1  
 C:Superfamily: nucleolin; ribonucleoprotein repeat homology

Query Match 11.8%; Score 61; DB 2; Length 635;  
 Best Local Similarity 33.3%; Pred. No. 86;  
 Matches 15; Conservative 8; Mismatches 20; Indels 2; Gaps 1;  
 Qy 5 TPPTLHEVMDLOPETTDLYXXYXQLNDSSEEDIDGPAGQAEPPDR 49  
 Db 89 TPAKGNVKAQPEPTTS--ESDSDDISDBEEVKKPAKAVPSK 131

RESULT 73  
 T40524  
 hypothetical protein SPBC530.08 - fission yeast (Schizosaccharomyces pombe)  
 C:Species: Schizosaccharomyces pombe  
 C>Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
 C:Accession: T40524  
 R:Lyme, M.; Wood, V.; Rajandream, M.A.; Barrell, B.G.; Rieger, M.  
 submitted to the EMBL Data Library, May 1998  
 A:Reference number: Z21934  
 A:Accession: T40524  
 A:Status: preliminary; translated from GB/EMBL/DDBJ  
 A:Molecule type: DNA  
 A:Residues: 1-815 <LYN>  
 A:Cross-references: UNIPROT:O59744; UNIPARC:UPI000006B51D; EMBL:AL023634; PIDN:CAA19174.1  
 C:Genetics:  
 A:Gene: SPDB:SPBC530.08  
 A:Map position: 2  
 F:26-62/Domain: GAL4 zinc binuclear cluster homology <GLA>

Query Match 11.8%; Score 61; DB 2; Length 815;  
 Best Local Similarity 40.0%; Pred. No. 1.1e+02;  
 Matches 20; Conservative 6; Mismatches 16; Indels 8; Gaps 4;  
 Qy 37 EIDGPAGQ--EPPRAHYNIYTFCKCSDSTLRCLVQS--THVD--ITLLE 80  
 Db 510 EADSPAMQALKVPDR--QTAFTLACKCVDSAIYCVQNLSHLSGKAKRTLD 557

RESULT 74  
 AB0007  
 probable DNA repair protein radc [imported] - Yersinia pestis (strain CO92)  
 C:Species: Yersinia pestis  
 C>Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 09-Jul-2004  
 C:Accession: AB0007

R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tibball, R.W.; Holden, M.T.G.; Prentice, M.B.  
 demo-Terraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davey, P.; Dougan, G.;  
 11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrett,  
 Nature 413, 523-527, 2001

A>Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.  
 A/Reference number: AB0001; MUID:21470413; PMID:11586360

A/Accession: AB0007

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-222 <KUR>

A/Cross-references: UNIPROT:Q8ZJP3; UNIPARC:UPI00001330CB; GB:AL590842; P1DN:CAC88916.1;

C/Genetics:

A/Gene: radC

C/Superfamily: DNA repair protein radC

Query Match 11.7%; Score 60.5; DB 2; Length 222;

Best Local Similarity 37.8%; Pred. No. 31;

Matches 17; Conservative 6; Mismatches 13; Indels 9; Gaps 1;

QY 41 PQAQEPDRAHNVITFCCKDSTLRVCVOSTHVDITLEDL 85

DB 174 PSQAEPDRAHNVITFCCKDSTLRVCVOSTHVDITLEDL 209

#### RESULT 75

S40936 hypothetical protein ZK632.4 - *Caenorhabditis elegans*

C/Species: *Caenorhabditis elegans*

C/Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 09-Jul-2004

C/Accession: S40936

R/Berks, M.

submitted to the EMBL Data Library, February 1993

A/Reference number: S40933

A/Accession: S40936

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-411 <BER>

A/Cross-references: UNIPROT:P34650; UNIPARC:UPI0000128B77; EMBL:Z22181

C/Genetics:

A/Intons: 44/3; 81/1; 147/1; 207/1

C/Superfamily: yeast mannose-6-phosphate isomerase

Query Match 11.7%; Score 60.5; DB 2; Length 411;

Best Local Similarity 23.6%; Pred. No. 61;

Matches 21; Conservative 17; Mismatches 40; Indels 11; Gaps 3;

QY 2 HGDPTLH---YMLDQPEPTDLYXXQLNDSSEEDIDGPQAEPDRAHNVITFC 58

DB 206 HEKTALEDEIVLFTYFGDVGVFAPILNYPKQ---PGEATFLEPNPHAYIKGDC 261

QY 59 CKC---DSTLRVCVOSTHVDITLEDL 83

DB 262 VECMAQSDNITRAGLTPKYIDVSLVEML 290

#### RESULT 76

C89134 protein F25G6.6 [imported] - *Caenorhabditis elegans*

C/Species: *Caenorhabditis elegans*

C/Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004

C/Accession: C89134

R/anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A>Title: Genome sequence of the nematode *C. elegans*: a platform for investigating biology

A/Reference number: A75000; MUID:99069613; PMID:9851916

A/Note: see websites genome.wustl.edu/gsc/C\_elegans/ and www.sanger.ac.uk/Projects/C\_elegans/

A/Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and

A/Accession: C89134

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-551 <STO>

A/Cross-references: UNIPROT:O15924; UNIPARC:UPI0000080118; GB:chr\_V; P1DN:AAC5799.1; P1

A/Note: Similar to asparagine synthetase; F25G6.6

C/Genetics:  
 A/Gene: F25G6.6  
 A/Map position: 5  
 C/Superfamily: asparagine synthase (glutamine-hydrolyzing)

Query Match 11.7%; Score 60.5; DB 2; Length 551;

Best Local Similarity 27.6%; Pred. No. 84;

Matches 24; Conservative 9; Mismatches 31; Indels 23; Gaps 3;

QY 14 DLQPEPTDLYXXQLNDSSEED-----EIDGPQAEPD---RAHNVITFCCKD 62

DB 476 DRPETEREYWRQIFEDFVYDKMGLVTKYKRTAAMRPDEKEMHLETETLDVKT 535

QY 63 STLRVCVOSTHVDITLEDL 89

DB 536 DLRLRRST-----GSLGV 550

#### RESULT 77

T14476 psIA protein - slime mold (*Dictyostelium discoideum*)

C/Species: *Dictyostelium discoideum*

C/Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004

C/Accession: T14476

R/Yasukawa, H.; Mohanty, S.; Firtel, R.A.

submitted to the EMBL Data Library, December 1997

A/Reference number: Z18117

A/Accession: T14476

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-1269 <YAS>

A/Cross-references: UNIPROT:O43993; UNIPARC:UPI000007CA46; EMBL:AF038919; NID:g2766695; I

A/Experimental source: strain Kax3

C/Genetics:

A/Gene: psIA

Query Match 11.7%; Score 60.5; DB 2; Length 1269;

Best Local Similarity 24.4%; Pred. No. 2.1e+02;

Matches 21; Conservative 17; Mismatches 33; Indels 15; Gaps 4;

QY 6 PTLHEVYLDQPEPTDLYXXQLNDSSEED-----EIDGPQAEPDRA-----HYNI 54

DB 349 PSIHKF--TKKHENTULFMSSTINDGEEDDDDDNDVDGDDNNKEXYDDTSNNKSDI 406

QY 55 VFPCCKDSTLRVCVOSTHVDITLEDL 80

DB 407 VKF--KDDITIVLVNRQRFQFSNFE 430

#### RESULT 78

A41685 SIL protein - human

N/Contains: SIL protein, short form

C/Species: Homo sapiens (man)

C/Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 09-Jul-2004

C/Accession: A41685

R/Aplan, P.D.; Lombardi, D.P.; Kirsch, I.R.

Mol. Cell. Biol. 11, 5462-5469, 1991

A>Title: Structural characterization of SIL, a gene frequently disrupted in T-cell acute

A/Reference number: A41685; MUID:92017825; PMID:1922059

A/Accession: A41685

A/Molecule type: mRNA

A/Residues: 1-1287 <APL>

A/Cross-references: UNIPROT:Q15468; UNIPARC:UPI000072CA6; GB:M74558; NID:G338087; P1DN:J

A/Note: exon/intron borders were determined by genomic DNA sequencing

C/Genetics:

A/Intons: 15/2; 51/2; 89/1; 151/3; 166/1; 213/1; 262/2; 291/2; 341/3; 378/2; 416/3; 739/

C/Superfamily: human SIL protein

C/Keywords: alternative splicing

F/1-1287/Product: SIL protein #statue predicted <MAT>

F/1-165,213-1287/Product: SIL protein, short form #statue predicted <ALT>

Query Match

11.7%; Score 60.5; DB 2; Length 1287;

```

Best Local Similarity 23.8%; Pred. No. 2.1e+02;
Matches 19; Conservative 11; Mismatches 23; Indels 27; Gaps 3;

Qy 23 YXXYXQLNDSSEEPEDIDPA-----GQAEPPRAHYNIIVFCKCD 62
Db 1126 YGLIQQSDNSDEEPPPNADSKSEYLLNQLNRISIPBQLGQKPSKNDHETIN-CSNCE 1184

Qy 63 STURLCVQSTHVDIRTEDL 82
Db 1185 SV-----GTNADTPVLRLNI 1198

RESULT 79
150090
cardoxypeptidase gp180 - Anas sp.
C/Species: Anas sp.
C/Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 09-Jul-2004
C/Accession: 150090
R./Kuraki, K.; Eng, F.; Ishikawa, T.; Turck, C.; Harada, F.; Ganem, D.
J. Biol. Chem. 270, 15022-15028, 1995
A./Title: gp180, a host cell glycoprotein that binds duck hepatitis B virus particles, is
A./Reference number: A57010; MUID:95318059; PMID:7797483
A./Accession: 150090
A./Status: preliminary; translated from GB/EMBL/DBJ
A./Molecule type: mRNA
A./Residues: 1-1389 <KUR>
A./Cross-references: UNIPROT:Q90240; UNIPARC:UPI00000FC41C; EMBL:U25126; NID:g1008477; PI

Query Match 11.7%; Score 60.5; DB 2; Length 1389;
Best Local Similarity 31.9%; Pred. No. 2.3e+02;
Matches 23; Conservative 1; Mismatches 23; Indels 25; Gaps 3;

Qy 1 MHGDTPTLHEYMIDLOPE-----TTDYXXYXQLN-DSSEEDID--- 39
Db 138 MHGDEPLARILLRLAGELVRCMGAGDERLGRLLNTTDLVLLPSLNPDPGFRAREGCGG 197

Qy 40 ----GPAQAE 47
Db 198 GGGGGGEGGGE 209

RESULT 80
H86502
excinnuclease ABC subunit A [imported] - Chlamydia pneumoniae (strain J138)
C/Species: Chlamydia pneumoniae, Chlamydia pneumoniae
C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C/Accession: H86502
R./Shirai, M.; Hirakawa, H.; Kinoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Is
Nucleic Acids Res. 28, 2311-2314, 2000
A./Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A./Reference number: A86491; MUID:20330349; PMID:10871362
A./Accession: H86502
A./Status: preliminary
A./Molecule type: DNA
A./Residues: 1-1826 <STO>
A./Cross-references: UNIPROT:Q92985; UNIPARC:UPI000016569B; GB:BA000008; NID:g9978469; PI
A./Experimental source: strain J138
C/Genetics:
A./Gene: uvrA
C./Superfamily: Chlamydia trachomatis probable excinnuclease ABC chain A; ATP-binding case

Query Match 11.7%; Score 60.5; DB 2; Length 1826;
Best Local Similarity 23.7%; Pred. No. 3e+02;
Matches 23; Conservative 17; Mismatches 32; Indels 25; Gaps 4;

Qy 10 EYMLDLOPETTDLYX-----XQLNDSSE-----EDIDGPAQAEPPRAHYN 53
Db 877 DYVLELGPBGDLGGYLLASCTPKDLIQLNTPRAKALAPYIEGSLDIPVKSPPSPKS 936

Qy 54 IVTFCKCDSTLRICVOST--HVDIRTEDLIMGTIG 88
Db 937 -----CDILIKDAYQNNIKHIDLALPRNSLIAIG 966

RESULT 81
D72120
excinnuclease ABC, chain A CP0678 [imported] - Chlamydia pneumoniae (strains CWL029 ar
C/Species: Chlamydia pneumoniae, Chlamydia pneumoniae
C/Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C/Accession: D72120; E81550
R./Kaiman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;
Nature Genet. 21, 385-389, 1999
A./Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
A./Reference number: A72000; MUID:99206606; PMID:10192288
A./Accession: D72120
A./Status: preliminary
A./Molecule type: DNA
A./Residues: 1-1826 <ARN>
A./Cross-references: UNIPROT:Q92985; UNIPARC:UPI0000137E7B; GB:AE001595; GB:AE001363; NID
A./Experimental source: strain CWL029
R./Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, J.
C.; Dodson, R.; Gwinn, M.; Nelson, W.; Deboy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A./Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A./Reference number: A81500; MUID:20150255; PMID:10684935
A./Accession: E81550
A./Status: preliminary
A./Molecule type: DNA
A./Residues: 1-1826 <REA>
A./Cross-references: UNIPARC:UPI0000137E7B; GB:AE002226; GB:AE002161; NID:g7189592; PIDN:f
A./Experimental source: strain AR39, HU cells
C/Genetics:
A./Gene: uvrA; CP0678
C./Superfamily: Chlamydia trachomatis probable excinnuclease ABC chain A; ATP-binding case
F./609-885/Domain: ATP-binding cassette homology <ABC>

Query Match 11.7%; Score 60.5; DB 2; Length 1826;
Best Local Similarity 23.7%; Pred. No. 3e+02;
Matches 23; Conservative 17; Mismatches 32; Indels 25; Gaps 4;

Qy 10 EYMLDLOPETTDLYX-----XQLNDSSE-----EDIDGPAQAEPPRAHYN 53
Db 877 DYVLELGPBGDLGGYLLASCTPKDLIQLNTPRAKALAPYIEGSLDIPVKSPPSPKS 936

Qy 54 IVTFCKCDSTLRICVOST--HVDIRTEDLIMGTIG 88
Db 937 -----CDILIKDAYQNNIKHIDLALPRNSLIAIG 966

RESULT 82
T03396
Invertase inhibitor homolog - common tobacco
C/Species: Nicotiana tabacum (common tobacco)
C/Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 31-Dec-2004
C/Accession: T03396
R./Greiner, S.; Krausgrill, S.; Rausch, T.
submitted to the EMBL Data Library, April 1997
A./Reference number: Z14924
A./Accession: T03396
A./Status: preliminary; translated from GB/EMBL/DBJ
A./Molecule type: mRNA
A./Residues: 1-172 <GRE>
A./Cross-references: UNIPROT:O49909; UNIPARC:UPI00000AC71C; EMBL:Y12806
A./Experimental source: strain petit havana
C./Superfamily: Ripening-related protein-like, contains similarity to pectinesterase

Query Match 11.6%; Score 60; DB 2; Length 172;
Best Local Similarity 38.1%; Pred. No. 27;
Matches 16; Conservative 6; Mismatches 14; Indels 6; Gaps 2;

Qy 53 NIVTFCKCDSTLRICVOSTHVDIRTE-----DLIMGTIGIV 90
Db 24 NIINTTCRATTNYPICITLHSDPRTSEAGADLT--TLGLV 63

RESULT 83

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RESULT 83

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E70341  
 Conserved hypothetical protein eq\_454 - Aquifex aeolicus  
 C/Species: Aquifex aeolicus  
 C/Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
 C/Accession: E70341  
 R/Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O'V.  
 Nature 392, 353-358, 1998  
 A/Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.  
 A/Reference number: A70300; MUID:98196666; PMID:9537320  
 A/Accession: E70341  
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A/Molecule type: DNA  
 A/Residues: 1-370 <NO>  
 A/Cross-references: UNIPROT:O66761; UNIPARC:UPI0000056374; GB:AE000690; GB:AE000657; NID  
 A/Experimental source: strain VFS  
 C/Genetic: A;Genetic: A  
 A/Residues: eq\_454  
 C/Superfamily: conserved hypothetical protein yodo

Query Match 11.6%; Score 60; DB 1; Length 370;  
 Best Local Similarity 33.3%; Pred. No. 62;  
 Matches 18; Conservative 8; Mismatches 26; Indels 2; Gaps 2;

Oy 30 DSSEEDIDGPAQAPDRAHYIVFCC-KCDSTRLCVSTHVDIRLTEDL 82  
 Db 94 DALKEBDIFG-LTHRYDRLVLTNTTFCAVYCHCKKRIFSQGERARTKEI 146

RESULT 84  
 protein P2E2.2 [imported] - Arabidopsis thaliana  
 C/Species: Arabidopsis thaliana (mouse-ear cress)  
 C/Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
 C/Accession: H86352  
 R/Theologis, A.; Eckert, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Alonso,  
 Chin, C.W.; Chung, M.K.; Com, L.; Conway, A.B.; Conway, A.R.; Cressy, T.H.; Dewar, K.;  
 anen, N.F.; Hughes, B.; Hutzar, L.  
 Nature 408, 816-820, 2000  
 A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lucos, J.S.; Matli, R.; Marziani,  
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
 A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon,  
 Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
 A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
 A/Reference number: A86141; MUID:21016719; PMID:11130712  
 A/Accession: H86352  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-465 <STO>  
 A/Cross-references: UNIPROT:Q9LM64; UNIPARC:UPI000004126E; GB:AE005172; NID:G9280695; PI  
 C/Genetic: A;Genetic: A  
 A/Map position: 1  
 C/Superfamily: Arabidopsis thaliana hypothetical protein F17J16.30

Query Match 11.6%; Score 60; DB 2; Length 465;  
 Best Local Similarity 25.0%; Pred. No. 79;  
 Matches 27; Conservative 17; Mismatches 36; Indels 28; Gaps 5;

Oy 4 DPTPL-----HEY---MLDLPETDLYXXQLNDSSEEDIDGPAQAPDR 50  
 Db 233 DTSGLVLDYSGHAYRTYTEMGLSEARLNLFWEGILNDSDEDDDFDGYGPRWEKRSK 292

Oy 51 HYNIVFCCKCDSTRLCVSTHVDIRLTEDLMTGLGIYVPTCSQRP 98  
 Db 293 -----DAGGLAMTS---NVKTLH-TSSDSELVHSLCKWMP 325

RESULT 85  
 S46281  
 P element - fruit fly (Drosophila ananassae)  
 C/Species: Drosophila bifasciata

C/Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004  
 C/Accession: S46281  
 R/Hagemann, S.; Miller, W.J.; Pinker, W.  
 Mol. Gen. Genet. 244, 168-175, 1994  
 A/Title: Two distinct P element subfamilies in the genome of Drosophila bifasciata.  
 A/Reference number: S46281; MUID:94329069; PMID:8052236  
 A/Accession: S46281  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-562 <HAG>  
 A/Cross-references: UNIPROT:Q9TX47; UNIPARC:UPI000017BE6B

Query Match 11.6%; Score 60; DB 2; Length 562;  
 Best Local Similarity 22.2%; Pred. No. 97;  
 Matches 26; Conservative 14; Mismatches 35; Indels 42; Gaps 5;

Oy 4 DPTPLHRYMDLOPE-----TTDI-----YXXQLNDSSE-----EDE-----I 38  
 Db 280 DVPTLYELIKGLHRRGVFVSVISDWAGNQRLMRELGISSEKTFQGHPEDEDLKFVFS 339

Oy 39 DGP-----AGQAPDRAHYIVFCC-KCDSTRLCVSTHVDIR 78  
 Db 340 DAPHLIKLVNHYLATGALINGQTLTKRSVEQITRCKKTDTITLFKNESHNVRS 396

RESULT 86  
 T37192  
 nebulin-related protein, skeletal muscle - mouse  
 C/Species: Mus musculus (house mouse)  
 C/Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
 C/Accession: T37192  
 R/Luo, G.; Zhang, J.O.; Nguyen, T.P.; Herrera, A.H.; Paterson, B.; Horowitz, R.  
 Cell Motil. Cytoskeleton 38, 75-90, 1997  
 A/Title: Complete cDNA sequence and tissue localization of N-RAP, a novel nebulin-related  
 A/Reference number: Z21630; MUID:97439586; PMID:9295142  
 A/Accession: T37192  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: mRNA  
 A/Residues: 1-1175 <LHO>  
 A/Cross-references: UNIPROT:Q35884; UNIPARC:UPI0000029C98; EMBL:U76618; NID:G2351567; PI  
 A/Function:  
 A/Description: supposed to play a role in anchoring the terminal actin filaments in the  
 A/Note: specifically expressed in skeletal and cardiac muscle  
 C/Keywords: skeletal muscle; tandem repeat

Query Match 11.6%; Score 60; DB 2; Length 1175;  
 Best Local Similarity 30.0%; Pred. No. 2.1e+02;  
 Matches 21; Conservative 8; Mismatches 37; Indels 4; Gaps 2;

Oy 11 YMDLPETDLYXXQLNDSSEEDIDGPAC---QAPDRAHYIVFCC-KCDSTRL 67  
 Db 405 YKADYKRDVVD-YNYLPLHSLILPNNDAGSECCQLQAEHDKKFSVTVTPQIVQAKIN 463

Oy 68 CVQSTHVDIR 77  
 Db 464 AQLSHVNR 473

RESULT 87  
 JC5500  
 phosphoinositide 3-kinase (EC 2.7.1.1) - human  
 C/Species: Homo sapiens (man)  
 C/Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
 C/Accession: JC5500  
 R/Brown, R.A.; Ho, L.K.F.; Weber-Hall, S.J.; Shipley, J.M.; Fry, M.J.  
 Biochem. Biophys. Res. Commun. 233, 537-544, 1997  
 A/Title: Identification and cDNA cloning of a novel mammalian C2 domain-containing phospho  
 A/Reference number: JC5500; MUID:97289668; PMID:9144573  
 A/Accession: JC5500  
 A/Molecule type: mRNA  
 A/Residues: 1-1634 <BRO>  
 A/Cross-references: UNIPROT:O00750; UNIPARC:UPI0000131B5A; GB:Y11312; NID:G2808446; PIDN:  
 A/Experimental source: breast cell

C;Comment: This enzyme is involved in receptor signal transduction, in a signalling complex.  
C;Genetics:  
A;Gene: GDB:PIK3CB; C2-PI3K; PI3K-C2beta  
A;Cross-references: GDB:9837703; OMIM:602838  
A;Map position: 1q32-1q32  
C;Superfamily: Hec2 phosphatidylinositol 3-kinase; protein kinase C C2 region homology  
C;Keywords: phosphotransferase  
F;156-162,169-174/Domain: SH3 #status predicted <SH3>  
F;1037-1320/Domain: catalytic #status predicted <CAT>  
F;1498-1612/Domain: protein kinase C C2 region homology <KC2A>

Query Match 11.5%; Score 60; DB 1; Length 1634;  
Best Local Similarity 25.8%; Pred. No. 3.1e+02;  
Matches 24; Conservative 17; Mismatches 36; Indels 16; Gaps 6;

Qy 11 YMLDLPETTL-----YXXQLNDSSSE-EDFIDGPAQAEPDRAHYIVTFCKCD 62  
Db 341 HMLDILSGSDIQYFLTGYVSAVTPSPHIGDEVMLKV-TVLCDRLO-BALTFTCNCS 398

Qy 63 STLRLCVQS---THVDIRTL--DLWGTGLI 89  
Db 399 STVDLLIYQTLCTYHDDLKANDVDGDFVLKPGCL 431

RESULT 88  
T39642  
conserved hypothetical protein SPBC1709.14 - fission yeast (Schizosaccharomyces pombe)  
C;Species: Schizosaccharomyces pombe  
C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
C;Accession: T39642  
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Rieger, M.  
submitted to the EMBL Data Library, October 1998  
A;Reference number: 221668  
A;Accession: T39642  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-333 <LYN>  
A;Cross-references: UNIPROT:O74739; UNIPARC:UPI000006C436; EMBL:AL031852; PIDs:CAA21253.  
A;Experimental source: strain 972h-; cosmid c1709  
C;Genetics:  
A;Gene: SPDB:SPBC1709.14  
A;Map position: 2  
A;Intons: 109/3; 168/3; 222/1; 235/1  
C;Superfamily: Saccharomyces cerevisiae hypothetical protein YPL096w

Query Match 11.5%; Score 59.5; DB 2; Length 333;  
Best Local Similarity 32.6%; Pred. No. 63;  
Matches 14; Conservative 6; Mismatches 20; Indels 3; Gaps 1;

Qy 8 LHEYMLDLPETTLVYXXQLNDSSSEDEIDG---PAGQNEP 47  
Db 267 LHEINIEFRSLTDSERKALEEERKEDLDGIMRVSQATP 309

RESULT 89  
A48355  
coat protein - pelargonium leaf curl virus  
C;Species: pelargonium leaf curl virus  
C;Date: 17-Feb-1994 #sequence\_revision 17-Feb-1994 #text\_change 09-Jul-2004  
C;Accession: A48355  
R;Li, Y.; Bachmann, S.; Maiss, E.; Commandeur, U.; Breyel, E.; Timpe, U.; Koenig, R.  
Arch. Virol. 129, 349-356, 1993  
A;Title: Nucleotide sequence of the coat protein gene of pelargonium leaf curl virus and  
A;Reference number: A48355; MUID:93228459; PMID:8470957  
A;Accession: A48355  
A;Molecule type: genomic RNA  
A;Residues: 1-389 <LII>  
A;Cross-references: UNIPROT:Q86586; UNIPARC:UPI00000F7BB9; GB:SS8174; NID:9299096; PIDs:  
A;Note: sequence extracted from NCBI backbone (NCBIN:129117, NCBIPI:129118)  
C;Superfamily: carnation mottle virus coat protein  
C;Keywords: coat protein, glycoprotein  
F;8,9,117,118,139,353/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 11.5%; Score 59.5; DB 1; Length 389;  
Best Local Similarity 26.8%; Pred. No. 74;  
Matches 26; Conservative 13; Mismatches 39; Indels 19; Gaps 5;

Qy 4 DTPLHEYMLDLP--ETDLYXXQLNDSSSEDEIDGPAQAEPDRAHYIV----- 55  
Db 154 DQYFNNVVLYVPLCATTEGVAVMYFDXDSERVE---PADRYE--LANYGVLEKAPW 208

Qy 56 ---TFCKCDSTRLCVQSTHVDIRTEEDLWGTGLI 89  
Db 209 AEATLNIPICDRIKRYCDSATVDKLD---LQQLGI 242

RESULT 90  
C96640  
hypothetical protein T25B24.14 (imported) - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C;Accession: C96640  
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;  
ansen, N.F.; Hughes, B.; Huizart, L.  
Nature 408, 816-820, 2000  
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luoro, J.S.; Maitl, R.; Marziani,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A;Reference number: A86141; MUID:21016719; PMID:11130712  
A;Accession: C96640  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-404 <STO>  
A;Cross-references: UNIPROT:Q9S199; UNIPARC:UPI00000A6CC0; GB:AE005173; NID:94585884; PIDs:  
A;Genes: T25B24.14  
A;Map position: 1

Query Match 11.5%; Score 59.5; DB 2; Length 404;  
Best Local Similarity 32.7%; Pred. No. 77;  
Matches 18; Conservative 5; Mismatches 23; Indels 9; Gaps 2;

Qy 5 TPTLHEYMLDLPETTLVYXXQLNDSSSEDEIDG-----PAGQNEP 54  
Db 338 TMLAHNVIRSQGSDSPFRHMEIVESYEGCDGNDGHPVPIVG---DKVMENI 388

RESULT 91  
C69455  
tungsten formylmethanofuran dehydrogenase, subunit F (fwdf) homolog - Archaeoglobus fulgidus  
C;Species: Archaeoglobus fulgidus  
C;Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 05-Oct-2004  
C;Accession: C69455  
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson,  
Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kitzness, E.F.;  
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.  
Nature 390, 364-370, 1997  
A;Authors: Uitterlinden, T.; Cotton, M.D.; Spriggs, T.; Artlich, P.; Kaime, B.P.; Sykes, S.;  
Smith, H.O.; Woese, C.R.; Venter, J.C.  
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeon  
A;Reference number: A69250; MUID:98049343; PMID:9389475  
A;Accession: C69455  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-438 <KLE>  
A;Cross-references: UNIPROT:Q28629; UNIPARC:UPI0000056C46; GB:AE000989; GB:AE000782; NID:  
C;Superfamily: formylmethanofuran dehydrogenase, subunit F; ferredoxin 2 [4Fe-4S] homolog  
F;28-94/Domain: ferredoxin 2 [4Fe-4S] homolog <FER3>

Query Match 11.5%; Score 59.5; DB 2; Length 438;  
Best Local Similarity 21.3%; Pred. No. 84;

Matches 19; Conservative 16; Mismatches 45; Indels 9; Gaps 2;

QY 5 PTLHEVMDLQPTTDLXXKQINDSSE-----EDIDGPAQAEPRRAHYNIVT 56  
 Db 106 SPWVYTKYKTECECTCYKVCPTNAIKREVKITRQOIIEKNKIEGKVEIDRDKNLCG 165

QY 57 FCCCKDSTLRQVSTH-VDIRTELDLLM 84  
 Db 166 ICABFCFVFKWKEKPEHEDVMPYSIDIL 194

RESULT 92  
 B71474  
 probable hep60 chaperonin, mitochondrial - Chlamydia trachomatis (serotype D, strain UM3  
 C/Species: Chlamydia trachomatis  
 C/Date: 13-Sep-1998 #sequence\_revision 13-Sep-1998 #text\_change 09-Jul-2004  
 C/Accession: B71474  
 R/Stephen, R.S.; Kaiman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell,  
 Science 282, 754-759, 1998  
 A/Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trac  
 A/Reference number: A71570; MUID:9900809; PMID:9784136  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-512 <ARN>  
 A/Cross-references: UNIPROT:O84760; UNIPARC:UPI000000339E; GB:AE001348; GB:AE001273; NID  
 A/Experimental source: serotype D, strain UM-3/Cx  
 C/Genetics:  
 A/Gene: CT755  
 C/Superfamily: chaperonin groEL  
 C/Keywords: mitochondrion

Query Match 11.5%; Score 59.5; DB 2; Length 512;  
 Best Local Similarity 24.3%; Pred. No. 1e+02;  
 Matches 26; Conservative 15; Mismatches 41; Indels 25; Gaps 4;

QY 4 DTPPLHVMMDLQPTTDL-----LYXXQQLNDSSEEDIDGPAQAEPRRAHY 52  
 Db 370 DTPPLHMLAKTLNSTGSEFVLGGAAALYATOSLSSEPHSQE-----EQAAV 419

QY 53 NIVFCCCKDSTLRQVSTHVDIRTELDLL--MGTIGVXPICSOX 97  
 Db 420 QIIQOTNR--TLEQLVNSVYMDKLVADKLCSTGTSIGRNVVSQ 464

RESULT 93  
 A85438  
 hypothetical protein A7437080 [imported] - Arabidopsis thaliana  
 C/Species: Arabidopsis thaliana (mouse-ear cress)  
 C/Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 05-Oct-2004  
 C/Accession: A85438  
 R/anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring  
 Nature 402, 769-777, 1999  
 A/Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.  
 A/Reference number: A85001; MUID:20083488; PMID:10617158  
 A/Accession: A85438  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-596 <STO>  
 A/Cross-references: UNIPROT:O23178; UNIPARC:UPI00000986AC; GB:NC\_001268; NID:97270657; F  
 C/Genetics:  
 A/Gene: A7437080  
 A/Map position: 4  
 C/Superfamily: Putative ternary complex factor MIP1

Query Match 11.5%; Score 59.5; DB 2; Length 596;  
 Best Local Similarity 26.1%; Pred. No. 1.2e+02;  
 Matches 23; Conservative 11; Mismatches 33; Indels 21; Gaps 2;

QY 10 EYMLDQPTTDLXXKQINDSSEEDIDGPAQAEPRRAHYNIVTFCCKDSTLRQV 69  
 Db 262 EAADKHSSESTKQLDRLADQDKAQSSE-----DXTL----- 300

QY 70 QSTHVDIRTELDLLMGTIGVXPICSOX 97  
 Db 301 QSGVNAVRSDDLKCLVTIIRISSK 328

RESULT 94  
 T10102  
 diphosphate-fructose-6-phosphate 1-phosphotransferase (EC 2.7.1.90) alpha chain - castor  
 N/Alternate names: 6-phosphofructokinase (pyrophosphate)  
 C/Species: Ricinus communis (castor bean)  
 C/Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004  
 C/Accession: T10102  
 R/Todd, J.F.; Blakeley, S.D.; Dennis, D.T.  
 Gene 152, 181-186, 1995  
 A/Title: Structure of the genes encoding the alpha- and beta-subunits of castor pyrophos  
 A/Reference number: Z16949; MUID:95137384; PMID:7835697  
 A/Accession: T10102  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 1-617 <TOD>  
 A/Cross-references: UNIPROT:Q41140; UNIPARC:UPI000013175D; EMBL:Z32849; NID:9483546; PID  
 C/Genetics:  
 A/Intons: 30/3; 88/2; 126/1; 151/1; 189/1; 211/3; 239/3; 257/3; 284/3; 316/1; 340/3; 37  
 C/Superfamily: pyrophosphate-dependent phosphofructokinase, PFB type; 6-phosphofructoki  
 C/Keywords: phosphotransferase

Query Match 11.5%; Score 59.5; DB 2; Length 617;  
 Best Local Similarity 23.3%; Pred. No. 1.2e+02;  
 Matches 24; Conservative 15; Mismatches 33; Indels 31; Gaps 4;

QY 6 PTLHEVMDLQPTTDLXXKQINDSSEDEI-----DGPAGAEPRRAHYNIVT 56  
 Db 505 PAIHPAVVDLKGK--YELRLNAVKFLMDLRYNCPQFEGPGDAKP----- 552

QY 57 FCCCKDSTLRQVSTH--DIRTELDLLMGTIGVXPICSOX 97  
 Db 553 -----ITLCVEDDQYMRKIKLQEYLDKVRIVPGCSQE 587

RESULT 95  
 E96793  
 hypothetical protein F14G6.15 [imported] - Arabidopsis thaliana  
 C/Species: Arabidopsis thaliana (mouse-ear cress)  
 C/Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 05-Oct-2004  
 C/Accession: E96793  
 R/Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;  
 Nature 408, 816-820, 2000  
 A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;  
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luoro, J.S.; Maitl, R.; Marziani,  
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
 A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon, I  
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
 A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
 A/Reference number: A86141; MUID:21016719; PMID:11130712  
 A/Accession: E96793  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-617 <STO>  
 A/Cross-references: UNIPARC:UPI0000048495; GB:AE005173; NID:96642673; PID:AAF20253.1; G  
 C/Genetics:  
 A/Gene: F14G6.15  
 A/Map position: 1  
 C/Superfamily: pyrophosphate-dependent phosphofructokinase, PFB type; 6-phosphofructokin

Query Match 11.5%; Score 59.5; DB 2; Length 617;  
 Best Local Similarity 24.0%; Pred. No. 1.2e+02;  
 Matches 25; Conservative 15; Mismatches 29; Indels 35; Gaps 5;

QY 6 PTLHEVMDLQPTTDLXXKQINDSSE--ED-----RIDGPAQAEPRRAHYNI 54  
 Db 505 PVIHPASVVDLKGKAYD-----LRQNAQKFLMDVMYRNPQVQYDGGADAK----- 551

Qy 55 VTFCCKCDSTLRLCVQSTHV--DIRTLEDLMGTGLGVXPICSQ 96  
 Db 552 -----AVSLCEVDQYKGIKKIQEYLDQYRTIVKPCSQ 586

## RESULT 96

T01622  
 probable salt-inducible protein At2g18940 (imported) - Arabidopsis thaliana  
 N/Alternate names: hypothetical protein F19F24.14  
 C/Species: Arabidopsis thaliana (mouse-ear cress)  
 C/Date: 19-Feb-1999 #sequence\_revision 19-Feb-1999 #text\_change 09-Jul-2004  
 C/Accession: T01622; E84570  
 R/Rounaley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul  
 submitted to the EMBL Data Library, April 1998  
 A/Description: Arabidopsis thaliana chromosome II BAC F19F24 genomic sequence.  
 A/Reference number: Z14153  
 A/Accession: T01622  
 A/Status: translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 1-822 <R0U>  
 A/Cross-references: UNIPROT:O64624; UNIPARC:UPI00000A9BDA; EMBL:AC003673; NID:G3004543;  
 A/Experimental source: cultivar Columbia  
 R/Lin, X.; Kaul, S.; Rounaley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanhaken, S.E.; Unayam, L.; Tallon, L.;  
 Euse, D.; Niemec, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
 Nature 402, 761-768, 1999  
 A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
 A/Reference number: A84420; MUID:20083487; PMID:10617137  
 A/Accession: E84570  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-822 <STO>  
 A/Cross-references: UNIPARC:UPI00000A9BDA; GB:AE002093; NID:G3004555; PIDN:AC09028.1; C  
 C/Genetics:  
 A/Gene: At2g18940; F19F24.14  
 A/Map position: 2

Query Match 11.5%; Score 59.5; DB 2; Length 822;  
 Best Local Similarity 30.0%; Pred. No. 1.7e+02;  
 Matches 18; Conservative 10; Mismatches 17; Indels 15; Gaps 3;

Qy 4 DTPTLHEYMLDLPETDLYXXYQANDSSEDEID-----GPAGQAEPPRAHYNIIV 55  
 Db 199 DKPIPLQGYLLDVRAYTITLHAYSR---TGKYEKAIDLEFRMKEMGPS---PTLVTVYNI 251

RESULT 97  
 F69189  
 protoporphyrin IX magnesium chelatase (EC 4.99.1.-) - Methanobacterium thermoautotrophic  
 C/Species: Methanobacterium thermoautotrophicum  
 C/Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004  
 C/Accession: F69189  
 R/Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;  
 Qu, D.; Spadafora, R.; Viscarte, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.  
 ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Neolling, J.; Reeve, J.N.  
 J. Bacteriol. 179, 7135-7155, 1997  
 A/Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: func  
 A/Reference number: A69000; MUID:98037514; PMID:9371463  
 A/Accession: F69189  
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA  
 A/Residues: 1-1708 <MTH>  
 A/Cross-references: UNIPROT:O26769; UNIPARC:UPI0000066625; GB:AE000847; GB:AE000666; NID  
 A/Experimental source: strain Delta H  
 C/Genetics:  
 A/Gene: MTH673  
 C/Superfamily: Methanobacterium thermoautotrophicum cobalamin biosynthesis protein N  
 C/Keywords: lyase

Query Match 11.5%; Score 59.5; DB 2; Length 1708;  
 Best Local Similarity 23.9%; Pred. No. 3.7e+02;  
 Matches 28; Conservative 12; Mismatches 46; Indels 31; Gaps 4;

Qy 3 GDPTLHEYMLD-----LQERTDLYXXYQAND-----SSEDEID 38  
 Db 853 GDPTSLYIYIMDGVGEGLOAKRGGLAVIIDHLRPLRLTKGLDGLAGLVSYEAT-- 910

Qy 39 DGPAQAEPPRAHYNIIVTFCCKCDSTLRLCVQSTHV--DIRTLEDLMGTGLGVXP 92  
 Db 911 --PTGNPMRDEYAKQIRETIIKLDLRDLGINATMTDDIDRVHVDLISITSTLMP 965

## RESULT 98

A33977  
 myosin heavy chain, nonmuscle - chicken  
 N/Contains: myosin ATPase (EC 3.6.4.1)  
 C/Species: Gallus gallus (chicken)  
 C/Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004  
 C/Accession: A33977; S06116; A43422  
 R/Shohet, R.V.; Conti, M.A.; Kawamoto, S.; Preston, Y.A.; Brill, D.A.; Adelstein, R.S.  
 Proc. Natl. Acad. Sci. U.S.A. 86, 7726-7730, 1989  
 A/Title: Cloning of the cDNA encoding the myosin heavy chain of a vertebrate cellular my  
 A/Reference number: A33977; MUID:90046668; PMID:2813355  
 A/Accession: A33977  
 A/Molecule type: mRNA  
 A/Residues: 1-1959 <SHO>  
 A/Cross-references: UNIPROT:P14105; UNIPARC:UPI000012PB7F; GB:M26510; NID:G212382; PIDN:  
 R/Katsuragawa, Y.; Yanagisawa, M.; Inoue, A.; Masaki, T.  
 Eur. J. Biochem. 184, 611-616, 1989  
 A/Title: Two distinct nonmuscle myosin-heavy-chain mRNAs are differentially expressed in

B.  
 A/Reference number: S06116; MUID:90032648; PMID:2806244  
 A/Accession: S06116  
 A/Status: not compared with conceptual translation  
 A/Molecule type: mRNA  
 A/Residues: 716-1008 <KAT>  
 A/Cross-references: UNIPARC:UPI0000173E31; GB:X17589  
 A/Note: this translation is not annotated in GenBank entry GCMCFMTH, release 114  
 R/Hodge, T.P.; Cross, R.; Kendrick-Jones, J.  
 J. Cell Biol. 118, 1085-1095, 1992

A/Title: Role of the COOH-terminal nonhelical tailpiece in the assembly of a vertebrate r  
 A/Reference number: A43422; MUID:92381096; PMID:1512291  
 A/Accession: A43422  
 A/Status: nucleic acid sequence not shown; not compared with conceptual translation  
 A/Molecule type: mRNA  
 A/Residues: 1900-1959 <HOD>  
 A/Cross-references: UNIPARC:UPI000008A46C  
 A/Experimental source: brush border  
 A/Note: sequence extracted from NCBI backbone (NCBI:P111947)  
 C/Superfamily: myosin heavy chain; myosin motor domain homology  
 C/Keywords: actin binding; ATP; coiled coil; hydrophobic; methylated amino acid; nucleotide  
 F/84-764/Domain: myosin motor domain homology <MMOT>  
 F/174-181/Region: nucleotide-binding motif A (P-loop)  
 F/552-565/Region: actin binding #status predicted  
 F/636-640/Region: actin binding #status predicted  
 F/837-1936/Domain: coiled coil #status predicted <COI>  
 F/837-1277/Region: S2  
 F/1278-1959/Region: light meromyosin  
 F/1937-1959/Domain: carboxyl-terminal <CBT>  
 F/125/Modified site: N6,N6,N6-trimethyllysine (Lys) #status predicted  
 F/180/Binding site: ATP (Lys) #status predicted  
 F/694/704/Active site: Cys #status predicted

Query Match 11.5%; Score 59.5; DB 1; Length 1959;  
 Best Local Similarity 27.8%; Pred. No. 4.2e+02;  
 Matches 15; Conservative 14; Mismatches 20; Indels 5; Gaps 2;

Qy 1 MEGDPTLHEYMLDLPETDLYXXYQANDSSEDEIDGPAGQAEPPRAHYNIIV 54  
 Db 1053 IEGDSSDIHQIARLQIQIAEL--KIQL---SKKEELQALARVEEAAQKQM 1101

RESULT 99  
 S57908  
 hypothetical 527k polypeptide - rice

C:Species: Oryza sativa (rice)

C>Date: 28-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 09-Jul-2004

C/Accession: S57908; S33529

R/Moriyama, H.; Nitte, T.; Fukuhara, T.

Mol. Gen. Genet. 248, 364-369, 1995

A>Title: Double-stranded RNA in rice: a novel RNA replicon in plants.

A/Reference number: S57908; MUID:96004703; PMID:7565598

A/Accession: S57908

A>Status: preliminary; nucleic acid sequence not shown

A/Molecule type: DNA

A/Residues: 1-4572 <MOR>

A/Cross-references: UNIPROT:Q40712; UNIPARC:UPI00001101CF; EMBL:D32136; MUID:9511666; PID

A/Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994

A/Note: only a part of the coding sequence is given

R/Fukuhara, T.; Moriyama, H.; Pak, J.Y.; Hyakutake, H.; Nitte, T.

Plant Mol. Biol. 21, 1121-1130, 1993

A>Title: Enigmatic double-stranded RNA in Japonica rice.

A/Reference number: S33529; MUID:93257627; PMID:8490131

A/Accession: S33529

A>Status: nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 3854-4370 <PUK>

A/Cross-references: UNIPARC:UPI0000179245; EMBL:D12639

A/Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1992

C:Superfamily: rice hypothetical 527k polypeptide

C:Keywords: polypeptide

Query Match 11.5%; Score 59.5; DB 2; Length 4572;

Best Local Similarity 23.6%; Pred. No. 1.1e+03;

Matches 26; Conservative 14; Mismatches 49; Indels 21; Gaps 4;

QY 7 TLHEVMDLPETTDLYXXQNDSSSE---EDEIDGPAGAEPPRAHNIIVTFCK-CD 62

DB 2664 TYHEES-DLENTQEKSETDGLDENSEALGLDDEVDGDNQSSSENVVYVVEKDMTKETD 2722

QY 63 STRLCTVQSTHVDIRTL-----DILMGTGLGIYVPICSQ 96

DB 2723 ATEKPSANDHKSVPTSDTEIKLPDSDDGTQISFTEIKPTITLPTPICVQ 2772

#### RESULT 100

AP1164

hypothetical protein lmo0718 [imported] - listeria monocytogenes (strain EGD-e)

C/Species: Listeria monocytogenes

C>Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 09-Jul-2004

C/Accession: AP1164

R/Glaeser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker

.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Duseurget, O.; Entian, K.D.; Feihl, H.

Science 294, 849-852, 2001

A/authors: Kreft, U.; Kuhn, M.; Kunst, F.; Kurapkai, G.; Madueno, E.; Maitournam, A.; Ma

ok, C.; Schluter, T.; Simoes, N.; Tixeront, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,

A>Title: Comparative genomics of Listeria species.

A/Reference number: AB1077; MUID:21537279; PMID:11679669

A/Accession: AP1164

A>Status: preliminary

A/Molecule type: DNA

A/Residues: 1-214 <GIA>

A/Cross-references: UNIPROT:Q8Y924; UNIPARC:UPI0000556BC; GB:NC\_003210; PIDN:CAC98796.1

A/Experimental source: strain EGD-e

C/Genetic:

A:Gene: lmo0718

Query Match 11.4%; Score 59; DB 2; Length 214;

Best Local Similarity 21.4%; Pred. No. 44;

Matches 15; Conservative 12; Mismatches 25; Indels 18; Gaps 1;

QY 11 YMDLQPETDLYXXQNDSSSEEDIDGPAGAEPPRAHNIIVTFCKCDSTRLCTVQ 70

DB 137 YMDIFNEESESEHYANLD-----EKQYKNIGPICNDAAAEIATK 178

QY 71 STHVDIRTL 80

DB 179 LTNEMLETTLE 188

Search completed: May 27, 2006, 05:17:20  
Job time : 22.8916 secs

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GenCore version 5.1.8  
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## OM protein - protein search, using sw model

Run on: May 27, 2006, 05:00:16 ; Search time 151.133 Seconds  
(Without alignments)  
599,815 Million cell updates/sec

Title: US-10-530-253-14ED  
Perfect score: 517  
Sequence: 1 MGDRTLTHERMIDLQPERTT.....LEDLMGTGIVXPCISQKP 98

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : UniProt\_7.2:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	512	99.0	98	1	VE7_HPV16
2	512	99.0	98	2	Q547B8_HPV16
3	512	99.0	98	2	Q778G4_HPV16
4	512	99.0	98	2	Q778G6_HPV16
5	512	99.0	98	2	Q778G8_HPV16
6	512	99.0	98	2	Q778G9_HPV16
7	512	99.0	98	2	Q778H1_HPV16
8	512	99.0	98	2	Q778H2_HPV16
9	512	99.0	98	2	Q778H7_HPV16
10	512	99.0	98	2	Q778H9_HPV16
11	512	99.0	98	2	Q778I0_HPV16
12	512	99.0	98	2	Q778I1_HPV16
13	512	99.0	98	2	Q778I3_HPV16
14	512	99.0	98	2	Q778I5_HPV16
15	512	99.0	98	2	Q778A1_HPV16
16	512	99.0	98	2	Q778V7_HPV16
17	508	98.3	98	2	Q12337_HPV16
18	507	98.1	98	2	Q11650_HPV16
19	507	98.1	98	2	Q778H3_HPV16
20	507	98.1	98	2	Q778H5_HPV16
21	507	98.1	98	2	Q8QRD3_HPV16
22	507	98.1	98	2	Q8QRD3_HPV16
23	507	98.1	98	2	Q2MJT4_HPV16
24	504	97.5	98	2	Q12338_HPV16
25	500	96.7	98	2	Q8V10_HPV16
26	499	96.5	98	2	Q8QRD4_HPV16
27	486	94.0	94	2	Q8B5P6_HPV16
28	478	92.5	93	2	Q9QDH6_HPV16
29	477	92.3	93	2	Q9QDH6_HPV16
30	477	92.3	93	2	Q9QDH4_HPV16
31	477	92.3	93	2	Q9QDH8_HPV16

32	406	78.5	77	2	Q8B5P5_9PAPI	Q8B5P5 human papil
33	381.5	73.8	99	1	VE7_HPV35	VE7_HPV35 human papil
34	381.5	73.8	99	2	Q76FP2_9PAPI	Q76FP2 human papil
35	372	72.0	98	1	VE7_HPV31	VE7_HPV31 human papil
36	367	71.0	98	2	Q6T377_HPV31	Q6T377 human papil
37	343	66.3	95	2	Q8B563_9PAPI	Q8B563 human papil
38	316	61.1	99	2	Q90724_HPV67	Q90724 human papil
39	295	57.1	97	1	VE7_HPV33	VE7_HPV33 human papil
40	294	56.9	99	1	VE7_HPV52	VE7_HPV52 human papil
41	289.5	56.0	98	1	VE7_HPV58	VE7_HPV58 human papil
42	289.5	56.0	98	2	Q547M4_HPV58	Q547M4 human papil
43	288.5	55.8	98	2	Q9QCZ1_HPV58	Q9QCZ1 human papil
44	286.5	55.4	98	2	Q8QSF0_HPV58	Q8QSF0 human papil
45	285.5	55.2	98	2	Q8QHN7_HPV58	Q8QHN7 human papil
46	285.5	55.2	98	2	Q8QH02_HPV58	Q8QH02 human papil
47	284.5	55.0	98	2	Q9QCZ2_HPV58	Q9QCZ2 human papil
48	283.5	54.8	98	2	Q8QSE8_HPV58	Q8QSE8 human papil
49	281.5	54.4	98	2	Q8QSE8_HPV58	Q8QSE8 human papil
50	247	47.8	98	2	Q9QLP4_9PAPI	Q9QLP4 human papil
51	245	47.4	98	1	VE7_HPV11	VE7_HPV11 human papil
52	243	47.0	98	1	VE7_HPV6B	VE7_HPV6B human papil
53	242	46.8	98	1	VE7_HPV6A	VE7_HPV6A human papil
54	222.5	43.0	97	1	VE7_HPV34	VE7_HPV34 human papil
55	221.5	42.8	98	2	Q8JNA0_9PAPI	Q8JNA0 human papil
56	221	42.7	43	2	Q91194_HPV16	Q91194 human papil
57	218.5	42.3	113	1	VE7_RHPV1	VE7_RHPV1 human papil
58	216	41.8	108	2	Q9WHG1_9PAPI	Q9WHG1 human papil
59	213	41.2	106	2	VE7_HPV45	VE7_HPV45 human papil
60	212	41.0	106	2	Q9Y4Y3_HUMAN	Q9Y4Y3 homo sapien
61	212	41.0	106	2	Q10609_HPV45	Q10609 human papil
62	211.5	40.9	95	2	Q8B5W9_9PAPI	Q8B5W9 human papil
63	209.5	40.5	105	1	VE7_HPV30	VE7_HPV30 human papil
64	208.5	40.3	105	1	VE7_HPV33	VE7_HPV33 human papil
65	207.5	40.1	90	2	Q56947_9PAPI	Q56947 human papil
66	207.5	40.1	97	2	Q82006_HPV73	Q82006 human papil
67	206.5	39.9	94	2	Q6EG08_9PAPI	Q6EG08 human papil
68	206	39.8	95	2	Q2VJC6_9PAPI	Q2VJC6 human papil
69	204.5	39.6	90	1	VE7_HPV29	VE7_HPV29 human papil
70	202.5	39.2	105	1	VE7_HPV18	VE7_HPV18 human papil
71	202.5	39.2	101	1	VE7_HPV13	VE7_HPV13 human papil
72	200.5	38.8	105	2	Q76Z96_HPV18	Q76Z96 human papil
73	200.5	38.6	94	2	Q6BG01_9PAPI	Q6BG01 human papil
74	199.5	38.6	105	2	Q9QNP7_HPV18	Q9QNP7 human papil
75	198.5	38.4	105	2	Q705H9_HPV43	Q705H9 human papil
76	198	38.3	105	2	Q9QNP6_HPV18	Q9QNP6 human papil
77	196.5	38.0	107	2	Q81965_HPV59	Q81965 human papil
78	195.5	37.8	98	1	VE7_PCpV1	VE7_PCpV1 human papil
79	194	37.5	98	1	Q8V9K9_HPV18	Q8V9K9 human papil
80	192.5	37.2	105	2	Q8B5X6_HPV54	Q8B5X6 human papil
81	191.5	37.0	95	2	Q9QNP5_HPV18	Q9QNP5 human papil
82	191.5	36.9	98	2	Q8UTC7_9PAPI	Q8UTC7 human papil
83	191	36.9	98	2	Q12IS3_HPV13	Q12IS3 human papil
84	190	36.8	98	2	Q98005_9PAPI	Q98005 human papil
85	189	36.6	96	2	VE7_HPV28	VE7_HPV28 human papil
86	186	36.0	87	1	VE7_HPV42	VE7_HPV42 human papil
87	183.5	35.5	93	1	VE7_HPV66	VE7_HPV66 human papil
88	183.5	35.5	105	1	Q37386_CCpV1	Q37386 common chim
89	180.5	34.9	99	2	VE7_HPV54	VE7_HPV54 human papil
90	179.5	34.7	95	1	VE7_HPV70	VE7_HPV70 human papil
91	179	34.6	109	1	VE7_HPV57	VE7_HPV57 human papil
92	178.5	34.5	92	1	VE7_HPV56	VE7_HPV56 human papil
93	178.5	34.5	105	1	VE7_HPV07	VE7_HPV07 human papil
94	178.5	34.5	111	1	VE7_HPV51	VE7_HPV51 human papil
95	178	34.4	101	1	VE7_HPV25	VE7_HPV25 human papil
96	176.5	33.9	97	1	VE7_HPV2A	VE7_HPV2A human papil
97	175.5	33.9	92	2	Q91S8_HPV82	Q91S8 human papil
98	175.5	33.9	100	2	Q2VUB9_9PAPI	Q2VUB9 human papil
99	174.5	33.8	96	2	VE7_HPV10	VE7_HPV10 human papil
100	173.5	33.6	86	1		

## ALIGNMENTS

RESULT 1  
 VET HPV16 STANDARD; PRT; 98 AA.  
 AC POS129;  
 DT 21-JUL-1986, integrated into UniProtKB/Swiss-Prot.  
 DT 21-JUL-1986, sequence version 1.  
 DT 07-FEB-2006, entry version 43.  
 DE Protein E7.  
 GN Name=E7;  
 OS Human papillomavirus type 16.  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 OC Alphapapillomavirus.  
 OX NCBI\_TaxID=333760;  
 RN NUCLEOTIDE SEQUENCE (GENOMIC DNA).  
 RP MEDLINE=85246220; PubMed=2390099;  
 RA Sedozi K., Krammer G., Durst M., Suhai S., Rowekamp W.G.;  
 RT "Human papillomavirus type 16 DNA sequence."; Virol  
 RL Virol 145:181-185 (1985).  
 RN NUCLEOTIDE SEQUENCE (GENOMIC DNA).  
 RP MEDLINE=90218027; PubMed=2157796;  
 RA Schneider-Maunoury S., Penau-Arnaudet G., Breitburd F., Orth G.;  
 RT "Expression of the human papillomavirus type 16 genome in SK-V cells, a line derived from a vulvar intraepithelial neoplasia."; J. Gen. Virol. 71:809-817 (1990).  
 RN NUCLEOTIDE SEQUENCE (GENOMIC DNA).  
 RP Song Y.S., Kee S.H., Kim J.W., Park N.H., Kang S.B., Lee H.P.;  
 RA Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.  
 RN NUCLEOTIDE SEQUENCE (GENOMIC DNA).  
 RP Torreggiani M.L., Buonaguro F.M., Meglio A., Buonaguro L.,  
 RA Beth-Giraldo E., Giraldo G.;  
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
 RN NUCLEOTIDE SEQUENCE (GENOMIC DNA).  
 RP STRAIN=Isolate African 1, and isolate European German 131;  
 RA Terat M., Fu L., Ma Z., Burk R.D.;  
 RT "Cloning and sequencing of non-European human papillomavirus (HPV) variant complete genomes from cervicovaginal cells by an overlapping PCR method."; Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.  
 RN FUNCTION.  
 RP MEDLINE=88223347; PubMed=2836062;  
 RA Phelps W.C., Yee C.L., Munger K., Howley P.M.;  
 RT "The human papillomavirus type 16 E7 gene encodes transactivation and transformation functions similar to those of adenovirus E1A."; Cell 53:539-547 (1988).  
 RL -1- FUNCTION: E7 protein has both transforming and trans-activating activities.  
 CC -1- MISCELLANEOUS: HPV16, in comparison to HPV types 6 and 11, is more often associated with malignant genital cancers in humans.  
 CC -1- SIMILARITY: Belongs to the papillomaviruses E7 protein family.  
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DR InterPro; IPR000148; Papv1\_E7.  
 DR Pfam; PF00527; E7; 1.  
 KW DNA-binding; Early protein; Oncogene; Transcription;  
 KW Transcription regulation.  
 FT CHAIN 1  
 FT MOTIF 58 61 /FTID=PRO\_0000133414.  
 FT MOTIF 91 94 C-XX-C motif-1.  
 FT MOTIF 91 94 C-XX-C motif-2.  
 SQ SEQUENCE 98 AA; 11022 MW; 9BD612534CD2C9EB CRC64;  
 Query Match 99.0%; Score 512; DB 1; Length 98;  
 Best Local Similarity 96.9%; Pred. No. 4.5e-52;  
 Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 MHGDTPLHEVMDLQPEETDLYXXYXOLNDSSEDEIDGPAGAEPRAHYNTVTCCK 60  
 DB 1 MHGDTPLHEVMDLQPEETDLYCYEGLNDSSEDEIDGPAGAEPRAHYNTVTCCK 60  
 QY 61 CDSTLRLCVOSTHYDITLEDLMGTIGIYXPCISQKP 98  
 DB 61 CDSTLRLCVOSTHYDITLEDLMGTIGIYXPCISQKP 98  
 RESULT 3  
 Q78G4 HPV16 PRELIMINARY; PRT; 98 AA.  
 AC Q78G4;  
 DT 10-MAY-2005, integrated into UniProtKB/TREMBL.  
 DT 10-MAY-2005, sequence version 1.  
 DT 07-FEB-2006, entry version 3.

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DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxId=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT Analysis of human papillomavirus type 16 E6 variants in relation to
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
CC -----
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CC -----
EMBL: AJ388069; CAB45131.1; -; Genomic_DNA.
DR GO: GO:0005622; C:intracellular; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR000148; Papv1_E7.
DR Pfam: PF00527; E7; 1.
FT NON TER 98
SQ SEQUENCE 98 AA; 11022 MW; 9BD612534CD2C9EB CRC64;

Query Match 99.0%; Score 512; DB 2; Length 98;
Best Local Similarity 96.9%; Pred. No. 4.5e-52;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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DB 1 MHGDTPLHRYMDLPETTDLYCYEQNDSSSEEDIDGPAGQAEPRAHYNIYTFCK 60
CC -----
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CC -----
EMBL: AJ388067; CAB45127.1; -; Genomic_DNA.
DR GO: GO:0005622; C:intracellular; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR000148; Papv1_E7.
DR Pfam: PF00527; E7; 1.
FT NON TER 98
SQ SEQUENCE 98 AA; 11022 MW; 9BD612534CD2C9EB CRC64;

RESULT 4
Q778G6 HPV16 PRELIMINARY; PRT; 98 AA.
AC Q778G6;
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 3.
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxId=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT Analysis of human papillomavirus type 16 E6 variants in relation to
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
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CC -----
EMBL: AJ388068; CAB45129.1; -; Genomic_DNA.
DR GO: GO:0005622; C:intracellular; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR000148; Papv1_E7.
DR Pfam: PF00527; E7; 1.
FT NON TER 98
SQ SEQUENCE 98 AA; 11022 MW; 9BD612534CD2C9EB CRC64;

Query Match 99.0%; Score 512; DB 2; Length 98;
Best Local Similarity 96.9%; Pred. No. 4.5e-52;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Best Local Similarity 96.9%; Pred. No. 4.5e-52;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDTPLHRYMDLPETTDLYXXYQNDSSSEEDIDGPAGQAEPRAHYNIYTFCK 60
DB 1 MHGDTPLHRYMDLPETTDLYCYEQNDSSSEEDIDGPAGQAEPRAHYNIYTFCK 60
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CC -----
EMBL: AJ388067; CAB45127.1; -; Genomic_DNA.
DR GO: GO:0005622; C:intracellular; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR000148; Papv1_E7.
DR Pfam: PF00527; E7; 1.
FT NON TER 98
SQ SEQUENCE 98 AA; 11022 MW; 9BD612534CD2C9EB CRC64;

Query Match 99.0%; Score 512; DB 2; Length 98;
Best Local Similarity 96.9%; Pred. No. 4.5e-52;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDTPLHRYMDLPETTDLYXXYQNDSSSEEDIDGPAGQAEPRAHYNIYTFCK 60
DB 1 MHGDTPLHRYMDLPETTDLYCYEQNDSSSEEDIDGPAGQAEPRAHYNIYTFCK 60
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CC -----
EMBL: AJ388067; CAB45127.1; -; Genomic_DNA.
DR GO: GO:0005622; C:intracellular; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR000148; Papv1_E7.
DR Pfam: PF00527; E7; 1.
FT NON TER 98
SQ SEQUENCE 98 AA; 11022 MW; 9BD612534CD2C9EB CRC64;

RESULT 6
Q778G9 HPV16 PRELIMINARY; PRT; 98 AA.
AC Q778G9;
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 3.
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxId=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20112892; PubMed=10644829;
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RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
CC -----
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CC -----
DR EMBL, AJ388066; CAB45125.1; -; Genomic_DNA.
DR GO, GO:0005622; C:intracellular; IEA.
DR GO, GO:0003700; P:transcription factor activity; IEA.
DR GO, GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro, IPR000148; Papv1_E7.
DR Pfam, PF00527; E7; 1.
FT NON_TER 98
SQ SEQUENCE 98 AA; 11022 MW; 9BD612534CD2C9EB CRC64;

Query Match 99.0%; Score 512; DB 2; Length 98;
Best Local Similarity 96.9%; Pred. No. 4.5e-52;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDPPTLHEHYMLDLOPETTDLYXXQLNDSSEDEIDGPAGQAEPRRAHNYIVTFCK 60
DB 1 MHGDPPTLHEHYMLDLOPETTDLYCYEQINDSSEDEIDGPAGQAEPRRAHNYIVTFCK 60
DB 61 CDSTLRLCVOSTHVDIRTLIEDLIMGTLGIYXPCISQKP 98
DB 61 CDSTLRLCVOSTHVDIRTLIEDLIMGTLGIYXPCISQKP 98

RESULT 7
ID 0778H1_HPV16 PRELIMINARY; PRT; 98 AA.
AC 0778H1;
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 10-MAY-2005, sequence version 1.
DE 07-FEB-2006, entry version 3.
DE E7 protein (fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_Taxid=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20112892; Pubmed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
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CC -----
DR EMBL, AJ388065; CAB45123.1; -; Genomic_DNA.
DR GO, GO:0005622; C:intracellular; IEA.
DR GO, GO:0003700; P:transcription factor activity; IEA.
DR GO, GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro, IPR000148; Papv1_E7.
DR Pfam, PF00527; E7; 1.
FT NON_TER 98
SQ SEQUENCE 98 AA; 11022 MW; 9BD612534CD2C9EB CRC64;

Query Match 99.0%; Score 512; DB 2; Length 98;
Best Local Similarity 96.9%; Pred. No. 4.5e-52;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDPPTLHEHYMLDLOPETTDLYXXQLNDSSEDEIDGPAGQAEPRRAHNYIVTFCK 60
DB 1 MHGDPPTLHEHYMLDLOPETTDLYCYEQINDSSEDEIDGPAGQAEPRRAHNYIVTFCK 60
DB 61 CDSTLRLCVOSTHVDIRTLIEDLIMGTLGIYXPCISQKP 98
DB 61 CDSTLRLCVOSTHVDIRTLIEDLIMGTLGIYXPCISQKP 98

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DB 61 CDSTLRLCVOSTHVDIRTLIEDLIMGTLGIYXPCISQKP 98

RESULT 8
ID 0778H2_HPV16 PRELIMINARY; PRT; 98 AA.
AC 0778H2;
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 10-MAY-2005, sequence version 1.
DE 07-FEB-2006, entry version 3.
DE E7 protein (fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_Taxid=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20112892; Pubmed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
CC -----
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CC -----
DR EMBL, AJ388064; CAB45121.1; -; Genomic_DNA.
DR GO, GO:0005622; C:intracellular; IEA.
DR GO, GO:0003700; P:transcription factor activity; IEA.
DR GO, GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro, IPR000148; Papv1_E7.
DR Pfam, PF00527; E7; 1.
FT NON_TER 98
SQ SEQUENCE 98 AA; 11022 MW; 9BD612534CD2C9EB CRC64;

Query Match 99.0%; Score 512; DB 2; Length 98;
Best Local Similarity 96.9%; Pred. No. 4.5e-52;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDPPTLHEHYMLDLOPETTDLYXXQLNDSSEDEIDGPAGQAEPRRAHNYIVTFCK 60
DB 1 MHGDPPTLHEHYMLDLOPETTDLYCYEQINDSSEDEIDGPAGQAEPRRAHNYIVTFCK 60
DB 61 CDSTLRLCVOSTHVDIRTLIEDLIMGTLGIYXPCISQKP 98
DB 61 CDSTLRLCVOSTHVDIRTLIEDLIMGTLGIYXPCISQKP 98

RESULT 9
ID 0778H7_HPV16 PRELIMINARY; PRT; 98 AA.
AC 0778H7;
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 10-MAY-2005, sequence version 1.
DE 07-FEB-2006, entry version 3.
DE E7 protein (fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_Taxid=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20112892; Pubmed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
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CC -----
DR EMBL: AJ388061; CAB45115.1; -; Genomic_DNA.
DR GO: GO:0005622; C:intracellular; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR000148; Papyl_E7.
DR Pfam: PF00527; E7; 1.
DR NON_TER 98
SQ SEQUENCE 98 AA; 11022 MW; 9BD612534CD2C9EB CRC64;

Query Match 99.0%; Score 512; DB 2; Length 98;
Best Local Similarity 96.9%; Pred. No. 4.5e-52;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MGGDTPLHEHYMDLQPEETDLYXXYQINDSSEEDIDGPAGAEPRAHYNIIVTFCK 60
Db 1 MGGDTPLHEHYMDLQPEETDLYXXYQINDSSEEDIDGPAGAEPRAHYNIIVTFCK 60
Cc CDSTLRKCVOSTHVDIRTELDLMGTLGIYCPICSKP 98
Db 61 CDSTLRKCVOSTHVDIRTELDLMGTLGIYCPICSKP 98

RESULT 10
07789 HPV16 PRELIMINARY; PRT; 98 AA.
ID 07789 HPV16
AC 07789;
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 10-MAY-2005, sequence version 1.
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OC NCBI_Taxid=333760;
OX [1]
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 B6 variants in relation to
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
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Cc EMBL: AJ388060; CAB45113.1; -; Genomic_DNA.
DR GO: GO:0005622; C:intracellular; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR000148; Papyl_E7.
DR Pfam: PF00527; E7; 1.
DR NON_TER 98
SQ SEQUENCE 98 AA; 11022 MW; 9BD612534CD2C9EB CRC64;

Query Match 99.0%; Score 512; DB 2; Length 98;
Best Local Similarity 96.9%; Pred. No. 4.5e-52;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MGGDTPLHEHYMDLQPEETDLYXXYQINDSSEEDIDGPAGAEPRAHYNIIVTFCK 60
Db 1 MGGDTPLHEHYMDLQPEETDLYXXYQINDSSEEDIDGPAGAEPRAHYNIIVTFCK 60
Cc CDSTLRKCVOSTHVDIRTELDLMGTLGIYCPICSKP 98
Db 61 CDSTLRKCVOSTHVDIRTELDLMGTLGIYCPICSKP 98

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DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 10-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OC NCBI_Taxid=333760;
OX [1]
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 B6 variants in relation to
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
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Cc EMBL: AJ388059; CAB45111.1; -; Genomic_DNA.
DR GO: GO:0005622; C:intracellular; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR000148; Papyl_E7.
DR Pfam: PF00527; E7; 1.
DR NON_TER 98
SQ SEQUENCE 98 AA; 11022 MW; 9BD612534CD2C9EB CRC64;

Query Match 99.0%; Score 512; DB 2; Length 98;
Best Local Similarity 96.9%; Pred. No. 4.5e-52;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MGGDTPLHEHYMDLQPEETDLYXXYQINDSSEEDIDGPAGAEPRAHYNIIVTFCK 60
Db 1 MGGDTPLHEHYMDLQPEETDLYXXYQINDSSEEDIDGPAGAEPRAHYNIIVTFCK 60
Cc CDSTLRKCVOSTHVDIRTELDLMGTLGIYCPICSKP 98
Db 61 CDSTLRKCVOSTHVDIRTELDLMGTLGIYCPICSKP 98

RESULT 12
077811 HPV16 PRELIMINARY; PRT; 98 AA.
ID 077811 HPV16
AC 077811;
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 10-MAY-2005, sequence version 1.
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OC NCBI_Taxid=333760;
OX [1]
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 B6 variants in relation to
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
CC -----
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Cc EMBL: AJ388058; CAB45109.1; -; Genomic_DNA.
DR GO: GO:0005622; C:intracellular; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR000148; Papyl_E7.
DR Pfam: PF00527; E7; 1.
DR NON_TER 98
SQ SEQUENCE 98 AA; 11022 MW; 9BD612534CD2C9EB CRC64;

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SQ SEQUENCE 98 AA; 11022 MW; 9BD612534CD2C9EB CRC64;

Query Match 99.0%; Score 512; DB 2; Length 98;  
Best Local Similarity 96.9%; Pred. No. 4.5e-52;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDTPLHEWMLDQPEPTTDLXXYXQANDSSEDEIDGPAQAEPDRAHYNIIVTFCK 60  
DB 1 MHGDTPLHEWMLDQPEPTTDLXXYXQANDSSEDEIDGPAQAEPDRAHYNIIVTFCK 60

QY 61 CDSTRLCVOSTHVDIRLTEDLMLGTLGIYVPCISQKP 98  
DB 61 CDSTRLCVOSTHVDIRLTEDLMLGTLGIYVPCISQKP 98

RESULT 13

Q77813\_HPV16 PRELIMINARY; PRT; 98 AA.  
AC Q77813;  
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.  
DT 07-FEB-2006, entry version 1.  
DE E7 protein (fragment).  
OS Human papillomavirus type 16.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Alphapapillomavirus.  
OX NCBI\_Taxid=333760;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=20112892; PubMed=10644829;  
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,  
Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;  
RT "Analysis of human papillomavirus type 16 E6 variants in relation to  
p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";  
RL J. Gen. Virol. 81:317-325(2000).  
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DR EMBL: AJ388057; CAB45107.1; -; Genomic\_DNA.  
DR GO: GO:0005622; C:intracellular; IEA.  
DR GO: GO:0003700; F:transcription factor activity; IEA.  
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
DR InterPro: IPR000148; Papv1\_E7.  
DR Pfam: PF00527; E7; 1.  
DR NON TER 98  
FT SEQUENCE 98 AA; 11022 MW; 9BD612534CD2C9EB CRC64;

Query Match 99.0%; Score 512; DB 2; Length 98;  
Best Local Similarity 96.9%; Pred. No. 4.5e-52;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDTPLHEWMLDQPEPTTDLXXYXQANDSSEDEIDGPAQAEPDRAHYNIIVTFCK 60  
DB 1 MHGDTPLHEWMLDQPEPTTDLXXYXQANDSSEDEIDGPAQAEPDRAHYNIIVTFCK 60

QY 61 CDSTRLCVOSTHVDIRLTEDLMLGTLGIYVPCISQKP 98  
DB 61 CDSTRLCVOSTHVDIRLTEDLMLGTLGIYVPCISQKP 98

RESULT 14

Q77815\_HPV16 PRELIMINARY; PRT; 98 AA.  
AC Q77815;  
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.  
DT 07-FEB-2006, entry version 1.  
DE E7 protein (fragment).  
OS Human papillomavirus type 16.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Alphapapillomavirus.  
OX NCBI\_Taxid=333760;

RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=20112892; PubMed=10644829;  
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,  
Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;  
RT "Analysis of human papillomavirus type 16 E6 variants in relation to  
p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";  
RL J. Gen. Virol. 81:317-325(2000).  
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DR EMBL: AJ388056; CAB45105.1; -; Genomic\_DNA.  
DR GO: GO:0005622; C:intracellular; IEA.  
DR GO: GO:0003700; F:transcription factor activity; IEA.  
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
DR InterPro: IPR000148; Papv1\_E7.  
DR Pfam: PF00527; E7; 1.  
DR NON TER 98  
FT SEQUENCE 98 AA; 11022 MW; 9BD612534CD2C9EB CRC64;

Query Match 99.0%; Score 512; DB 2; Length 98;  
Best Local Similarity 96.9%; Pred. No. 4.5e-52;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDTPLHEWMLDQPEPTTDLXXYXQANDSSEDEIDGPAQAEPDRAHYNIIVTFCK 60  
DB 1 MHGDTPLHEWMLDQPEPTTDLXXYXQANDSSEDEIDGPAQAEPDRAHYNIIVTFCK 60

QY 61 CDSTRLCVOSTHVDIRLTEDLMLGTLGIYVPCISQKP 98  
DB 61 CDSTRLCVOSTHVDIRLTEDLMLGTLGIYVPCISQKP 98

RESULT 15

Q77A11\_HPV16 PRELIMINARY; PRT; 98 AA.  
AC Q77A11;  
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.  
DT 07-FEB-2006, entry version 1.  
DE E7 protein (fragment).  
OS Human papillomavirus type 16.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Alphapapillomavirus.  
OX NCBI\_Taxid=333760;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=20112892; PubMed=10644829;  
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,  
Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;  
RT "Analysis of human papillomavirus type 16 E6 variants in relation to  
p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";  
RL J. Gen. Virol. 81:317-325(2000).  
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DR EMBL: AJ242681; CAB45382.1; -; Genomic\_DNA.  
DR GO: GO:0005622; C:intracellular; IEA.  
DR GO: GO:0003700; F:transcription factor activity; IEA.  
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
DR InterPro: IPR000148; Papv1\_E7.  
DR Pfam: PF00527; E7; 1.  
DR NON TER 98  
FT SEQUENCE 98 AA; 11022 MW; 9BD612534CD2C9EB CRC64;

Query Match 99.0%; Score 512; DB 2; Length 98;  
Best Local Similarity 96.9%; Pred. No. 4.5e-52;

Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGDPTLHEHYMDLQPTTDLXXYXOLNDSSEEDIDGPAQAEPRDRAHYNIVTFCK 60  
DB 1 MGDPTLHEHYMDLQPTTDLXXYXOLNDSSEEDIDGPAQAEPRDRAHYNIVTFCK 60

QY 61 CDSTLRVCVSTHVDIRTLTLEDLMGTLGTYXPCISQKP 98  
DB 61 CDSTLRVCVSTHVDIRTLTLEDLMGTLGTYXPCISQKP 98

RESULT 16  
07GV7 HPV16 PRELIMINARY; PRT; 98 AA.  
AC 07GV7; 10-MAY-2005, integrated into UniProtKB/TrEMBL.  
DT 10-MAY-2005, sequence version 1.  
DE 07-FEB-2006, entry version 7.  
DE E7 protein (Early transforming protein E7).  
GN Name=E7;  
OS Human papillomavirus type 16.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Alphapapillomavirus.  
OX NCBI\_Taxid=333760;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Terai M., Burk R.D.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=QV16396E; QV15521E, QV15351AA, QV18158E, QV17722E, and  
RC QV15331AA;  
RX PubMed=15890941; DOI=10.1128/JVI.79.11.7014-7023.2005;  
RA Chen Z., Terai M., Fu L., Herrero R., Desalle R., Burk R.D.;  
RT "Diversifying selection in human papillomavirus type 16 lineages based  
RT on complete genome analyses.";  
RL J. Virol. 79:7014-7023(2005).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=99434235; PubMed=10502513; DOI=10.1006/viro.1999.9868;  
RA Flores E.R., Allen-Hoffmann B.L., Lee D., Sattler C.A., Lambert P.F.;  
RT "Establishment of the human papillomavirus type 16 (HPV-16) life cycle  
RT in an immortalized human foreskin keratinocyte cell line.";  
RL Virology 262:344-354(1999).  
RN [4]  
RP NUCLEOTIDE SEQUENCE.  
RA Terai M., Ma Z., Burk R.D.;  
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=2242222; PubMed=12355268; DOI=10.1007/s00239-002-2344-Y;  
RA DeFilippis V.R., Ayala F.J., Villarreal L.P.;  
RT "Evidence of diversifying selection in human papillomavirus type 16 E6  
RT but not E7 oncogenes.";  
RL J. Mol. Evol. 55:491-499(2002).  
RN [6]  
RP NUCLEOTIDE SEQUENCE.  
RX STRAIN=QEH-2076, QEH-186, PWM-Q42, QEH-525, QEH-453, QEH-501, QEH-561,  
RC QEH-1220, QEH-400, PWM-Q27, QEH-318, and PWM-Q39;  
RX MEDLINE=22182962; PubMed=12195358; DOI=10.1086/332048;  
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,  
RA Cheung J.L.K., Xu L.Y., Cheng A.F.;  
RT "Human papillomavirus type 16 intracyclic variant infection and risk  
RT for cervical neoplasia in southern China.";  
RL J. Infect. Dis. 186:696-700(2002).  
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CC  
CC EMBL; AF402678; AAC05409.1; -; Genomic DNA.  
CC EMBL; AY686580; AAV91653.1; -; Genomic DNA.  
CC EMBL; AY686581; AAV91651.1; -; Genomic DNA.  
CC EMBL; AY686582; AAV91659.1; -; Genomic DNA.

DR EMBL; AY686583; AAV91677.1; -; Genomic DNA.  
DR EMBL; AY686584; AAV91685.1; -; Genomic DNA.  
DR EMBL; AF125673; AAD33253.1; -; Genomic DNA.  
DR EMBL; AF472508; AAO15698.1; -; Genomic DNA.  
DR EMBL; AY089951; AAM11876.1; -; Genomic DNA.  
DR EMBL; AY089952; AAM11878.1; -; Genomic DNA.  
DR EMBL; AY089953; AAM11880.1; -; Genomic DNA.  
DR EMBL; AY089954; AAM11882.1; -; Genomic DNA.  
DR EMBL; AY089955; AAM11884.1; -; Genomic DNA.  
DR EMBL; AF486328; AAL96640.1; -; Genomic DNA.  
DR EMBL; AF486335; AAL96640.1; -; Genomic DNA.  
DR EMBL; AF486337; AAL96642.1; -; Genomic DNA.  
DR EMBL; AF486339; AAL96644.1; -; Genomic DNA.  
DR EMBL; AF486340; AAL96645.1; -; Genomic DNA.  
DR EMBL; AF486341; AAL96646.1; -; Genomic DNA.  
DR EMBL; AF486342; AAL96647.1; -; Genomic DNA.  
DR EMBL; AF486343; AAL96648.1; -; Genomic DNA.  
DR EMBL; AF486347; AAL96652.1; -; Genomic DNA.  
DR EMBL; AF486348; AAL96653.1; -; Genomic DNA.  
DR EMBL; AF486349; AAL96654.1; -; Genomic DNA.  
DR EMBL; AF486352; AAL96657.1; -; Genomic DNA.  
DR EMBL; AY686579; AAV91645.1; -; Genomic DNA.  
DR GO; GO:0005622; C:intracellular; IEA.  
DR GO; GO:0003700; F:transcription factor activity; IEA.  
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
DR InterPro; IPR000146; Papv1\_E7.  
DR Pfam; PF00527; E7; 1.  
SQ SEQUENCE 98 AA; 11022 MW; 9BD612534CD2C9EB CRC64;

Query Match 99.0%; Score 512; DB 2; Length 98;  
Best Local Similarity 96.9%; Pred. No. 4, 5e-52;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGDPTLHEHYMDLQPTTDLXXYXOLNDSSEEDIDGPAQAEPRDRAHYNIVTFCK 60  
DB 1 MGDPTLHEHYMDLQPTTDLXXYXOLNDSSEEDIDGPAQAEPRDRAHYNIVTFCK 60

QY 61 CDSTLRVCVSTHVDIRTLTLEDLMGTLGTYXPCISQKP 98  
DB 61 CDSTLRVCVSTHVDIRTLTLEDLMGTLGTYXPCISQKP 98

RESULT 17  
012337 HPV16 PRELIMINARY; PRT; 98 AA.  
AC 012337;  
DT 01-JUL-1997, integrated into UniProtKB/TrEMBL.  
DT 01-JUL-1997, sequence version 1.  
DE 07-FEB-2006, entry version 21.  
DE E7 protein.  
OS Human papillomavirus type 16.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Alphapapillomavirus.  
OX NCBI\_Taxid=333760;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=97437474; PubMed=9292007;  
RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,  
RA Beth-Giraldo E., Giraldo G.;  
RT "Sequence variations and viral genomic state of human papillomavirus  
RT type 16 in penile carcinomas from Ugandan patients.";  
RL J. Gen. Virol. 78:2199-2208(1997).  
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CC  
CC EMBL; AF003021; AAB70738.1; -; Genomic DNA.  
CC GO; GO:0005622; C:intracellular; IEA.  
CC GO; GO:0003700; F:transcription factor activity; IEA.  
CC GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
CC InterPro; IPR000148; Papv1\_E7.  
CC Pfam; PF00527; E7; 1.  
SQ SEQUENCE 98 AA; 11056 MW; 19DEB8F14CD2C705 CRC64;

Query Match 98.3%; Score 508; DB 2; Length 98;  
 Best Local Similarity 95.9%; Pred. No. 1.3e-51;  
 Matches 94; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MHGDPFLHEHYMDLQPEETDLYXXQLNDSSEDEIDGPAGQAEPRRAHYNIYTFCK 60  
 Db 1 MHGDPFLHEHYMDLQPEETDLYCYEQPDSSEDEIDGPAGQAEPRRAHYNIYTFCK 60

Oy 61 CDSTLRVCVOSTHVDIRTEEDLMGTGIVXPCISQKP 98  
 Db 61 CDSTLRVCVOSTHVDIRTEEDLMGTGIVXPCISQKP 98

RESULT 18  
 ID 01650 HPV16 PRELIMINARY; PRT; 98 AA.  
 AC 011650;  
 DT 01-JUL-1997, integrated into UniProtKB/TrEMBL.  
 DT 01-JUL-1997, sequence version 1.  
 DT 07-FEB-2006, entry version 24.  
 DE Putative transforming protein E7.  
 OS Human papillomavirus type 16.  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 OC Alphapapillomavirus.  
 NCBI\_TaxID=333760;  
 RX MEDLINE=97407827; PubMed=9264576; DOI=10.1006/gyno.1997.4756;  
 RA Song Y.-S., Kee S.-H., Kim J.-W., Park N.-H., Kang S.-B., Chang W.-H.,  
 Lee H.-P.;  
 RT "Major sequence variants in E7 gene of human papillomavirus type 16  
 from cervical cancerous and noncancerous lesions of Korean women.";  
 RL Gynecol. Oncol. 66:275-281(1997).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Song Y.-S., Kee S.-H., Kim J.-W., Park N.-H., Kang S.-B., Chang W.-H.,  
 Lee H.-P.;  
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Terafi M., Ma Z., Burk R.D.;  
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=22182962; PubMed=12195358; DOI=10.1086/342048;  
 RA Chan P.-K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,  
 Cheung J.L.K., Xu L.Y., Cheng A.F.;  
 RT "Human papillomavirus type 16 intratypic variant infection and risk  
 for cervical neoplasia in southern China.";  
 RL J. Infect. Dis. 186:696-700(2002).  
 RN [5]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Terafi M., Fu L., Ma Z., Burk R.D.;  
 RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.  
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 CC -----  
 CC EMBL: U76404; AAC58243.1; -; Genomic DNA.  
 CC EMBL: AF472509; AA015706.1; -; Genomic DNA.  
 CC EMBL: AF486326; AAL96631.1; -; Genomic DNA.  
 CC EMBL: AF486327; AAL96632.1; -; Genomic DNA.  
 CC EMBL: AF486330; AAL96635.1; -; Genomic DNA.  
 CC EMBL: AF486331; AAL96636.1; -; Genomic DNA.  
 CC EMBL: AF486332; AAL96637.1; -; Genomic DNA.  
 CC EMBL: AF486333; AAL96638.1; -; Genomic DNA.  
 CC EMBL: AF486334; AAL96639.1; -; Genomic DNA.  
 CC EMBL: AF486336; AAL96641.1; -; Genomic DNA.  
 CC EMBL: AF486338; AAL96643.1; -; Genomic DNA.  
 CC EMBL: AF486346; AAL96651.1; -; Genomic DNA.  
 CC EMBL: AF486350; AAL96655.1; -; Genomic DNA.  
 CC EMBL: AF486351; AAL96656.1; -; Genomic DNA.

DR EMBL: AF534061; AAQ10404.1; -; Genomic DNA.  
 DR GO: GO:0005622; C:intracellular; IEA.  
 DR GO: GO:0003700; F:transcription factor activity; IEA.  
 DR GO: GO:0006355; F:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro: IPR000148; Papv1\_E7.  
 DR Pfam: PF00527; E7; 1.  
 SQ SEQUENCE 98 AA; 10995 MW; 81E53B534CC3281B CRC64;

Query Match 98.1%; Score 507; DB 2; Length 98;  
 Best Local Similarity 95.9%; Pred. No. 1.7e-51;  
 Matches 94; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDPFLHEHYMDLQPEETDLYXXQLNDSSEDEIDGPAGQAEPRRAHYNIYTFCK 60  
 Db 1 MHGDPFLHEHYMDLQPEETDLYCYEQPDSSEDEIDGPAGQAEPRRAHYNIYTFCK 60

Oy 61 CDSTLRVCVOSTHVDIRTEEDLMGTGIVXPCISQKP 98  
 Db 61 CDSTLRVCVOSTHVDIRTEEDLMGTGIVXPCISQKP 98

RESULT 19  
 ID 07783 HPV16 PRELIMINARY; PRT; 98 AA.  
 AC 07783;  
 DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.  
 DT 05-JUL-2004, sequence version 1.  
 DT 07-FEB-2006, entry version 9.  
 DE E7 protein (fragment).  
 OS Human papillomavirus type 16.  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 OC Alphapapillomavirus.  
 NCBI\_TaxID=333760;  
 RX MEDLINE=20112892; PubMed=10644829;  
 RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,  
 Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;  
 RT "Analysis of human papillomavirus type 16 E6 variants in relation to  
 p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";  
 RL J. Gen. Virol. 81:317-325(2000).  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=20112892; PubMed=10644829;  
 RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,  
 Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;  
 RT "Analysis of human papillomavirus type 16 E6 variants in relation to  
 p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";  
 RL J. Gen. Virol. 81:317-325(2000).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Terafi M., Fu L., Ma Z., Burk R.D.;  
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Terafi M., Fu L., Ma Z., Burk R.D.;  
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=22182962; PubMed=12195358; DOI=10.1086/342048;  
 RA Chan P.-K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,  
 Cheung J.L.K., Xu L.Y., Cheng A.F.;  
 RT "Human papillomavirus type 16 intratypic variant infection and risk  
 for cervical neoplasia in southern China.";  
 RL J. Infect. Dis. 186:696-700(2002).  
 RN [5]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Terafi M., Fu L., Ma Z., Burk R.D.;  
 RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.  
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 CC -----  
 CC EMBL: AJ388063; CAB45119.1; -; Genomic DNA.  
 CC EMBL: GO:0005622; C:intracellular; IEA.  
 CC EMBL: GO:0003700; F:transcription factor activity; IEA.  
 CC EMBL: GO:0006355; F:regulation of transcription, DNA-dependent; IEA.  
 CC EMBL: InterPro: IPR000148; Papv1\_E7.  
 CC EMBL: Pfam: PF00527; E7; 1.  
 CC EMBL: NON TER 98  
 SQ SEQUENCE 98 AA; 10995 MW; 81E53B534CC3281B CRC64;

Query Match 98.1%; Score 507; DB 2; Length 98;  
 Best Local Similarity 95.9%; Pred. No. 1.7e-51;  
 Matches 94; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDPFLHEHYMDLQPEETDLYXXQLNDSSEDEIDGPAGQAEPRRAHYNIYTFCK 60  
 Db 1 MHGDPFLHEHYMDLQPEETDLYCYEQPDSSEDEIDGPAGQAEPRRAHYNIYTFCK 60

Oy 61 CDSTLRVCVOSTHVDIRTEEDLMGTGIVXPCISQKP 98  
 Db 61 CDSTLRVCVOSTHVDIRTEEDLMGTGIVXPCISQKP 98

RESULT 20  
 ID 07785 HPV16 PRELIMINARY; PRT; 98 AA.  
 AC 07785;  
 DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.  
 DT 05-JUL-2004, sequence version 1.

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DT 07-FEB-2006, entry version 9.
DE E7 protein (fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_Taxid=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20112892; Pubmed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Heijmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
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CC -----
DE E7 protein.
DR GO: 0005622; C:intracellular; IEA.
DR GO: 0003700; F:transcription factor activity; IEA.
DR GO: 0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR000148; Papv1_E7.
DR Pfam: PF00527; E7; 1.
DR NON_TER 98
SQ SEQUENCE 98 AA; 10995 MW; 81E53B534CC3281B CRC64;

Query Match 98.1%; Score 507; DB 2; Length 98;
Best Local Similarity 95.9%; Pred. No. 1.7e-51;
Matches 94; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGGDPTLHEHYMDLQPETTDLYXXYQLNDSSEEDIDGPAGQAEPRRAHYNIIVTFCK 60
DB 1 MGGDPTLHEHYMDLQPETTDLYCYEQLNDSSEEDIDGPAGQAEPRRAHYNIIVTFCK 60

QY 61 CDSTLRLCVQSTHYVDIRITLEDLMGTLGIYXPCISQKP 98
DB 61 CDSTLRLCVQSTHYVDIRITLEDLMGTLGIYXPCISQKP 98

RESULT 21
O8ORD2 HPV16 PRELIMINARY; PRT; 98 AA.
ID O8ORD2 HPV16 PRELIMINARY; PRT; 98 AA.
AC O8ORD2;
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2002, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE E7 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_Taxid=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22182962; Pubmed=12195358; DOI=10.1086/342048;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
RT "Human papillomavirus type 16 intracyclic variant infection and risk
RT for cervical neoplasia in southern China.";
RL J. Infect. Dis. 186:696-700(2002).
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CC -----
DE E7 protein.
DR GO: 0005622; C:intracellular; IEA.
DR GO: 0003700; F:transcription factor activity; IEA.
DR GO: 0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR000148; Papv1_E7.
DR Pfam: PF00527; E7; 1.
DR SEQUENCE 98 AA; 11045 MW; 9CAF8C534CD76C4B CRC64;

Query Match 98.1%; Score 507; DB 2; Length 98;
Best Local Similarity 95.9%; Pred. No. 1.7e-51;
Matches 94; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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Best Local Similarity 95.9%; Pred. No. 1.7e-51;
Matches 94; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGGDPTLHEHYMDLQPETTDLYXXYQLNDSSEEDIDGPAGQAEPRRAHYNIIVTFCK 60
DB 1 MGGDPTLHEHYMDLQPETTDLYCYEQLNDSSEEDIDGPAGQAEPRRAHYNIIVTFCK 60

QY 61 CDSTLRLCVQSTHYVDIRITLEDLMGTLGIYXPCISQKP 98
DB 61 CDSTLRLCVQSTHYVDIRITLEDLMGTLGIYXPCISQKP 98

RESULT 22
O8ORD3 HPV16 PRELIMINARY; PRT; 98 AA.
ID O8ORD3 HPV16 PRELIMINARY; PRT; 98 AA.
AC O8ORD3;
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2002, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE E7 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_Taxid=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22182962; Pubmed=12195358; DOI=10.1086/342048;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
RT "Human papillomavirus type 16 intracyclic variant infection and risk
RT for cervical neoplasia in southern China.";
RL J. Infect. Dis. 186:696-700(2002).
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CC -----
DE E7 protein.
DR GO: 0005622; C:intracellular; IEA.
DR GO: 0003700; F:transcription factor activity; IEA.
DR GO: 0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR000148; Papv1_E7.
DR Pfam: PF00527; E7; 1.
DR SEQUENCE 98 AA; 11021 MW; 9BD6125946D2C3B1 CRC64;

Query Match 98.1%; Score 507; DB 2; Length 98;
Best Local Similarity 95.9%; Pred. No. 1.7e-51;
Matches 94; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGGDPTLHEHYMDLQPETTDLYXXYQLNDSSEEDIDGPAGQAEPRRAHYNIIVTFCK 60
DB 1 MGGDPTLHEHYMDLQPETTDLYCYEQLNDSSEEDIDGPAGQAEPRRAHYNIIVTFCK 60

QY 61 CDSTLRLCVQSTHYVDIRITLEDLMGTLGIYXPCISQKP 98
DB 61 CDSTLRLCVQSTHYVDIRITLEDLMGTLGIYXPCISQKP 98

RESULT 23
O2MJT4 HPV16 PRELIMINARY; PRT; 98 AA.
ID O2MJT4 HPV16 PRELIMINARY; PRT; 98 AA.
AC O2MJT4;
DT 07-FEB-2006, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, sequence version 1.
DT 07-FEB-2006, entry version 1.
DE E7 protein.
GN Name=E7;
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_Taxid=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Meshkat Z., Hassan Z.M., Soleimanjahi H., Mahmoudi M., Mirshahabi H.,

```

RA Ghafari S.R., Sabokbar T.;  
 RT "Cloning and sequence analysis of Human papillomavirus type 16 E7 gene  
 in Iran."  
 RL Submitted (DEC-2005) to the EMBL/GenBank/DBJ databases.  
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 CC -----  
 DR EMBL: DQ333401; ABC54573.1; -; Genomic DNA.  
 SQ SEQUENCE 98 AA; 10992 MW; 9BD6125357D379EB CRC64;

Query Match 98.1%; Score 507; DB 2; Length 98;  
 Best Local Similarity 95.9%; Pred. No. 1.7e-51;  
 Matches 94; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 MHGDTPLHEHYMLDQEPETDLYXXQLNDSSEEDIDGPAGAEPRRAHNYITFCCK 60  
 DB 1 MHGDTPLHEHYMLDQEPETDLYCYEQLNDSSEEDIDGPAGAEPRRAHNYITFCCK 60  
 OY 61 CDSTLRCLCVOSTHVDIRLTEDLMGTGIVXPCISQKP 98  
 DB 61 CDSTLRCLCVOSTHVDIRLTEDLMGTGIVCPICSQKP 98

RESULT 24  
 ID 013338 HPV16 PRELIMINARY; PRT; 98 AA.  
 AC 013338

DT 01-JUL-1997, integrated into UniProtKB/TrEMBL.

DT 01-JUL-1997, sequence version 1.

DT 07-FEB-2006, entry version 20.

DE E7 protein.

OS Human papillomavirus type 16.

OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;

OC Alphapapillomavirus.

OX NCBI\_TaxID=333760;

NP NUCLEOTIDE SEQUENCE.

RX MEDLINE=97437474; PubMed=9292007;

RA Tonesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,

RA Beth-Giraldo E., Giraldo G.;

RT "Sequence variations and viral genomic state of human papillomavirus

RT type 16 in penile carcinomas from Ugandan patients.";

RL J. Gen. Virol. 78:2199-2208(1997).

RN [2]

NP NUCLEOTIDE SEQUENCE.

RA Jinhui X., Xinxing W., Yun T.;

RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.

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CC -----

CC EMBL: AF003032; AAB70739.1; -; Genomic DNA.

DR EMBL: AF477385; AAM03025.1; -; Genomic DNA.

DR GO: GO:0005622; C:intracellular; IEA.

DR GO: GO:0003700; F:transcription factor activity; IEA.

DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

DR InterPro: IPR000148; Papv1\_E7.

DR Pfam: PF00527; E7; 1.

DR SEQUENCE 98 AA; 10969 MW; 9BD612534CCBA59B CRC64;

Query Match 97.5%; Score 504; DB 2; Length 98;

Best Local Similarity 95.9%; Pred. No. 3.9e-51;

Matches 94; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 MHGDTPLHEHYMLDQEPETDLYXXQLNDSSEEDIDGPAGAEPRRAHNYITFCCK 60

DB 1 MHGDTPLHEHYMLDQEPETDLYCYEQLNDSSEEDIDGPAGAEPRRAHNYITFCCK 60

OY 61 CDSTLRCLCVOSTHVDIRLTEDLMGTGIVXPCISQKP 98

DB 61 CDSTLRCLCVOSTHVDIRLTEDLMGTGIVCPICSQKP 98

OY 61 CDSTLRCLCVOSTHVDIRLTEDLMGTGIVXPCISQKP 98

DB 61 CDSTLRCLCVOSTHVDIRLTEDLMGTGIVCPICSQKP 98

OY 61 CDSTLRCLCVOSTHVDIRLTEDLMGTGIVXPCISQKP 98

DB 61 CDSTLRCLCVOSTHVDIRLTEDLMGTGIVCPICSQKP 98

RESULT 25  
 ID 08V1J0 HPV16 PRELIMINARY; PRT; 98 AA.  
 AC 08V1J0

DT 01-MAR-2002, integrated into UniProtKB/TrEMBL.

DT 01-MAR-2002, sequence version 1.

DT 07-FEB-2006, entry version 11.

DE E7 protein.

OS Human papillomavirus type 16.

OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;

OC Alphapapillomavirus.

OX NCBI\_TaxID=333760;

NP [1]

NP NUCLEOTIDE SEQUENCE.

RA Jinhui X., Xinxing W., Yun T.;

RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.

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CC -----

CC EMBL: AF461264; AAL66736.1; -; Genomic DNA.

DR GO: GO:0005622; C:intracellular; IEA.

DR GO: GO:0003700; F:transcription factor activity; IEA.

DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

DR InterPro: IPR000148; Papv1\_E7.

DR Pfam: PF00527; E7; 1.

DR SEQUENCE 98 AA; 10997 MW; 9BD610834CCBA59B CRC64;

Query Match 96.7%; Score 500; DB 2; Length 98;

Best Local Similarity 94.9%; Pred. No. 1.2e-50;

Matches 93; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 MHGDTPLHEHYMLDQEPETDLYXXQLNDSSEEDIDGPAGAEPRRAHNYITFCCK 60  
 DB 1 MHGDTPLHEHYMLDQEPETDLYCYEQLNDSSEEDIDGPAGAEPRRAHNYITFCCK 60  
 OY 61 CDSTLRCLCVOSTHVDIRLTEDLMGTGIVXPCISQKP 98  
 DB 61 CDSTLRCLCVOSTHVDIRLTEDLMGTGIVCPICSRKP 98

RESULT 26  
 ID 08ORD4 HPV16 PRELIMINARY; PRT; 98 AA.  
 AC 08ORD4

DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.

DT 01-JUN-2002, sequence version 1.

DT 07-FEB-2006, entry version 10.

DE E7 protein.

OS Human papillomavirus type 16.

OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;

OC Alphapapillomavirus.

OX NCBI\_TaxID=333760;

NP [1]

NP NUCLEOTIDE SEQUENCE.

RX MEDLINE=22182962; PubMed=12195358; DOI=10.1086/342048;

RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,

RA Cheung J.L.K., Xu L.Y., Cheng A.F.;

RT "Human papillomavirus type 16 intratypic variant infection and risk

RT for cervical neoplasia in southern China.";

RL J. Infect. Dis. 186:696-700(2002).

RN [1]

NP NUCLEOTIDE SEQUENCE.

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CC -----

CC EMBL: AF46329; AAL96634.1; -; Genomic DNA.

DR GO: GO:0005622; C:intracellular; IEA.

DR GO: GO:0003700; F:transcription factor activity; IEA.

DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

DR InterPro: IPR000148; Papv1\_E7.

DR Pfam: PF00527; E7; 1.

DR SEQUENCE 98 AA; 11025 MW; 86E24B234CC3281B CRC64;

Query Match 96.5%; Score 499; DB 2; Length 98;  
 Best Local Similarity 94.9%; Pred. No. 1,5e-50;  
 Matches 93; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MHGDTPLHEHYMDLOPETTDLYXXYQOLNDSSEEDSIDDPAGQAEPRRAHYNIVTFCK 60  
 DB 1 MHGDTPLHEHYMDLOPETTDLYXXYQOLNDSSEEDSIDDPAGQAEPRRAHYNIVTFCK 60

QY 61 CDSTLRACVSTHVDIRTTEDLMGTGIVXPC 98  
 DB 61 CDSTLRACVSTHVDIRTTEDLMGTGIVXPC 98

RESULT 27  
 Q98SP6\_HPV16 PRELIMINARY; PRT; 94 AA.  
 AC Q98SP6;  
 DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.  
 DT 01-MAR-2003, sequence version 1.  
 DT 07-FEB-2006, entry version 10.  
 DE E7 oncoprotein (Fragment).  
 OS Human papillomavirus type 16.  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 OC Alphapapillomavirus.  
 OX NCBI\_TaxID=333760;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Ponglikitmongkol M., Vaeaeooteacharn K.,  
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
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 CC EMBL: AF469197; AAO15692.1; -; Genomic\_DNA.  
 DR GO: GO:0005622; C:intracellular; IEA.  
 DR GO: GO:0003700; F:transcription factor activity; IEA.  
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro: IPR000148; Papv1\_E7.  
 DR Pfam: PF00527; E7; 1.  
 FT NON TER 94  
 FT SEQUENCE 94 AA; 10555 MW; 7CC3281BB2AE2C8A CRC64;

Query Match 94.0%; Score 486; DB 2; Length 94;  
 Best Local Similarity 95.7%; Pred. No. 4.9e-45;  
 Matches 90; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDTPLHEHYMDLOPETTDLYXXYQOLNDSSEEDSIDDPAGQAEPRRAHYNIVTFCK 60  
 DB 1 MHGDTPLHEHYMDLOPETTDLYXXYQOLNDSSEEDSIDDPAGQAEPRRAHYNIVTFCK 60

QY 61 CDSTLRACVSTHVDIRTTEDLMGTGIVXPC 94  
 DB 61 CDSTLRACVSTHVDIRTTEDLMGTGIVXPC 94

RESULT 28  
 Q9QDH6\_HPV16 PRELIMINARY; PRT; 93 AA.  
 AC Q9QDH6;  
 DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.  
 DT 01-MAY-2000, sequence version 1.  
 DT 07-FEB-2006, entry version 14.  
 DE E7 protein (Fragment).  
 OS Human papillomavirus type 16.  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 OC Alphapapillomavirus.  
 OX NCBI\_TaxID=333760;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Lee H.P., Song Y.S., Kim J.W., Park N.H., Kang S.B.,  
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
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 CC EMBL: AF187867; AAF13395.1; -; Genomic\_DNA.  
 DR GO: GO:0005622; C:intracellular; IEA.  
 DR GO: GO:0003700; F:transcription factor activity; IEA.  
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro: IPR000148; Papv1\_E7.  
 DR Pfam: PF00527; E7; 1.  
 FT NON TER 93  
 FT SEQUENCE 93 AA; 10513 MW; 92C7054341326A1F CRC64;

Query Match 92.5%; Score 478; DB 2; Length 93;  
 Best Local Similarity 95.7%; Pred. No. 4.2e-48;  
 Matches 89; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MHGDTPLHEHYMDLOPETTDLYXXYQOLNDSSEEDSIDDPAGQAEPRRAHYNIVTFCK 60  
 DB 1 MHGDTPLHEHYMDLOPETTDLYXXYQOLNDSSEEDSIDDPAGQAEPRRAHYNIVTFCK 60

QY 61 CDSTLRACVSTHVDIRTTEDLMGTGIVXPI 93  
 DB 61 CDSTLRACVSTHVDIRTTEDLMGTGIVXPI 93

RESULT 29  
 Q9QDH2\_HPV16 PRELIMINARY; PRT; 93 AA.  
 AC Q9QDH2;  
 DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.  
 DT 01-MAY-2000, sequence version 1.  
 DT 07-FEB-2006, entry version 14.  
 DE E7 protein (Fragment).  
 OS Human papillomavirus type 16.  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 OC Alphapapillomavirus.  
 OX NCBI\_TaxID=333760;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Lee H.P., Song Y.S., Kim J.W., Park N.H., Kang S.B.,  
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
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 CC EMBL: AF187869; AAF13399.1; -; Genomic\_DNA.  
 DR GO: GO:0005622; C:intracellular; IEA.  
 DR GO: GO:0003700; F:transcription factor activity; IEA.  
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro: IPR000148; Papv1\_E7.  
 DR Pfam: PF00527; E7; 1.  
 FT NON TER 93  
 FT SEQUENCE 93 AA; 10452 MW; 83281BB2AE2C8A1F CRC64;

Query Match 92.3%; Score 477; DB 2; Length 93;  
 Best Local Similarity 95.7%; Pred. No. 5.6e-48;  
 Matches 89; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDTPLHEHYMDLOPETTDLYXXYQOLNDSSEEDSIDDPAGQAEPRRAHYNIVTFCK 60  
 DB 1 MHGDTPLHEHYMDLOPETTDLYXXYQOLNDSSEEDSIDDPAGQAEPRRAHYNIVTFCK 60

QY 61 CDSTLRACVSTHVDIRTTEDLMGTGIVXPI 93  
 DB 61 CDSTLRACVSTHVDIRTTEDLMGTGIVXPI 93

RESULT 30  
 Q9QDH4\_HPV16 PRELIMINARY; PRT; 93 AA.  
 AC Q9QDH4;  
 DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.  
 DT 01-MAY-2000, sequence version 1.

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 CC EMBL: AF187867; AAF13395.1; -; Genomic\_DNA.  
 DR GO: GO:0005622; C:intracellular; IEA.  
 DR GO: GO:0003700; F:transcription factor activity; IEA.  
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro: IPR000148; Papv1\_E7.  
 DR Pfam: PF00527; E7; 1.  
 FT NON TER 93  
 FT SEQUENCE 93 AA; 10513 MW; 92C7054341326A1F CRC64;

Query Match 92.5%; Score 478; DB 2; Length 93;  
 Best Local Similarity 95.7%; Pred. No. 4.2e-48;  
 Matches 89; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MHGDTPLHEHYMDLOPETTDLYXXYQOLNDSSEEDSIDDPAGQAEPRRAHYNIVTFCK 60  
 DB 1 MHGDTPLHEHYMDLOPETTDLYXXYQOLNDSSEEDSIDDPAGQAEPRRAHYNIVTFCK 60

QY 61 CDSTLRACVSTHVDIRTTEDLMGTGIVXPI 93  
 DB 61 CDSTLRACVSTHVDIRTTEDLMGTGIVXPI 93

RESULT 29  
 Q9QDH2\_HPV16 PRELIMINARY; PRT; 93 AA.  
 AC Q9QDH2;  
 DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.  
 DT 01-MAY-2000, sequence version 1.  
 DT 07-FEB-2006, entry version 14.  
 DE E7 protein (Fragment).  
 OS Human papillomavirus type 16.  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 OC Alphapapillomavirus.  
 OX NCBI\_TaxID=333760;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Lee H.P., Song Y.S., Kim J.W., Park N.H., Kang S.B.,  
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
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 CC EMBL: AF187869; AAF13399.1; -; Genomic\_DNA.  
 DR GO: GO:0005622; C:intracellular; IEA.  
 DR GO: GO:0003700; F:transcription factor activity; IEA.  
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro: IPR000148; Papv1\_E7.  
 DR Pfam: PF00527; E7; 1.  
 FT NON TER 93  
 FT SEQUENCE 93 AA; 10452 MW; 83281BB2AE2C8A1F CRC64;

Query Match 92.3%; Score 477; DB 2; Length 93;  
 Best Local Similarity 95.7%; Pred. No. 5.6e-48;  
 Matches 89; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDTPLHEHYMDLOPETTDLYXXYQOLNDSSEEDSIDDPAGQAEPRRAHYNIVTFCK 60  
 DB 1 MHGDTPLHEHYMDLOPETTDLYXXYQOLNDSSEEDSIDDPAGQAEPRRAHYNIVTFCK 60

QY 61 CDSTLRACVSTHVDIRTTEDLMGTGIVXPI 93  
 DB 61 CDSTLRACVSTHVDIRTTEDLMGTGIVXPI 93

RESULT 30  
 Q9QDH4\_HPV16 PRELIMINARY; PRT; 93 AA.  
 AC Q9QDH4;  
 DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.  
 DT 01-MAY-2000, sequence version 1.

DT 07-FEB-2006, entry version 14.  
 DE E7 protein (Fragment).  
 OS Human papillomavirus type 16.  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 OC Alphapapillomavirus.  
 NCBI\_TaxID=333760;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;  
 RL Submitted (SFP-1999) to the EMBL/GenBank/DBJ databases.  
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 CC -----  
 DR EMBL: AF187868; AAF13397.1; -: Genomic\_DNA.  
 DR GO: GO:0005622; C:intracellular; IEA.  
 DR GO: GO:0003700; F:transcription factor activity; IEA.  
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro: IPR000148; Papv1\_E7.  
 DR Pfam: PF00527; E7; 1.  
 FT NON TER 93 93  
 SQ SEQUENCE 93 AA; 10452 MW; 83281BB2AE2C6A1F CRC64;

Query Match 92.3%; Score 477; DB 2; Length 93;  
 Best Local Similarity 95.7%; Pred. No. 5.6e-48;  
 Matches 89; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEMYMLDLPETTDLYXXYXQLNDSSEDEIDGPAGQAEPRRAHYNIVTFCK 60  
 Db 1 MHGDTPLHEMYMLDLPETTDLYCYEQLSDSSEDEIDGPAGQAEPRRAHYNIVTFCK 60  
 61 CDSTLRLCVOSTHVDIRTLIEDLMTGLGVXPI 93  
 Db 61 CDSTLRLCVOSTHVDIRTLIEDLMTGLGVXPI 93

RESULT 31  
 ID Q9QDH8 HPV16 PRELIMINARY; PRT; 93 AA.  
 AC Q9QDH8;  
 DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.  
 DT 07-FEB-2006, sequence version 1.  
 DT 01-MAY-2000, entry version 14.  
 DE E7 protein (Fragment).  
 OS Human papillomavirus type 16.  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 OC Alphapapillomavirus.  
 NCBI\_TaxID=333760;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;  
 RL Submitted (SFP-1999) to the EMBL/GenBank/DBJ databases.  
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 CC -----  
 DR EMBL: AF187866; AAF13393.1; -: Genomic\_DNA.  
 DR GO: GO:0005622; C:intracellular; IEA.  
 DR GO: GO:0003700; F:transcription factor activity; IEA.  
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro: IPR000148; Papv1\_E7.  
 DR Pfam: PF00527; E7; 1.  
 FT NON TER 93 93  
 SQ SEQUENCE 93 AA; 10452 MW; 83281BB2AE2C6A1F CRC64;

Query Match 92.3%; Score 477; DB 2; Length 93;  
 Best Local Similarity 95.7%; Pred. No. 5.6e-48;  
 Matches 89; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEMYMLDLPETTDLYXXYXQLNDSSEDEIDGPAGQAEPRRAHYNIVTFCK 60  
 Db 1 MHGDTPLHEMYMLDLPETTDLYCYEQLSDSSEDEIDGPAGQAEPRRAHYNIVTFCK 60

Qy 61 CDSTLRLCVOSTHVDIRTLIEDLMTGLGVXPI 93  
 Db 61 CDSTLRLCVOSTHVDIRTLIEDLMTGLGVXPI 93

RESULT 32  
 ID Q8B5P5 9PAPI PRELIMINARY; PRT; 77 AA.  
 AC Q8B5P5;  
 DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.  
 DT 01-MAR-2003, sequence version 1.  
 DT 07-FEB-2006, entry version 11.  
 DE E7 protein (Fragment).  
 OS Human papillomavirus.  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 OC Unclassified Papillomaviridae.  
 NCBI\_TaxID=10566;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Ponglikitmongkol M., Vaeeteewoatcharn K.;  
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
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 CC -----  
 DR EMBL: AF469198; AAO15694.1; -: Genomic\_DNA.  
 DR GO: GO:0005622; C:intracellular; IEA.  
 DR GO: GO:0003700; F:transcription factor activity; IEA.  
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro: IPR000148; Papv1\_E7.  
 DR Pfam: PF00527; E7; 1.  
 FT NON TER 77 77  
 SQ SEQUENCE 77 AA; 8782 MW; C5DE3A7E546AC31B CRC64;

Query Match 78.5%; Score 406; DB 2; Length 77;  
 Best Local Similarity 96.1%; Pred. No. 1e-39;  
 Matches 74; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEMYMLDLPETTDLYXXYXQLNDSSEDEIDGPAGQAEPRRAHYNIVTFCK 60  
 Db 1 MHGDTPLHEMYMLDLPETTDLYCYEQLSDSSEDEIDGPAGQAEPRRAHYNIVTFCK 60  
 61 CDSTLRLCVOSTHVDIR 77  
 Db 61 CDSTLRLCVOSTHVDIR 77

RESULT 33  
 ID VE7 HPV35 STANDARD; PRT; 99 AA.  
 AC P27230;  
 DT 01-AUG-1992, integrated into UniProtKB/Swiss-Prot.  
 DT 01-AUG-1992, sequence version 1.  
 DT 07-FEB-2006, entry version 32.  
 DE Protein E7.  
 GN Name=E7;  
 OS Human papillomavirus type 35.  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 OC Alphapapillomavirus.  
 NCBI\_TaxID=10587;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
 RC STRAIN=Isolate 35H;  
 RX MEDLINE=94265501; PubMed=8205838;  
 RA Delius H., Hofmann B.;  
 RT Primer-directed sequencing of human papillomavirus types.;  
 RL Curr. Top. Microbiol. Immunol. 186:13-31 (1994).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
 RX MEDLINE=9214753; PubMed=1310198;  
 RA Merich J.E., Pontsler A.V., Rice S.M., McGraw K.A., Dubenak T.W.;  
 RT "The phylogenetic relationship and complete nucleotide sequence of human papillomavirus type 35.";

RL Virology 186:770-776(1992).  
CC -1- FUNCTION: E7 protein has both transforming and trans-activating  
CC activities.  
CC -1- SIMILARITY: Belongs to the papillomaviruses E7 protein family.  
CC -----  
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CC -----  
DR EMBL: W74117; AAA46967.1; -; Genomic\_DNA.  
DR EMBL: X74477; CAAS5262.1; -; Genomic\_DNA.  
DR PIR: F40824; W7ML35.  
DR InterPro: IPR000148; Papv1\_E7.  
DR Pfam: PF00527; E7; 1.  
KW DNA-binding; Early protein; Oncogene; Transcription;  
KW Transcription regulation.  
FT CHAIN 1  
FT Protein E7.  
FT /FTId=PRO\_0000133433.  
FT MOTIF 59 62 C-XX-C motif-1.  
FT MOTIF 92 95 C-XX-C motif-2.  
SQ SEQUENCE 99 AA; 10954 MW; 8EAA8F248051E226 CRC64;  
  
Query Match 73.8%; Score 381.5; DB 1; Length 99;  
Best Local Similarity 73.5%; Pred. No. 1,1e-36;  
Matches 72; Conservative 11; Mismatches 14; Indels 1; Gaps 1;  
  
QY 1 MHGDTPLHEHYMDLQPEETDLYXXQLNDS--EEBEIDGPGAGPDRAHNIIVTFCC 59  
DB 1 MHGEITTLQDYVDLQPEATDLYCYEQLCSSSEEBEDTIDGPAQAPDTSNNIIVTSCC 60  
DB 61 KCATRLACVQSTHIDIRKEDLMGTFGIVCPGCSQR 98  
  
RESULT 34  
Q76WP2\_9PAPI PRELIMINARY; PRT; 99 AA.  
AC Q76WP2;  
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.  
DT 05-JUL-2004, sequence version 1.  
DT 07-FEB-2006, entry version 10.  
DE E7 protein.  
OS Human papillomavirus.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC unclassified Papillomaviridae.  
ON NCBI\_Taxid=10566;  
RX 1  
RP NUCLEOTIDE SEQUENCE.  
RA Fujinaga K.;  
RL Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.  
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CC -----  
DR EMBL: D10597; BAA01448.1; -; Genomic\_DNA.  
DR GO: GO:0005622; C:intracellular; IEA.  
DR GO: GO:0003700; F:transcription factor activity; IEA.  
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
DR InterPro: IPR000148; Papv1\_E7.  
DR Pfam: PF00527; E7; 1.  
SQ SEQUENCE 99 AA; 10954 MW; 8EAA8F248051E226 CRC64;  
  
Query Match 73.8%; Score 381.5; DB 2; Length 99;  
Best Local Similarity 73.5%; Pred. No. 1,1e-36;  
Matches 72; Conservative 11; Mismatches 14; Indels 1; Gaps 1;  
  
QY 1 MHGDTPLHEHYMDLQPEETDLYXXQLNDS--EEBEIDGPGAGPDRAHNIIVTFCC 59  
DB 1 MHGEITTLQDYVDLQPEATDLYCYEQLCSSSEEBEDTIDGPAQAPDTSNNIIVTSCC 60  
DB 61 KCATRLACVQSTHIDIRKEDLMGTFGIVCPGCSQR 98

RESULT 35  
VE7\_HP31 STANDARD; PRT; 98 AA.  
ID VE7\_HP31  
AC P17387;  
DT 01-AUG-1990, integrated into UniProtKB/Swiss-Prot.  
DT 01-AUG-1990, sequence version 1.  
DT 07-FEB-2006, entry version 34.  
DE Protein E7.  
GN Name=E7;  
OS Human papillomavirus type 31.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Alphapapillomavirus.  
ON NCBI\_Taxid=10585;  
RX 1  
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
RX MEDLINE=89299478; PubMed=2545036;  
RA Goldborough M.D., Dielvestre D., Temple G.F., Lorincz A.T.;  
RT "Nucleotide sequence of human papillomavirus type 31: a cervical  
neoplasia-associated virus."  
RL Virology 171:306-311(1989).  
CC -1- FUNCTION: E7 protein has both transforming and trans-activating  
CC activities.  
CC -1- SIMILARITY: Belongs to the papillomaviruses E7 protein family.  
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CC -----  
DR EMBL: J04353; AAA46951.1; -; Genomic\_DNA.  
DR PIR: B32444; W7ML31.  
DR InterPro: IPR000148; Papv1\_E7.  
DR Pfam: PF00527; E7; 1.  
KW DNA-binding; Early protein; Oncogene; Transcription;  
KW Transcription regulation.  
FT CHAIN 1  
FT Protein E7.  
FT /FTId=PRO\_0000133429.  
FT MOTIF 58 61 C-XX-C motif-1.  
FT MOTIF 91 94 C-XX-C motif-2.  
SQ SEQUENCE 98 AA; 10918 MW; 793B7F5BC734E9B CRC64;  
  
Query Match 72.0%; Score 372; DB 1; Length 98;  
Best Local Similarity 71.1%; Pred. No. 1,4e-35;  
Matches 69; Conservative 12; Mismatches 16; Indels 0; Gaps 0;  
  
QY 1 MHGDTPLHEHYMDLQPEETDLYXXQLNDSSEBEIDGPGAGPDRAHNIIVTFCC 60  
DB 1 MHGEITTLQDYVDLQPEATDLYCYEQLPSSDEBDVIDSPAGAPDTSNNIIVTFCCQ 60  
DB 61 CKSTRLACVQSTGVDIRIQELMGSGFIVCPNCSTR 97  
  
RESULT 36  
Q6T377\_HP31 PRELIMINARY; PRT; 98 AA.  
ID Q6T377\_HP31  
AC Q6T377;  
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.  
DT 05-JUL-2004, sequence version 1.  
DT 07-FEB-2006, entry version 9.  
DE E7 transforming protein variant.  
OS Human papillomavirus type 31.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Alphapapillomavirus.  
ON NCBI\_Taxid=10585;  
RX 1  
RP NUCLEOTIDE SEQUENCE.  
RA Friedler M., Fitzky B., Durst M., Zwerschke W., Jansen-Durr P.;  
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
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CC -----
DR EMBL: AY38621; AAR13015.1; -; Genomic_DNA.
DR GO: GO:0005622; C:intracellular; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR000148; Papv1_E7.
DR Pfam: PF00527; E7; 1.
SQ SEQUENCE 98 AA; 10917 MW; 9D31DFP1CF9064B1 CRC64;

Query Match
Best Local Similarity 71.0%; Score 367; DB 2; Length 98;
Matches 67; Conservative 15; Mismatches 15; Indels 0; Gaps 0;

Qy 1 MHGDPPTLHEXYMLDLOPETTDLYXXYXQLNDSSEDEIDGPAQAEPPRAHNYITVFCCK 60
Db 1 MRGEPFLQDVLLQPKATDHCYEQLPDSSEEDVDSDPAQAKPDTSNYITVFCCK 60

Qy 61 CDSTLRICVOSTVHDVIRLTEDLLMGTGIVXPICSQK 97
Db 61 CESTLRICVOSTVQVDIRLTQELMGSFGIVCPNCSTR 97

RESULT 37
Q8B563_9PAPI PRELIMINARY; PRT; 65 AA.
AC Q8B563;
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003, sequence version 1.
DE 07-FEB-2006, entry version 11.
OS E7 protein (fragment).
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Unclassified Papillomaviridae.
OX NCBI_Taxid=10566;

RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Ponglikitmongkol M., Vaelewootcharn K.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
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DR EMBL: AF548023; AAC16240.1; -; Genomic_DNA.
DR GO: GO:0005622; C:intracellular; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR000148; Papv1_E7.
DR Pfam: PF00527; E7; 1.
FT NON_TER
SQ SEQUENCE 65 AA; 7373 MW; E9D7AD7923700195 CRC64;

Query Match
Best Local Similarity 66.3%; Score 343; DB 2; Length 65;
Matches 62; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MHGDPPTLHEXYMLDLOPETTDLYXXYXQLNDSSEDEIDGPAQAEPPRAHNYITVFCCK 60
Db 1 MHGEPFLHXYMLDLOPETTDLYCYEQLPDSSEEDVDSDPAQAKPDTSNYITVFCCK 60

Qy 61 CDSTL 65
Db 61 CDSTL 65

RESULT 38
O90724_HPV67 PRELIMINARY; PRT; 99 AA.
AC O90724;
DT 01-NOV-1998, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1998, sequence version 1.
DT 07-FEB-2006, entry version 17.
DE ORF E7.
OS Human papillomavirus type 67.

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OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_Taxid=37120;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99073695; PubMed=9857984; DOI=10.1023/A:1008002905588;
RA Kiril Y., Matsukura T.;
RT "Nucleotide sequence and phylogenetic classification of human
RT papillomavirus type 67."
RL Virus Genes 17:117-121(1998).
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DR EMBL: D21208; BA28853.1; -; Genomic_DNA.
DR GO: GO:0005622; C:intracellular; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR000148; Papv1_E7.
DR Pfam: PF00527; E7; 1.
SQ SEQUENCE 99 AA; 11157 MW; 81A4A636D7588C44 CRC64;

Query Match
Best Local Similarity 61.1%; Score 316; DB 2; Length 99;
Matches 59; Conservative 17; Mismatches 21; Indels 2; Gaps 1;

Qy 1 MHGDPPTLHEXYMLDLOPETTDLYXXYXQLNDSSEDEI--DGPAGQAEPPRAHNYITVFC 58
Db 1 MRGDKATLDYLDLKEETDLYCYEQLPDSSEEDVGVKDRPDGAKPDTTNHIVTVC 60

Qy 59 CKDSTLRICVOSTVHDVIRLTEDLLMGTGIVXPICSQK 97
Db 61 NICECTRLCIHSTADVIRTQGLMWTGIVPTCAQQ 99

RESULT 39
VE7 HPV33 STANDARD; PRT; 97 AA.
ID P06429;
DT 01-JAN-1988, integrated into UniProtKB/Swiss-Prot.
DT 01-JAN-1988, sequence version 1.
DT 07-FEB-2006, entry version 40.
DE Protein E7.
GN Name=E7;
OS Human papillomavirus type 33.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_Taxid=10586;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=86200464; PubMed=3009902;
RA Cole S.T., Streeck R.E.;
RT "Genome organization and nucleotide sequence of human papillomavirus
RT type 33, which is associated with cervical cancer."
RL J. Virol. 58:991-995(1986).
RN [2]
RP NUCLEOTIDE SEQUENCE [MRNA].
RX MEDLINE=92219410; PubMed=1313922;
RA Snijders P.J.F., van den Brule A.J.C., Schrijnemakers H.F.J.,
RA Raaphorst P.M.C., Meijer C.J.L.M., Walboomers J.M.M.;
RT "Human papillomavirus type 33 in a tonsillar carcinoma generates its
RT putative E7 mRNA via two 86* transcript species which are terminated
RT at different early region poly(A) sites."
RL J. Virol. 66:3172-3178(1992).
CC -----
CC -1- FUNCTION: E7 protein has both transforming and trans-activating
CC activities.
CC -1- SIMILARITY: Belongs to the papillomaviruses E7 protein family.
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DR EMBL: M12732; AAA46959.1; -; Genomic_DNA.
DR EMBL: X64084; CAA45430.1; -; mRNA.

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DR EMBL: X64085; CAA5434.1; -; mRNA.
DR PIR: A03689; W7ML33.
DR InterPro: IPR000148; Papv1_E7.
DR Pfam: PF00527; E7; 1.
DR DNA-binding; Early protein; Oncogene; Transcription;
KW Transcription regulation.
FT CHAIN 1 97 Protein E7.
FT MOTIF 58 61 /FTid=PRO_0000133431.
FT MOTIF 91 94 C-XX-C motif-1.
FT MOTIF 94 96 C-XX-C motif-2.
SQ SEQUENCE 97 AA; 10837 MW; 699DCFF74343243C8 CRC64;

Query March 57.1%; Score 295; DB 1; Length 97;
Best Local Similarity 57.7%; Pred. No. 1.6e-26;
Matches 56; Conservative 16; Mismatches 25; Indels 0; Gaps 0.

QY 1 MHGDPPTLHEHYMLDLQPEPTDLYXXYXQLNDSSEDEDEIDGAGCAEPDRAHNYIVTFCK 60
D 1 MRGKHPTLKEVYLDLPEPTDLYCYEQSDSDSDEBGLDRPDGQAQNPATADYIVTCGHT 60
QY 61 CDSTLRCLCVGOSTHVDIRFLTEDLNGTGLGVXPICSQK 97
D 61 CNTTVRLCVNSTASDLRTIQQLMGTVNIVCPCTAQ 97

RESULT 40
VE7_HPV52 STANDARD; PRT; 99 AA.
ID_VE7_HPV52
AC P36831;
DT 01-JUN-1994, integrated into UniProtKB/Swiss-Prot.
DT 01-JUN-1994, sequence version 1.
DT 07-FEB-2006, entry version 32.
DE Protein E7.
DE Name=E7;
OS Human papillomavirus type 52.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
CX NCBI_TaxID=10618;
[1]
RX NCBIOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=91258022; PubMed=1646174;
RA Takami Y., Kondoh G., Saito J., Noda K., Sudiro T.M.,
RA Sjahrudinman A., Warra U.C., Yuseido M., Hakura A.;
RT "Cloning and characterization of human papillomavirus type 52 from
RT cervical carcinoma in Indonesia.";
RL Int. J. Cancer 48:516-522(1991).
-1- FUNCTION: E7 protein has both transforming and trans-activating
activities.
-1- SIMILARITY: Belongs to the papillomaviruses E7 protein family.
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CC -----
DR EMBL: X74481; CA52586.1; -; Genomic_DNA.
DR PIR: S36574; S36574.
DR InterPro: IPR000148; Papv1_E7.
DR Pfam: PF00527; E7; 1.
KW DNA-binding; Early protein; Oncogene; Transcription;
KW Transcription regulation.
FT CHAIN 1 99 Protein E7.
FT MOTIF 60 63 /FTid=PRO_0000133448.
FT MOTIF 93 96 C-XX-C motif-1.
FT MOTIF 96 98 C-XX-C motif-2.
SQ SEQUENCE 99 AA; 11032 MW; 55CFRA02B4DFE96F CRC64;

Query Match 56.9%; Score 294; DB 1; Length 99;
Best Local Similarity 57.1%; Pred. No. 2.2e-26;

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[illegible]

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Db      61 TCGTTRLCINSTTTDVRTLQQLMGTCCTIVCPSCAQO 98

RESULT 42
OS47M4_HPV58      PRELIMINARY; PRT; 98 AA.
ID   OS47M4_HPV58
AC   OS47M4;
DT   24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT   24-MAY-2005, sequence version 1.
DE   07-FEB-2006, entry version 4.
DE   E7 protein.
GN   Name=E7;
OS   Human papillomavirus type 58.
OC   Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC   Alphapapillomavirus.
OX   NCBI_TaxId=10598;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=E6/E7-HK-7, E6/E7-HK-9, E6/E7-HK-12, and E6/E7-HK-5;
RX   MEDLINE=22176796; PubMed=12189229; DOI=10.1093/jnci/94.16.1249;
RA   Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA   Cheung J.L.K., Cheng A.F.;
RT   "Association of human papillomavirus type 58 variant with the risk of
RT   cervical cancer.";
RL   J. Natl. Cancer Inst. 94:1249-1253(2002).
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DR   EMBL; AF478138; ALA85383.1; -; Genomic_DNA.
DR   EMBL; AF478140; ALA85385.1; -; Genomic_DNA.
DR   EMBL; AF478143; ALA85388.1; -; Genomic_DNA.
DR   EMBL; AF478146; ALA85391.1; -; Genomic_DNA.
DR   GO; GO:0005622; C:intracellular; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
SQ   SEQUENCE 98 AA; 10819 MW; D719944F3CF48D12 CRC64;

Query Match      56.0%; Score 289.5; DB 2; Length 98;
Best Local Similarity 57.1%; Pred. No. 7.2e-26;
Matches 56; Conservative 16; Mismatches 25; Indels 1; Gaps 1;

Qy      1 MHGDPPLHRYMDLQPEPTDLYXXQLNDSSSEED-EIDGPAGQEPDRAHNIYVFCC 59
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1 MRGNPPLRRIYIDLHPEPTDLFCYEQLCSDEDEGLRPPGQAQAPATANIYIVICCY 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      60 KCDSTRLCVQSTHVDIRTEEDLLMGTLGIVXPCSQK 97
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 TCGTTRLCINSTTTDVRTLQQLMGTCCTIVCPSCAQO 98
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 43
OSQC21_HPV58      PRELIMINARY; PRT; 98 AA.
ID   OSQC21_HPV58
AC   OSQC21;
DT   01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT   01-MAY-2000, sequence version 1.
DE   07-FEB-2006, entry version 17.
DE   E7 protein.
OS   Human papillomavirus type 58.
OC   Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC   Alphapapillomavirus.
OX   NCBI_TaxId=10598;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=E7-HK-2;
RA   Chan P.K.S., Lam C.W., Chan M.Y.M., Li W.W.H., Cheung J.L.K.,
RA   Cheng A.F.;
RT   Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=E6/E7-HK-1, E6/E7-HK-11, E6/E7-HK-14, E6/E7-HK-15, and
RC   E6/E7-HK-16;

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RX   MEDLINE=22176796; PubMed=12189229; DOI=10.1093/jnci/94.16.1249;
RA   Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA   Cheung J.L.K., Cheng A.F.;
RT   "Association of human papillomavirus type 58 variant with the risk of
RT   cervical cancer.";
RL   J. Natl. Cancer Inst. 94:1249-1253(2002).
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CC   Distributed under the Creative Commons Attribution-NonDerivs license
-----
DR   EMBL; AF192270; AAF15691.1; -; Genomic_DNA.
DR   EMBL; AF478132; ALA85377.1; -; Genomic_DNA.
DR   EMBL; AF478142; ALA85387.1; -; Genomic_DNA.
DR   EMBL; AF478146; ALA85391.1; -; Genomic_DNA.
DR   EMBL; AF478147; ALA85392.1; -; Genomic_DNA.
DR   EMBL; AF478145; ALA85390.1; -; Genomic_DNA.
DR   GO; GO:0005622; C:intracellular; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   InterPro; IPR000148; Papv1_E7.
DR   Pfam; PF00527; E7; 1.
SQ   SEQUENCE 98 AA; 10976 MW; D70C8D4DD4CE5D12 CRC64;

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Query Match      55.8%; Score 288.5; DB 2; Length 98;
Best Local Similarity 57.1%; Pred. No. 9.4e-26;
Matches 56; Conservative 16; Mismatches 25; Indels 1; Gaps 1;

Qy      1 MHGDPPLHRYMDLQPEPTDLYXXQLNDSSSEED-EIDGPAGQEPDRAHNIYVFCC 59
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1 MRGNPPLRRIYIDLHPEPTDLFCYEQLCSDEDEGLRPPGQAQAPATANIYIVICCY 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      60 KCDSTRLCVQSTHVDIRTEEDLLMGTLGIVXPCSQK 97
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 TCGTTRLCINSTTTDVRTLQQLMGTCCTIVCPSCAQO 98
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 44
OSQSF0_HPV58      PRELIMINARY; PRT; 98 AA.
ID   OSQSF0_HPV58
AC   OSQSF0;
DT   01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT   01-JUN-2002, sequence version 1.
DE   07-FEB-2006, entry version 11.
DE   E7 protein.
OS   Human papillomavirus type 58.
OC   Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC   Alphapapillomavirus.
OX   NCBI_TaxId=10598;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=E6/E7-HK-8;
RX   MEDLINE=22176796; PubMed=12189229; DOI=10.1093/jnci/94.16.1249;
RA   Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA   Cheung J.L.K., Cheng A.F.;
RT   "Association of human papillomavirus type 58 variant with the risk of
RT   cervical cancer.";
RL   J. Natl. Cancer Inst. 94:1249-1253(2002).
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-----
DR   EMBL; AF478139; ALA85384.1; -; Genomic_DNA.
DR   GO; GO:0005622; C:intracellular; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   InterPro; IPR000148; Papv1_E7.
DR   Pfam; PF00527; E7; 1.
SQ   SEQUENCE 98 AA; 10833 MW; 8248D5321354CC9 CRC64;

Query Match      55.4%; Score 286.5; DB 2; Length 98;
Best Local Similarity 56.1%; Pred. No. 1.6e-25;
Matches 55; Conservative 17; Mismatches 25; Indels 1; Gaps 1;

```

```

QY 1 MGGDTPLHEHYMDLOPETDLYXXYQNDSSSEED-EIDGPAQAEPDRAHYNYTFCC 59
DB 1 MRNNPTLREYIIDLHPETDLCFYEQLCSSDDEIGLDGPDGQAPATANYIYTCY 60
QY 60 KCDSTRLCVQSTHVDIRTELDLMTGLGIVAPICSOX 97
DB 61 TCSTYRLCTINSTATVETRTIQQLMGTCTIVCPSCAQ 98

RESULT 45
080H02 HPV58 PRELIMINARY; PRT; 98 AA.
AC 080H02, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2002, sequence version 1.
DE 07-FEB-2006, entry version 12.
DE E7 protein.
OS Human papillomavirus type 58.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OC NCBI_TaxID=10598;
OX NCBI_TaxID=10598;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=E6/E7-HK-3, and E6/E7-HK-4; DOI=10.1093/jnci/94.16.1249;
RX MEDLINE=22176796; PubMed=12189229; Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.L.K., Cheng A.F.;
RT "Association of human papillomavirus type 58 variant with the risk of
RT cervical cancer.";
RL J. Natl. Cancer Inst. 94:1249-1253(2002).
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CC
CC EMBL: AF478134; AL85379.1; -; Genomic DNA.
CC EMBL: AF478135; AL85380.1; -; Genomic DNA.
CC GO: GO:0005622; C:intracellular; IEA.
CC GO: GO:0003700; F:transcription factor activity; IEA.
CC GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
CC InterPro: IPR000148; Papy1_E7.
CC Pfam: PF00527; E7; 1.
CC SEQUENCE 98 AA; 10791 MW; D719984F3CEC3A42 CRC64;
SQ

Query Match 55.2%; Score 285.5; DB 2; Length 98;
Best Local Similarity 57.1%; Pred. No. 2.1e-25;
Matches 56; Conservative 15; Mismatches 26; Indels 1; Gaps 1;

QY 1 MGGDTPLHEHYMDLOPETDLYXXYQNDSSSEED-EIDGPAQAEPDRAHYNYTFCC 59
DB 1 MRNNPTLREYIIDLHPETDLCFYEQLCSSDDEIGLDGPDGQAPATANYIYTCY 60
QY 60 KCDSTRLCVQSTHVDIRTELDLMTGLGIVAPICSOX 97
DB 61 TCSTYRLCTINSTATVETRTIQQLMGTCTIVCPSCAQ 98

RESULT 46
080H02 HPV58 PRELIMINARY; PRT; 98 AA.
AC 080H02, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2002, sequence version 1.
DE 07-FEB-2006, entry version 12.
DE E7 protein.
OS Human papillomavirus type 58.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OC NCBI_TaxID=10598;
OX NCBI_TaxID=10598;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=E6/E7-HK-17, and E6/E7-HK-18; DOI=10.1093/jnci/94.16.1249;
RX MEDLINE=22176796; PubMed=12189229; Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RT "Association of human papillomavirus type 58 variant with the risk of
RT cervical cancer.";
RL J. Natl. Cancer Inst. 94:1249-1253(2002).
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CC
CC EMBL: AF478134; AL85379.1; -; Genomic DNA.
CC EMBL: AF478135; AL85380.1; -; Genomic DNA.
CC GO: GO:0005622; C:intracellular; IEA.
CC GO: GO:0003700; F:transcription factor activity; IEA.
CC GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
CC InterPro: IPR000148; Papy1_E7.
CC Pfam: PF00527; E7; 1.
CC SEQUENCE 98 AA; 10861 MW; ED3C57B911355721 CRC64;
SQ

Query Match 55.0%; Score 284.5; DB 2; Length 98;
Best Local Similarity 56.1%; Pred. No. 2.8e-25;
Matches 55; Conservative 17; Mismatches 25; Indels 1; Gaps 1;

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RA Cheung J.L.K., Cheng A.F.;
RT "Association of human papillomavirus type 58 variant with the risk of
RT cervical cancer.";
RL J. Natl. Cancer Inst. 94:1249-1253(2002).
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CC
CC EMBL: AF478148; AL85393.1; -; Genomic DNA.
CC EMBL: AF478149; AL85394.1; -; Genomic DNA.
CC GO: GO:0005622; C:intracellular; IEA.
CC GO: GO:0003700; F:transcription factor activity; IEA.
CC GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
CC InterPro: IPR000148; Papy1_E7.
CC Pfam: PF00527; E7; 1.
CC SEQUENCE 98 AA; 10803 MW; 824BD4F3CF48C9 CRC64;
SQ

Query Match 55.2%; Score 285.5; DB 2; Length 98;
Best Local Similarity 56.1%; Pred. No. 2.1e-25;
Matches 55; Conservative 17; Mismatches 25; Indels 1; Gaps 1;

QY 1 MGGDTPLHEHYMDLOPETDLYXXYQNDSSSEED-EIDGPAQAEPDRAHYNYTFCC 59
DB 1 MRNNPTLREYIIDLHPETDLCFYEQLCSSDDEIGLDGPDGQAPATANYIYTCY 60
QY 60 KCDSTRLCVQSTHVDIRTELDLMTGLGIVAPICSOX 97
DB 61 TCSTYRLCTINSTATVETRTIQQLMGTCTIVCPSCAQ 98

RESULT 47
09QC22 HPV58 PRELIMINARY; PRT; 98 AA.
AC 09QC22;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DE 07-FEB-2006, entry version 16.
DE E7 protein.
OS Human papillomavirus type 58.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OC NCBI_TaxID=10598;
OX NCBI_TaxID=10598;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=E7-HK-1;
RX Chan P.K.S., Lam C.W., Chan M.Y.M., Li W.W.H., Cheung J.L.K.,
RA Cheng A.F.;
RT Submitted (Oct-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=E6/E7-HK-2, and E6/E7-HK-6; DOI=10.1093/jnci/94.16.1249;
RX MEDLINE=22176796; PubMed=12189229; Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.L.K., Cheng A.F.;
RT "Association of human papillomavirus type 58 variant with the risk of
RT cervical cancer.";
RL J. Natl. Cancer Inst. 94:1249-1253(2002).
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CC
CC EMBL: AF192269; AF13690.1; -; Genomic DNA.
CC EMBL: AF478133; AL85378.1; -; Genomic DNA.
CC EMBL: AF478137; AL85382.1; -; Genomic DNA.
CC GO: GO:0005622; C:intracellular; IEA.
CC GO: GO:0003700; F:transcription factor activity; IEA.
CC GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
CC InterPro: IPR000148; Papy1_E7.
CC Pfam: PF00527; E7; 1.
CC SEQUENCE 98 AA; 10861 MW; ED3C57B911355721 CRC64;
SQ

Query Match 55.0%; Score 284.5; DB 2; Length 98;
Best Local Similarity 56.1%; Pred. No. 2.8e-25;
Matches 55; Conservative 17; Mismatches 25; Indels 1; Gaps 1;

```

```

Matches 55; Conservative 16; Mismatches 26; Indels 1; Gaps 1;

Qy 1 MHGDPPTLHEHYMDLQPEPTTDLXXYXQLNDSSEED-EIDGPAGQAEPPRAHYNIVTFCC 59
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MRGNPPTLRBYILDHPEPDLFCYEQLCDSSDEDEICLDPGDAQAPATANYIYITCCY 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 60 KCDSTLRCLVOSTHVDIRTEEDLGMGTGIXPICSQK 97
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 TCSITVRLCINSTTVDRTLQQLMGTCITVCPSCAQQ 98
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 48
Q0QSE9_HPV58 PRELIMINARY; PRT; 98 AA.
AC Q0QSE9;
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2002, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE E7 protein.
OS Human papillomavirus type 58.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxId=10598;
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=E6/E7-HK-10;
RX MEDLINE=22176796; PubMed=12189229; DOI=10.1093/jnci/94.16.1249;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
  Cheung J.L.K., Cheng A.F.;
RT "Association of human papillomavirus type 58 variant with the risk of
  cervical cancer.";
RL J. Natl. Cancer Inst. 94:1249-1253(2002).
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  Distributed under the Creative Commons Attribution-NonDerivs license
-----
CC EMBL; AF478141; AAL85386.1; -; Genomic_DNA.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000148; Papv1_E7.
DR Pfam; PF00527; E7; 1.
DR NCBI_TaxId=10598;
SQ SEQUENCE 98 AA; 10833 MW; ED24DEA180BC4F8A8 CRC64;

Query Match 54.8%; Score 283.5; DB 2; Length 98;
Best Local Similarity 56.1%; Pred. No. 3.7e-25;
Matches 55; Conservative 16; Mismatches 26; Indels 1; Gaps 1;

Qy 1 MHGDPPTLHEHYMDLQPEPTTDLXXYXQLNDSSEED-EIDGPAGQAEPPRAHYNIVTFCC 59
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MRGNPPTLRBYILDHPEPDLFCYEQLCDSSDEDEICLDPGDAQAPATANYIYITCCY 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 60 KCDSTLRCLVOSTHVDIRTEEDLGMGTGIXPICSQK 97
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 TCSITVRLCINSTTVDRTLQQLMGTCITVCPSCAQQ 98
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 49
Q0QSE8_HPV58 PRELIMINARY; PRT; 98 AA.
AC Q0QSE8;
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2002, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE E7 protein.
OS Human papillomavirus type 58.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxId=10598;
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=E6/E7-HK-13;
RX MEDLINE=22176796; PubMed=12189229; DOI=10.1093/jnci/94.16.1249;

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RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
  Cheung J.L.K., Cheng A.F.;
RT "Association of human papillomavirus type 58 variant with the risk of
  cervical cancer.";
RL J. Natl. Cancer Inst. 94:1249-1253(2002).
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-----
CC EMBL; AF478144; AAL85389.1; -; Genomic_DNA.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000148; Papv1_E7.
DR Pfam; PF00527; E7; 1.
DR NCBI_TaxId=10598;
SQ SEQUENCE 98 AA; 10998 MW; D70C8D4620711D12 CRC64;

Query Match 54.4%; Score 281.5; DB 2; Length 98;
Best Local Similarity 56.1%; Pred. No. 6.3e-25;
Matches 55; Conservative 16; Mismatches 26; Indels 1; Gaps 1;

Qy 1 MHGDPPTLHEHYMDLQPEPTTDLXXYXQLNDSSEED-EIDGPAGQAEPPRAHYNIVTFCC 59
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MRGNPPTLRBYILDHPEPDLFCYEQLCDSSDEDEICLDPGDAQAPATANYIYITCCY 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 60 KCDSTLRCLVOSTHVDIRTEEDLGMGTGIXPICSQK 97
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 TCHTIVRLCINSTTVDRTLQQLMGTCITVCPSCAQQ 98
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 50
Q0QLP4_9PAPI PRELIMINARY; PRT; 98 AA.
AC Q0QLP4;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE E7.
OS Human papillomavirus type 6.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxId=31552;
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=Human papillomavirus type 6vc;
RX MEDLINE=99429608; PubMed=10501500;
RA Kovelman R., Bilzer G.K., Roman A., Brown D.R., Barbosa M.S.;
RT "Human papillomavirus type 6: Classification of clinical isolates and
  functional analysis of E2 proteins.";
RL J. Gen. Virol. 80:2445-2451(1999).
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-----
CC EMBL; AF092392; AAF0065.1; -; Genomic_DNA.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000148; Papv1_E7.
DR Pfam; PF00527; E7; 1.
DR NCBI_TaxId=31552;
SQ SEQUENCE 98 AA; 10903 MW; 74DD65095A39DDB5 CRC64;

Query Match 47.8%; Score 247; DB 2; Length 98;
Best Local Similarity 53.5%; Pred. No. 7.3e-21;
Matches 53; Conservative 14; Mismatches 28; Indels 4; Gaps 3;

Qy 1 MHGDPPTLHEHYMDLQPEPTTDLXXYXQLNDSSEED-DEIDGPAGQAEPPRAHYNIVTFCC 58
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MGRNHTVTKOIVDLQPPDVGALHCYEQLVDSSEDEVDDGQ--DSQPLKQHYQIVTCC 58
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 59 CKCDSTLRCLVOSTHVDIRTEEDLGMGTGIXPICSQK 97
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 59 CGDSDNVRLVQCTETDIREVQQLLGTITNIVPICAPK 97
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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RESULT 51
VE7_HPV11 STANDARD; PRT; 98 AA.
AC P04020;
DT 23-OCT-1986, integrated into UniProtKB/Swiss-Prot.
DT 23-OCT-1986, sequence version 1.
DE Protein E7.
GN Name=E7;
OS Human papillomavirus type 11.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=10580;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=86181601; PubMed=3008427;
RA Dartmann K., Schwarz E., Gissmann L., Zur Hausen H.;
RT "The nucleotide sequence and genome organization of human papilloma
virus type 11."
RL Virology 151:124-130(1986).
RN [2]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RA Fife K.H., Fan L., Fritsch M.H., Bryan J., Brown D.R.;
RT "Association of human papillomavirus 11 DNA with squamous-cell
carcinoma of the tongue."
RL Submitted (OCT-1994) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: E7 protein has both transforming and trans-activating
activities.
CC -1- SIMILARITY: Belongs to the papillomaviruses E7 protein family;
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DR EMBL: M4119; AAA46928.1; -; Genomic_DNA.
DR EMBL: L36108; AAA21704.1; -; Genomic_DNA.
DR PIR: A03690; W7ML11.
DR InterPro: IPR000148; Papv1_E7.
DR Pfam: PF00527; E7; 1.
DR DNA-binding; Early protein; Oncogene; Transcription;
KM Transcription regulation.
FT CHAIN 1 98 Protein E7.
FT MOTIF 58 61 /FTID=PRO_0000133410.
FT MOTIF 91 94 C-XX-C motif-1.
FT MOTIF 91 94 C-XX-C motif-2.
SQ SEQUENCE 98 AA; 10889 MW; AACAA9A60C933E1F6 CRC64;

Query Match 47.4%; Score 245; DB 1; Length 98;
Best Local Similarity 53.0%; Pred. No. 1.3e-20;
Matches 53; Conservative 14; Mismatches 29; Indels 4; Gaps 3;

QY 1 MGGDTPLHEHYMDLQ-PETTDLYXXQLNDSEER-DEIDGPAQAEPRAHYNYTFC 58
DB 1 MGGRLVTLKDIYDLQPPPVGHLHCYQLDSSSEDEVKQD--KQDAQLPQHYQITCC 58
QY 59 CKCDSTLRICVSGSTHVDIRTLDELMTGLTGIYXPCISOK 98
DB 59 CGCDSNRLVVECTDGIROLDLLGLTINIVCPICAPKE 98

RESULT 52
VE7_HPV6B STANDARD; PRT; 98 AA.
AC P04664;
DT 01-JAN-1988, integrated into UniProtKB/Swiss-Prot.
DT 01-JAN-1988, sequence version 1.
DE Protein E7.
GN Name=E7;
OS Human papillomavirus type 6b.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.

```

```

OX NCBI_TaxID=10600;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=84131949; PubMed=6321162;
RA Schwarz E., Durr M., Demankowski C., Lattermann O., Zech R.,
RA Wolfepberger E., Suhai S., Zur Hausen H.;
RT "DNA sequence and genome organization of genital human papillomavirus
type 6b."
RL EMBL J. 2:2341-2348(1983).
CC -1- FUNCTION: E7 protein has both transforming and trans-activating
activities.
CC -1- SIMILARITY: Belongs to the papillomaviruses E7 protein family;
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DR EMBL: X00203; CA25019.1; -; Genomic_DNA.
DR PIR: D20558; W7ML6.
DR InterPro: IPR000148; Papv1_E7.
DR Pfam: PF00527; E7; 1.
DR DNA-binding; Early protein; Oncogene; Transcription;
KM Transcription regulation.
FT CHAIN 1 98 Protein E7.
FT MOTIF 58 61 /FTID=PRO_0000133405.
FT MOTIF 91 94 C-XX-C motif-1.
FT MOTIF 91 94 C-XX-C motif-2.
SQ SEQUENCE 98 AA; 10887 MW; 997CB5095A3C4CD CRC64;

Query Match 47.0%; Score 243; DB 1; Length 98;
Best Local Similarity 52.5%; Pred. No. 2.2e-20;
Matches 52; Conservative 15; Mismatches 28; Indels 4; Gaps 3;

QY 1 MGGDTPLHEHYMDLQ-PETTDLYXXQLNDSEER-DEIDGPAQAEPRAHYNYTFC 58
DB 1 MGGRLVTLKDIYDLQPPPVGHLHCYQLDSSSEDEVKQD--DSQPLKQHFQVTC 58
QY 59 CKCDSTLRICVSGSTHVDIRTLDELMTGLTGIYXPCISOK 97
DB 59 CGCDSNRLVVECTDGIROLDLLGLTINIVCPICAPK 97

RESULT 53
VE7_HPV6A STANDARD; PRT; 98 AA.
AC Q84292;
DT 15-JUL-1998, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1996, sequence version 1.
DE Protein E7.
GN Name=E7;
OS Human papillomavirus type 6a.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=37122;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=95297152; PubMed=778283;
RA Hofmann K.J., Cook J.C., Joyce J.G., Brown D.R., Schultz L.D.,
RA George H.A., Rosolowsky M., Fife K.H., Jansen K.U.;
RT "Sequence determination of human papillomavirus type 6a and assembly
of virus-like particles in Saccharomyces cerevisiae."
RL Virology 209:506-518(1995).
CC -1- FUNCTION: E7 protein has both transforming and trans-activating
activities.
CC -1- SIMILARITY: Belongs to the papillomaviruses E7 protein family;
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NonDerivs License
DR EMBL: L41216; AA04212.1; -; Genomic_DNA.
DR InterPro: IPR000148; Papv1_E7.
DR Pfam: PF00527; E7; 1.
KM DNA-binding; Early protein; Oncogene; Transcription;

```

```

KM Transcription regulation.
FT CHAIN 1 98 Protein E7.
FT MOTIF 58 61 /FTid=PRO_0000133404.
FT MOTIF 91 94 C-XX-C motif-1.
SQ SEQUENCE 98 AA; 10888 MW; 997CBDA5A39C4CD CRC64;

Query Match 46.8%; Score 242; DB 1; Length 98;
Best Local Similarity 52.5%; Pred. No. 2.8e-20;
Matches 52; Conservative 15; Mismatches 28; Indels 4; Gaps 3;

QY 1 MHGDTPLHEHYMDLQ-PETTDLYXXYQLNDSSEED-DEIDGPAQAPDRRAHYNYTF 58
DB 1 MHGSHVTLKDIIDLQPPDPVGLHCYEQLVDSSEDEVDEVDGQ--DSQPLKHFQIVTCC 58
QY 59 CKCDSTLRCLVQSTHVDIRTLIEDLLMGTLGIVXPICSQK 97
DB 59 CGCDSNVRLVVOCTETDIREVOQLLGLTIVCPICAPK 97

RESULT 54
VE7_HPV34 STANDARD; PRT; 97 AA.
ID VE7_HPV34
AC P36828;
DT 01-JUN-1994, integrated into UniProtKB/Swiss-Prot.
DT 01-JUN-1994, sequence version 1.
DT 07-FEB-2006, entry version 32.
DE Protein E7.
GN Name=E7;
OS Human papillomavirus type 34.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxId=333764;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=94265501; PubMed=8205838;
RA Delius H., Hofmann B.;
RT "Primer-directed sequencing of human papillomavirus types.";
RL Curr. Top. Microbiol. Immunol. 186:13-31(1994).
CC -1- FUNCTION: E7 protein has both transforming and trans-activating
CC activities.
CC -1- SIMILARITY: Belongs to the papillomaviruses E7 protein family.
CC -----
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CC -----
EMBL: X74476; CA52556.1; -; Genomic_DNA.
DR PTR; S36516;
DR InterPro; IPR000148; Papv1_E7.
DR Pfam; PF00527; E7; 1.
KM DNA-binding; Early protein; Oncogene; Transcription;
KM Transcription regulation.
FT CHAIN 1 97 Protein E7.
FT MOTIF 57 60 /FTid=PRO_0000133432.
FT MOTIF 90 93 C-XX-C motif-1.
SQ SEQUENCE 97 AA; 10985 MW; 19E3C9D1F12BF4F6 CRC64;

Query Match 43.0%; Score 222.5; DB 1; Length 97;
Best Local Similarity 49.0%; Pred. No. 5.5e-16;
Matches 48; Conservative 18; Mismatches 29; Indels 3; Gaps 3;

QY 1 MHGDTPLHEHYMDLQPET--TDLYXXYQLNDSSEEDIDGPAQAPDRRAHYNYTF 59
DB 1 MHGKPEVQDVLVDLKTETEDLTCYEST--DNSDEDEBTSHL--ERQAEGQWYIVTDCS 58
QY 60 KCDSTLRCLVQSTHVDIRTLIEDLLMGTLGIVXPICSQK 97
DB 59 RCGSTVCLTTESTADLLVLEDDLGAALKIVCPICRSRR 96

RESULT 55
O8JNAO_9PAPI

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ID O8JNAO_9PAPI PRELIMINARY; PRT; 98 AA.
AC O8JNAO;
DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2002, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE Putative transforming protein E7.
OS Human papillomavirus - cand90.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxId=333769;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22079881; PubMed=12085327; DOI=10.1086/340824;
RA Terai M., Burk R.D.;
RT "Identification and characterization of 3 novel genital human
RT papillomaviruses by overlapping polymerase chain reaction: candHPV89,
RL J. Infect. Dis. 185:1794-1797(2002).
CC -----
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CC -----
EMBL: AY057438; AAL14205.1; -; Genomic_DNA.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000148; Papv1_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 98 AA; 10944 MW; 4978F2A03847E5A2 CRC64;

Query Match 42.8%; Score 221.5; DB 2; Length 98;
Best Local Similarity 45.9%; Pred. No. 7.4e-18;
Matches 45; Conservative 17; Mismatches 33; Indels 3; Gaps 2;

QY 1 MHGDTPLHEHYMDLQ-PETTDLYXXYQLNDSSEEDIDG--PAGQAPDRRAHYNYTF 57
DB 1 MHGQRPFLKDIFFLQPDVDLHCNEQLASSEEDNRDEGQPTPTPEPAQQAIVTVIS 60
QY 58 CKCDSTLRCLVQSTHVDIRTLIEDLLMGTLGIVXPIC 95
DB 61 CCRCCCTVRLVSGHAEIRQQLBLLGALHIVCPICA 98

RESULT 56
O91194_HPV16 PRELIMINARY; PRT; 43 AA.
ID O91194_HPV16
AC O91194;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 12.
DE Truncated E7 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxId=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Zhao M., Wu X.X., Ding X.H.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
CC -----
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CC -----
EMBL: AF393782; AAK84003.1; -; Genomic_DNA.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000148; Papv1_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 43 AA; 4903 MW; 19A57D4E52FB14D6 CRC64;

Query Match 42.7%; Score 221; DB 2; Length 43;
Best Local Similarity 95.3%; Pred. No. 3.1e-18;

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Matches 41; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MHGDTPTLHEMYMDLQPTTDLXXYYQLNDSSEEDIDGPAG 43  
 DB 1 MHGDTPTLHEMYMDLQPTTDLXXYYQLNDSSEEDIDGPAG 43

RESULT 57  
 VE7\_RHPV1 STANDARD; PRT; 113 AA.  
 AC P2161;  
 DT 01-AUG-1991, integrated into UniProtKB/Swiss-Prot.  
 DT 07-FEB-2006, entry version 32.  
 DE Protein E7.  
 GN Name=E7;  
 OS Rhesus papillomavirus type 1 (Rhpv 1).  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 OC Alphapapillomavirus.  
 OX NCBI\_TaxID=10570;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE (GENOMIC DNA).  
 RX MEDLINE=9135018; PubMed=1847267;  
 RA Ostrow R.S., Labresh K.V., Faras A.J.;  
 RT "Characterization of the complete RHPV 1 genomic sequence and an  
 integration locus from a metastatic tumor.";  
 RL Virology 181:424-429(1991).  
 CC -1- FUNCTION: E7 protein has both transforming and trans-activating  
 activities.  
 CC -1- SIMILARITY: Belongs to the papillomaviruses E7 protein family.  
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EMBL: M60184; AAA79312.1; -; Genomic\_DNA.  
 DR PIR: B38503; W7MLR1.  
 DR InterPro: IPR000148; Papv1\_E7.  
 DR Pfam: PF00527; E7; 1.  
 KW DNA-binding; Early protein; Oncogene; Transcription;  
 KW Transcription regulation.  
 FT CHAIN 1 113 Protein E7.  
 FT MOTIF 73 76 /FTId=PRO\_0000133470.  
 FT MOTIF 106 109 C-XX-C motif-2.  
 FT MOTIF 106 109 C-XX-C motif-1.  
 SQ SEQUENCE 113 AA; 12818 MW; 9C404BDAC1298306 CRC64;

Query Match 42.3%; Score 218.5; DB 1; Length 113;  
 Best Local Similarity 43.8%; Pred. No. 2e-17;  
 Matches 49; Conservative 13; Mismatches 35; Indels 15; Gaps 2;

QY 1 MHGDTPTLHEMYMDLQPTTDLXXYYQLNDSSEEDIDGPAGQAEPRAH----- 51  
 DB 1 MIGHKPTLIEDIVDLQFPQGPVDMCYEQLSDSSDEDEVDHNNHNNQCHQHARPEV 60

QY 52 -----YNIYTFCKCKDSTLRCTVOSTHVDIRTLEDLMGTGLGVXPICSK 97  
 DB 61 PEDGDCYRIVSDCYSCCKPRLVVSSEHLELVLEDLMTGLDITVCSCASR 112

RESULT 58  
 Q9WHG1\_9PAPI PRELIMINARY; PRT; 108 AA.  
 AC Q9WHG1;  
 DT 01-NOV-1999, integrated into UniProtKB/TrEMBL.  
 DT 01-NOV-1999, sequence version 1.  
 DT 07-FEB-2006, entry version 17.  
 DE Putative transforming protein E7.  
 OS Human papillomavirus - Cande85.  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 OC Alphapapillomavirus.  
 OX NCBI\_TaxID=151757;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.

RA MEDLINE=20047972; PubMed=10580054;  
 RA Chow V.T., Leong P.W.;  
 RT "Complete nucleotide sequence, genomic organization and phylogenetic  
 analysis of a novel genital human papillomavirus type, HLT7474-S.";  
 RL J. Gen. Virol. 80:2923-2929(1999).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Chow V.T.K., Leong W.F.;  
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
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EMBL: AF131950; AM24182.1; -; Genomic\_DNA.  
 DR GO: GO:0005622; C:intracellular; IEA.  
 DR GO: GO:0003700; F:transcription factor activity; IEA.  
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro: IPR000148; Papv1\_E7.  
 DR Pfam: PF00527; E7; 1.  
 SQ SEQUENCE 108 AA; 12355 MW; B1F84D7DA0F384FB CRC64;

Query Match 41.8%; Score 216; DB 2; Length 108;  
 Best Local Similarity 39.0%; Pred. No. 3.7e-17;  
 Matches 41; Conservative 22; Mismatches 32; Indels 10; Gaps 2;

QY 1 MHGDTPTLHEMYMDLQPTTDLXXYYQLNDSSEEDIDGPAGQAEPRAH----- 50  
 DB 1 MHGKPTLHEMYMDLQPTTDLXXYYQLNDSSEEDIDGPAGQAEPRAH----- 60

QY 51 HNYIVTFCKCKDSTLRCTVOSTHVDIRTLEDLMGTGLGVXPICS 95  
 DB 61 RHITCCVCKCKEASLQVSSAADLRDLQQLPLGTLISFLCPICA 105

RESULT 59  
 VE7\_HPVA5 STANDARD; PRT; 106 AA.  
 AC P21736;  
 DT 01-MAY-1991, integrated into UniProtKB/Swiss-Prot.  
 DT 01-JUN-1994, sequence version 2.  
 DT 07-FEB-2006, entry version 33.  
 DE Protein E7.  
 GN Name=E7;  
 OS Human papillomavirus type 45.  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 OC Alphapapillomavirus.  
 OX NCBI\_TaxID=10593;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE (GENOMIC DNA).  
 RX MEDLINE=94255501; PubMed=8205838;  
 RA Delius H., Hofmann B.;  
 RT "Primer-directed sequencing of human papillomavirus types.";  
 RL Curr. Top. Microbiol. Immunol. 186:13-31(1994).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE (GENOMIC DNA).  
 RA Kaplan J.B., Burk R.D.;  
 RL Submitted (AUG-1990) to the EMBL/GenBank/DBJ databases.  
 CC  
 CC -1- FUNCTION: E7 protein has both transforming and trans-activating  
 activities.  
 CC -1- SIMILARITY: Belongs to the papillomaviruses E7 protein family.  
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EMBL: X74479; CA452574.1; -; Genomic\_DNA.  
 DR EMBL: M38198; AAA46974.1; -; Genomic\_DNA.  
 DR PIR: S36562; S36562.  
 DR InterPro: IPR000148; Papv1\_E7.  
 DR Pfam: PF00527; E7; 1.  
 KW DNA-binding; Early protein; Oncogene; Transcription;  
 KW Transcription regulation.  
 FT CHAIN 1 106 Protein E7.  
 FT /FTId=PRO\_0000133442.

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FT MOTIF 64 67 C-XX-C motif-1.
FT MOTIF 99 102 C-XX-C motif-2.
FT CONFLICT 3 3 G -> E (in Ref. 2).
FT CONFLICT 5 5 R -> Q (in Ref. 2).
SQ SEQUENCE 106 AA; 12050 MW; 4C53808A7285AD41 CRC64;

Query Match
Best Local Similarity 41.2%; Score 213; DB 1; Length 106;
Matches 46; Conservative 15; Mismatches 32; Indels 12; Gaps 3;

QY 1 MHGDTPTLHEMYLDLPET---TDLYXXYXQLNDSSEEDIDG-----PAGQAEPPRA 50
D 1 MHGGRATLQELIVLHPQNEIDPVDLLCYEQLSSESEENDEADGVSHAQLPARRAEPQR- 59
QY 51 HYNIVTFCKCKDSTLRCLCVOSTHVDIRTELDLNGTLGIYXPICS 95
D 60 -HKILCVCKCKDGRILETVSSADRLTLQQLFLSTLSFVCPWCA 103

RESULT 60
QY4Y3_HUMAN PRELIMINARY; PRT; 106 AA.
AC QY4Y3;
DT 01-NOV-1999, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1999, sequence version 1.
DT 07-FEB-2006, entry version 12.
DE E7 protein.
GN Name=HPV45 E7;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
RX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sastre-Garau X., Favre M., Couturier J., Orth G.;
RT "Distinct patterns of alteration of myc genes associated with
RT integration of human papillomavirus type 16 on type 45 in two genital
RT tumours.";
RL J. Gen. Virol. 81:198-199(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Favre M.G.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AJ242956; CAB44707.1; -; Genomic_DNA.
DR LinkHub; QY4Y3; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000148; Papv1_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 106 AA; 11977 MW; 1912D1DE742F6BED CRC64;

Query Match
Best Local Similarity 41.0%; Score 212; DB 2; Length 106;
Matches 46; Conservative 15; Mismatches 32; Indels 12; Gaps 3;

QY 1 MHGDTPTLHEMYLDLPET---TDLYXXYXQLNDSSEEDIDG-----PAGQAEPPRA 50
D 1 MHGGRATLQELIVLHPQNEIDPVDLLCYEQLSSESEENDEADGVSHAQLPARRAEPQR- 59
QY 51 HYNIVTFCKCKDSTLRCLCVOSTHVDIRTELDLNGTLGIYXPICS 95
D 60 -HKILCVCKCKDGRILETVSSADRLTLQQLFLSTLSFVCPWCA 103

RESULT 61
QY4Y3_HUMAN PRELIMINARY; PRT; 106 AA.
ID 010609_HP45
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```
AC 010609;
DT 01-JUN-1997, integrated into UniProtKB/TrEMBL.
DT 01-JUN-1997, sequence version 1.
DT 07-FEB-2006, entry version 21.
DE Oncoprotein E7.
OS Human papillomavirus type 45.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=10593;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sastre-Garau X., Favre M., Couturier J., Orth G.;
RT "Distinct patterns of alteration of myc genes associated with
RT integration of HPV16 or HPV45 DNA in two genital tumors.";
RL J. Gen. Virol. 0:0-0(0).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Favre M.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; Y13218; CA473661.1; -; Genomic_DNA.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000148; Papv1_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 106 AA; 11977 MW; 1912D1DE742F6BED CRC64;

Query Match
Best Local Similarity 43.8%; Pred. No. 1,1e-16;
Matches 46; Conservative 15; Mismatches 32; Indels 12; Gaps 3;

QY 1 MHGDTPTLHEMYLDLPET---TDLYXXYXQLNDSSEEDIDG-----PAGQAEPPRA 50
D 1 MHGGRATLQELIVLHPQNEIDPVDLLCYEQLSSESEENDEADGVSHAQLPARRAEPQR- 59
QY 51 HYNIVTFCKCKDSTLRCLCVOSTHVDIRTELDLNGTLGIYXPICS 95
D 60 -HKILCVCKCKDGRILETVSSADRLTLQQLFLSTLSFVCPWCA 103

RESULT 62
QBSW9_9PAPI PRELIMINARY; PRT; 95 AA.
ID QBSW9_9PAPI
AC QBSW9;
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE Putative transforming protein E7.
OS Human papillomavirus type 74.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=44028;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Terai W., Burk R.D.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AF436130; AAO15456.1; -; Genomic_DNA.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000148; Papv1_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 95 AA; 10448 MW; 6ADCFE5E772AA767 CRC64;

Query Match
Best Local Similarity 40.9%; Score 211.5; DB 2; Length 95;
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Best Local Similarity 48.5%; Pred. No. 1,1e-16;  
Matches 47; Conservative 10; Mismatches 37; Indels 3; Gaps 1;

QY 1 MHGDTPLHEHYMDLOPETDLYXXYQNLDSSEEDIDEPAGQEPDRAHYNIPTFCK 60  
DB 1 MHGKVPFLKEIVLQIQDPVGLLQNEQDSSSEEDVDEL---ATQATQHTQPYQIVTCCEV 57  
QY 61 CDSTLRLCVOSTHVDIRTDLELDMGTGIXYPCISOK 97  
DB 58 CNRSRLRVQCTGPDINNHLHTLLGLTSLVCPICAPK 94

## RESULT 63

VE7\_HPVS30 STANDARD; PRT; 105 AA.

AC P36826;  
DT 01-JUN-1994, integrated into UniProtKB/Swiss-Prot.  
DT 01-JUN-1994, sequence version 1.  
DT 07-FEB-2006, entry version 31.  
DE Protein E7.  
GN Name=E7;  
OS Human papillomavirus type 30.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Alphapapillomavirus.  
OX NCBI\_TaxId=10611;

RN [1]  
RX NUCLEOTIDE SEQUENCE (GENOMIC DNA).  
RX MEDLINE=94265501; PubMed=8205838;

RA Delius H., Hofmann B.,  
RA "Primer-directed sequencing of human papillomavirus types.",  
RL Curr. Top. Microbiol. Immunol. 186:13-31(1994).

CC -1- FUNCTION: E7 protein has both transforming and trans-activating activities.  
CC -1- SIMILARITY: Belongs to the papillomaviruses E7 protein family.  
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CC EMBL; X74474; CAAS2544.1; -; Genomic\_DNA.  
DR PIR; S36504; S36504.  
DR InterPro; IPR000148; Papv1\_E7.  
DR Pfam; PF00527; E7; 1.  
KM DNA-binding; Early protein; Oncogene; Transcription;  
KM Transcription regulation.  
FT CHAIN 1 105  
FT MOTIF 65 68 /FTid=PRO\_0000133428.  
FT MOTIF 98 101 C-XX-C motif-2.  
SQ SEQUENCE 105 AA; 12001 MW; 6166758B14B44D67 CRC64;

Query Match 40.5%; Score 209.5; DB 1; Length 105;  
Best Local Similarity 45.2%; Pred. No. 2,1e-16;  
Matches 47; Conservative 17; Mismatches 33; Indels 7; Gaps 4;

QY 1 MHGDTPLHEHYMDLOPETDLYXXYQNLDSSEEDIDEPAGQEPDRAHYNIPTFCK 60  
DB 1 MHGKVPFLKEIVLQIQDPVGLLQNEQDSSSEEDVDEL---ATQATQHTQPYQIVTCCEV 57  
QY 54 IYVFCKCDSSTLRLCVOSTHVDIRTDLELDMGTGIXYPCISOK 97  
DB 61 INTQCCRCESLVAQLAVQSTPEKELRALQOMLMGALVELVCPICATR 104

## RESULT 64

VE7\_HPVS3 STANDARD; PRT; 105 AA.

AC P36832;  
DT 01-JUN-1994, integrated into UniProtKB/Swiss-Prot.  
DT 01-JUN-1994, sequence version 1.  
DT 07-FEB-2006, entry version 32.  
DE Protein E7.  
GN Name=E7;  
OS Human papillomavirus type 53.

OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Alphapapillomavirus.  
OX NCBI\_TaxId=333765;

RN [1]  
RX NUCLEOTIDE SEQUENCE (GENOMIC DNA).  
RX MEDLINE=94265501; PubMed=8205838;  
RA Delius H., Hofmann B.,  
RA "Primer-directed sequencing of human papillomavirus types.",  
RL Curr. Top. Microbiol. Immunol. 186:13-31(1994).  
CC -1- FUNCTION: E7 protein has both transforming and trans-activating activities.  
CC -1- SIMILARITY: Belongs to the papillomaviruses E7 protein family.  
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CC EMBL; X74482; CAAS2592.1; -; Genomic\_DNA.  
DR PIR; S36528; S36528.  
DR InterPro; IPR000148; Papv1\_E7.  
DR Pfam; PF00527; E7; 1.  
KM DNA-binding; Early protein; Oncogene; Transcription;  
KM Transcription regulation.  
FT CHAIN 1 105  
FT MOTIF 65 68 /FTid=PRO\_0000133449.  
FT MOTIF 98 101 C-XX-C motif-1.  
SQ SEQUENCE 105 AA; 12162 MW; DEAYE2B8D0C1F7EC CRC64;

Query Match 43.3%; Score 208.5; DB 1; Length 105;  
Best Local Similarity 40.3%; Pred. No. 2,7e-16;  
Matches 45; Conservative 23; Mismatches 29; Indels 7; Gaps 4;

QY 1 MHGDTPLHEHYMDLOPETDLYXXYQNLDSSEEDIDEPAGQEPDRAHYNIPTFCK 60  
DB 1 MHGKVPFLKEIVLQIQDPVGLLQNEQDSSSEEDVDEL---ATQATQHTQPYQIVTCCEV 57  
QY 54 IYVFCKCDSSTLRLCVOSTHVDIRTDLELDMGTGIXYPCISOK 97  
DB 61 INTQCCRCESLVAQLAVQSTPEKELRALQOMLMGALVELVCPICATR 104

## RESULT 65

056947\_9PAPI PRELIMINARY; PRT; 90 AA.

AC 056947;  
DT 01-JUN-1998, integrated into UniProtKB/TrEMBL.  
DT 01-JUN-1998, sequence version 1.  
DT 07-FEB-2006, entry version 20.  
DE E7 protein.  
OS Human papillomavirus type 77.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Alphapapillomavirus.  
OX NCBI\_TaxId=69966;  
RN [1]  
RX NUCLEOTIDE SEQUENCE.  
RX MEDLINE=98118461; PubMed=9454709; DOI=10.1006/viro.1997.8943;  
RA Delius H., Saegling B., Bergmann K., Shamin V., de Villiers E.M.;  
RA "The genomes of three of four novel HPV types, defined by differences  
RT of their L1 genes, show high conservation of the E7 gene and the  
RT L1R";  
RL Virology 240:359-365(1998).

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CC EMBL; Y15175; CAAT5464.1; -; Genomic\_DNA.  
DR GO; GO:0005522; C:intracellular; IEA.  
DR GO; GO:0003700; F:transcription factor activity; IEA.  
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
DR InterPro; IPR000148; Papv1\_E7.  
DR Pfam; PF00527; E7; 1.  
SQ SEQUENCE 90 AA; 9971 MW; ABAB4EADABACF33B CRC64;

Query Match 40.1%; Score 207.5; DB 2; Length 90;  
Best Local Similarity 49.5%; Pred. No. 3e-16;  
Matches 47; Conservative 11; Mismatches 32; Indels 5; Gaps 2;  
QY 1 MHGPTLHEXMDLOPETTDLYXXQLNDSSEBDEIDGPAQAEPDRAHNYITFCCK 60  
DB 1 MHGKPTVKDLELDLAPLAVPLLCNEQL-DSSDEBDCID---VVEPAQAAYRVVTLCTK 55  
QY 61 CDSLTRLCVOSTHVDIRTELDLMGTGIVXPIC 95  
DB 56 CSSTLRLVESSEADIRAFQELRLTKIVCPRA 90  
RESULT 66  
Q82006 HPV73  
ID Q82006 HPV73 PRELIMINARY; PRT; 97 AA.  
AC Q82006;  
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.  
DT 01-NOV-1996, sequence version 1.  
DT 07-FEB-2006, entry version 20.  
DE E7 protein.  
OS Human papillomavirus type 73.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Alphapapillomavirus.  
OX NCBI\_Taxid=51033;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=96213783; PubMed=9635859;  
RA DOI=10.1002/(SICI)1097-0215(19960516)66:4<453::AID-IC73.0.CO;2-V;  
RA Voelter C., He Y., Delius H., Roy-Burman A., Greenspan J.S.,  
RA Greenspan D., de Villiers E.-M.,  
RT "Novel HPV types present in oral papillomatous lesions from patients  
RT with HIV infection."  
RL Int. J. Cancer 66:453-456(1996).  
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CC -----  
EMBL: X94165; CAA63883.1; -; Genomic DNA.  
DR GO: GO:0005622; C:intracellular; IEA.  
DR GO: GO:0003700; F:transcription factor activity; IEA.  
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
DR InterPro: IPR000148; PapiV\_E7.  
DR Pfam: PF00527; E7; 1.  
SQ SEQUENCE 97 AA; 10970 MW; 651D0345D048F022 CRC64;  
Query Match 40.1%; Score 207.5; DB 2; Length 97;  
Best Local Similarity 48.5%; Pred. No. 3.2e-16;  
Matches 47; Conservative 14; Mismatches 33; Indels 3; Gaps 3;  
QY 1 MHGPTLHEXMDLOPET-TDLYXXYQLNDSSEBDEIDGPAQAEPDRAHNYITFCCK 59  
DB 1 MHGKPTVKDLELDLAPLAVPLLCNEQL-DSSDEBDCID---VVEPAQAAYRVVTLCTK 58  
QY 60 KCDSTLRLCVOSTHVDIRTELDLMGTGIVXPIC 96  
DB 59 KCQCTVCAIESNKADLRVIEELMGTGIVCPIC 95  
RESULT 67  
Q6EG08\_9PAPI  
ID Q6EG08\_9PAPI PRELIMINARY; PRT; 94 AA.  
AC Q6EG08;  
DT 16-AUG-2004, integrated into UniProtKB/TrEMBL.  
DT 16-AUG-2004, sequence version 1.  
DT 07-FEB-2006, entry version 13.  
DE Putative transforming protein E7.  
GN Name=E7;  
OS Human papillomavirus type 71.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Alphapapillomavirus.  
OX NCBI\_Taxid=120686;  
RN [1]

RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Qv22792;  
RX PubMed=16306621; DOI=10.1128/JVI.79.24.15503-15510.2005;  
RA Narechania A., Chen Z., Desalle R., Burk R.D.;  
RT "Phylogenetic incongruence among Oncogenic Genital Alpha Human  
RT Papillomaviruses."  
RL J. Virol. 79:15503-15510(2005).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Qv22792;  
RA Fu L., Burk R.D.;  
RT "Correction of HPV71 sequences."  
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RA Fu L., Burk R.D.;  
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
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CC -----  
EMBL: AY330621; AAQ95185.1; -; Genomic DNA.  
DR EMBL: AY330623; AAQ95199.1; -; Genomic DNA.  
DR EMBL: AY330620; AAQ95178.1; -; Genomic DNA.  
DR GO: GO:0005622; C:intracellular; IEA.  
DR GO: GO:0003700; F:transcription factor activity; IEA.  
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
DR InterPro: IPR000148; PapiV\_E7.  
DR Pfam: PF00527; E7; 1.  
SQ SEQUENCE 94 AA; 10571 MW; 04C1C6DCC3E0DB9C CRC64;  
Query Match 39.9%; Score 206.5; DB 2; Length 94;  
Best Local Similarity 44.7%; Pred. No. 4.1e-16;  
Matches 42; Conservative 15; Mismatches 36; Indels 1; Gaps 1;  
QY 1 MHGPTLHEXMDLOPETTDLYXXQLNDSSEBDEIDGPAQAEPDRAHNYITFCCK 60  
DB 1 MRGQCTKIDIVQLQPEVVDLYCHEQFASSEBDEIDGPAQAEPDRAHNYITFCCK 59  
QY 61 CDSLTRLCVOSTHVDIRTELDLMGTGIVXPIC 94  
DB 60 CCRARLVESSEADIRAFQELRLTKIVCPIC 93  
RESULT 68  
Q2VUC6\_9PAPI  
ID Q2VUC6\_9PAPI PRELIMINARY; PRT; 95 AA.  
AC Q2VUC6;  
DT 10-JAN-2006, integrated into UniProtKB/TrEMBL.  
DT 10-JAN-2006, sequence version 1.  
DT 07-FEB-2006, entry version 3.  
DE E7 protein.  
OS Human papillomavirus type 106.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Alphapapillomavirus.  
OX NCBI\_Taxid=338326;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Qv28897;  
RX PubMed=16306621; DOI=10.1128/JVI.79.24.15503-15510.2005;  
RA Narechania A., Chen Z., Desalle R., Burk R.D.;  
RT "Phylogenetic incongruence among Oncogenic Genital Alpha Human  
RT Papillomaviruses."  
RL J. Virol. 79:15503-15510(2005).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Qv28897;  
RX PubMed=16306621; DOI=10.1128/JVI.79.24.15503-15510.2005;  
RA Narechania A., Chen Z., Desalle R., Burk R.D.;  
RT "Phylogenetic incongruence among Oncogenic Genital Alpha Human  
RT Papillomaviruses."  
RL J. Virol. 79:15503-15510(2005).  
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CC -----  
EMBL: DQ080082; AA339514.1; -; Genomic DNA.  
DR EMBL: DQ080082; AA339514.1; -; Genomic DNA.  
SQ SEQUENCE 95 AA; 10541 MW; FDD5E210EE230741 CRC64;  
Query Match 39.8%; Score 206; DB 2; Length 95;  
Best Local Similarity 41.7%; Pred. No. 4.7e-16;  
Matches 42; Conservative 15; Mismatches 36; Indels 1; Gaps 1;

Matches 40; Conservative 20; Mismatches 34; Indels 2; Gaps 2;

QY 1 MHGDTPTLHEWMLD-OPETTDLYXXQLNDSSEDEIDGPAGQAEPPRAHNYITPCC 59  
 DB 1 MHGQPTLKDQILLETDEPDVADLHCNEQFASSEEDNREDEO-PTEPAQAVRVLTCCC 59

QY 60 KCDSTLRCLVOSTHVDIRTELDLMTGLGIVXPICS 95  
 DB 60 RCGRAVLVSSGHAELRVQLLELLGALGIVCPHCA 95

RESULT 69  
 VET\_HPV29  
 ID\_VET\_HPV29 STANDARD; PRT; 90 AA.  
 AC P50784;  
 DT 01-OCT-1996, integrated into UniProtKB/Swiss-Prot.  
 DT 07-FEB-2006, sequence version 1.  
 DE Protein E7.  
 GN Name=E7;  
 OS Human papillomavirus type 29.  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 OC Alphapapillomavirus.  
 OX NCBI\_TaxId=37112;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
 RA Delius H.; (OCT-1995) to the EMBL/GenBank/DBJ databases.  
 RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: E7 protein has both transforming and trans-activating activities.  
 CC -1- SIMILARITY: Belongs to the papillomaviruses E7 protein family.  
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 CC -----  
 DR EMBL: U31784; AAA79430.1; -; Genomic\_DNA.  
 DR InterPro: IPR000148; Papv1\_E7.  
 DR Pfam: PF00527; E7; 1.  
 DR DNA-binding; Early protein; Oncogene; Transcription;  
 KW Transcription regulation.  
 FT CHAIN 1 90  
 FT MOTIF 53 56 /PRTD=PRO\_0000133427.  
 FT MOTIF 86 89 C-XX-C motif-2.  
 FT MOTIF 90 90 C-XX-C motif-1.  
 SQ SEQUENCE 90 AA; 9971 MW; 2DFX0BA8584CE6C CRC64;

Query Match 39.6%; Score 204.5; DB 1; Length 90;  
 Best Local Similarity 48.4%; Pred. No. 6,7e-16;  
 Matches 46; Conservative 12; Mismatches 32; Indels 5; Gaps 2;

QY 1 MHGDTPTLHEWMLD-OPETTDLYXXQLNDSSEDEIDGPAGQAEPPRAHNYITPCC 60  
 DB 1 MHGPKPTVKDIELDLAEAVPLVNEQL-DSSDEDCID----VPEAQAQAVRVLTCTK 55

QY 61 CDSTLRCLVOSTHVDIRTELDLMTGLGIVXPICS 95  
 DB 56 CSTTLRLVSSSEADIRAFQELLRLTKIVCPHCA 90

RESULT 70  
 VET\_HPV18  
 ID\_VET\_HPV18 STANDARD; PRT; 105 AA.  
 AC P66788;  
 DT 01-JAN-1988, integrated into UniProtKB/Swiss-Prot.  
 DT 01-APR-1990, sequence version 2.  
 DT 07-FEB-2006, entry version 40.  
 DE Protein E7.  
 GN Name=E7;  
 OS Human papillomavirus type 18.  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 OC Alphapapillomavirus.  
 OX NCBI\_TaxId=333761;  
 RN [1]

RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
 RX MEDLINE=87283882; PubMed=3039146;  
 RA Cole S.T., Dano O.;  
 RT "Nucleotide sequence and comparative analysis of the human  
 RT papillomavirus type 18 genome. Phylogeny of papillomaviruses and  
 RT repeated structure of the E6 and E7 gene products."  
 RL J. Mol. Biol. 193:599-608 (1987).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE [MRNA].  
 RX MEDLINE=88188247; PubMed=2833614;  
 RA Inagaki Y., Tsunokawa Y., Takebe N., Nawa H., Nakanishi S., Terada M.,  
 RA Sugimura T.;  
 RT "Nucleotide sequences of cDNAs for human papillomavirus type 18  
 RT transcripts in HeLa cells."  
 RL J. Virol. 62:1640-1646 (1988).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
 RX MEDLINE=87053870; PubMed=3023067;  
 RA Schneider-Gaedcke A., Schwarz E.;  
 RT "Different human cervical carcinoma cell lines show similar  
 RT transcription patterns of human papillomavirus type 18 early genes."  
 RL EMO J. 5:2285-2292 (1987).  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
 RX MEDLINE=87218459; PubMed=3034571;  
 RA Sedorf K., Oltendorf T., Kraemer G., Roewekamp W.;  
 RT "Identification of early proteins of the human papilloma viruses type  
 RT 16 (HPV 16) and type 18 (HPV 18) in cervical carcinoma cells."  
 RL EMO J. 6:139-144 (1987).  
 CC -1- FUNCTION: E7 protein has both transforming and trans-activating activities.  
 CC -1- SIMILARITY: Belongs to the papillomaviruses E7 protein family.  
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 CC -----  
 DR EMBL: X05015; CAA28665.1; -; Genomic\_DNA.  
 DR EMBL: M20324; AAA99513.1; -; mRNA.  
 DR EMBL: M20325; AAA99515.1; -; mRNA.  
 DR EMBL: M26798; AAA46947.1; -; Genomic\_DNA.  
 DR EMBL: X04773; CAA28467.1; -; Genomic\_DNA.  
 DR EMBL: A06324; CAA00540.1; -; Unassigned\_DNA.  
 DR EMBL: A06328; CAA00543.1; -; Unassigned\_DNA.  
 DR PIR: B26165; W7ML18.  
 DR InterPro: IPR000148; Papv1\_E7.  
 DR Pfam: PF00527; E7; 1.  
 DR DNA-binding; Early protein; Oncogene; Transcription;  
 KW Transcription regulation.  
 FT CHAIN 1 105  
 FT MOTIF 63 66 /PRTD=PRO\_0000133416.  
 FT MOTIF 98 101 C-XX-C motif-1.  
 FT MOTIF 99 101 C-XX-C motif-2.  
 FT CONFLICT 73 73 K -> E (in Ref. 1 and 4).  
 SQ SEQUENCE 105 AA; 11995 MW; 2CDB119534D0186A CRC64;

Query Match 39.2%; Score 202.5; DB 1; Length 105;  
 Best Local Similarity 39.6%; Pred. No. 1.4e-15;  
 Matches 42; Conservative 21; Mismatches 32; Indels 11; Gaps 3;

QY 1 MHGDTPTLHEWMLD-OPET---TDLYXXQLNDSSEDEIDG-----PAGQAEPPRAH 51  
 DB 1 MHGPKATLDQIVLHLEQNIPTVDLCHBQLSSEEDNDIDGNNHGLPARARAPQR-- 58

QY 52 YNIVTFCCKDSSTLRCLVOSTHVDIRTELDLMTGLGIVXPICSQK 97  
 DB 59 HTMLCMCKCEKARIKLVESASADLRAFQQLFNTLSFVCPWCASQ 104

RESULT 71  
 Q6PGP1\_HUMAN  
 ID\_Q6PGP1\_HUMAN PRELIMINARY; PRT; 105 AA.  
 AC Q6PGP1;  
 DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.



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CC -----
DR EMBL; AF262282; AAP20595.1; -; Genomic_DNA.
DR EMBL; AF339139; AAL34458.1; -; Genomic_DNA.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000148; Papyl_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 105 AA; 11996 MW; 24799BB534D0186A CRC64;

Query Match
Best Local Similarity 38.6%; Score 200.5; DB 2; Length 105;
Matches 42; Conservative 20; Mismatches 33; Indels 11; Gaps 3;

QY 1 MHGDTPTLHEMYLDLPET---TDLYXXYQNDSSSEEDIDG-----PAGQAEPRRAH 51
DB 1 MHGPKATLDIVVHLEPQNEIPVDLCHQLSDSSEENDEIDGVNHQHLPARRAEPOR-- 58
QY 52 YNIVTFCKCDSTLRLCVOSTHVDIRTLLEDLMGTGTYXPCSQ 97
DB 59 HTMLCMCKCKEARIELVBSADDLRAFOQLFNTLSFVCPWCASQ 104

RESULT 74
Q6EGQ1_9PAP1 PRELIMINARY; PRT; 94 AA.
AC Q6EGQ1;
DT 16-AUG-2004, integrated into UniProtKB/TrEMBL.
DT 16-FEB-2006, entry version 11.
DE Putative transforming protein E7.
OS Human papillomavirus type 71.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OC NCBI_TaxID=120686;
RN [1]
RA NUCLEOTIDE SEQUENCE.
RA Fu L., Burk R.D.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AY330622; AAQ95192.1; -; Genomic_DNA.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000148; Papyl_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 94 AA; 10499 MW; 07A1C6DC1E2DB9E CRC64;

Query Match
Best Local Similarity 38.6%; Score 199.5; DB 2; Length 94;
Matches 41; Conservative 15; Mismatches 37; Indels 1; Gaps 1;

QY 1 MHGDTPTLHEMYLDLPETTDLYXXYQNDSSSEEDIDGPAQAEPRRAHYNIVTFCK 60
DB 1 MRGQCCITKQIVVQLQPEVVDLVCHQEPASDDEGDNVDGQ-PTBAQQAQYRVVSYCGR 59
QY 61 CDSLRLCVOSTHVDIRTLLEDLMGTGTYXPC 94
DB 60 CCRVRLVBSDEADIRALQQLLGLTLVCPIC 93

RESULT 75
Q9QNP7_HPV18 PRELIMINARY; PRT; 105 AA.
AC Q9QNP7;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 07-FEB-2006, entry version 14.
DE E7 protein.

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OS Human papillomavirus type 18.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OC NCBI_TaxID=333761;
RN [1]
RA NUCLEOTIDE SEQUENCE.
RA Laaseri M., Gul'ko L., Vinokurova S., Kiseleva N., Veiko V.,
RA Kiselev P.,
RT Cloning of E6 and E7 Genes of Human Papilloma Virus Type 18 and
RT Transformation Potential of E7 Gene and its Mutants.";
RL Virus Genes 182:139-149(1999).
RN [2]
RA NUCLEOTIDE SEQUENCE.
RA Veiko V.P.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; Y18491; CAB53097.1; -; Genomic_DNA.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000148; Papyl_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 105 AA; 12010 MW; 24799BB534D4496A CRC64;

Query Match
Best Local Similarity 38.4%; Score 198.5; DB 2; Length 105;
Matches 42; Conservative 20; Mismatches 33; Indels 11; Gaps 3;

QY 1 MHGDTPTLHEMYLDLPET---TDLYXXYQNDSSSEEDIDG-----PAGQAEPRRAH 51
DB 1 MHGPKATLDIVVHLEPQNEIPVDLCHQLSDSSEENDEIDGVNHQHLPARRAEPOR-- 58
QY 52 YNIVTFCKCDSTLRLCVOSTHVDIRTLLEDLMGTGTYXPCSQ 97
DB 59 HTMLCMCKCKEARIELVBSADDLRAFOQLFNTLSFVCPWCASQ 104

RESULT 76
Q705H9_HPV43 PRELIMINARY; PRT; 99 AA.
AC Q705H9;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE E7 protein.
OS Human papillomavirus type 43.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OC NCBI_TaxID=10591;
RN [1]
RA NUCLEOTIDE SEQUENCE.
RA MEDLINE=9259065; Pubmed=2542593;
RA Loeferich A.T., Quinn A.P., Goldborough M.D., Schmidt B.J.,
RA Temple G.F.;
RT Cloning and partial DNA sequencing of two new human papillomavirus
RT types associated with condylomas and low-grade cervical neoplasia.";
RL J. Virol. 63:2829-2833(1989).
RN [2]
RA NUCLEOTIDE SEQUENCE.
RA Matsukura T., Delius H., Sugase M.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
RN [3]
RA NUCLEOTIDE SEQUENCE.
RA de Villiers E.M.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AJ620205; CAF05784.1; -; Genomic_DNA.

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DR	GO: GO:00056622; C:intracellular; IEA.
DR	GO: GO:0003760; P:transcription factor activity; IEA.
DR	GO: GO:000635; P:regulation of transcription, DNA-dependent; IEA.
DR	InterPro: IPRO00148; Papri_E7.
DR	Pfam: PF00527; E7; 1.1187 MW; CAE98EACB2C34EE3 CRC64;
SD	SEQUENCE 99 AA; 11187 MW; CAE98EACB2C34EE3 CRC64;
Query Match	
Best Local Similarity	38.3%; Score 198; DB 2; Length 99;
Matches	44; Conservative 14; Mismatches 36; Indels 2; Gaps 2;
Oy	1 MHGDPITLAEVWLDLQPEETDLYXXOINDSEEDSIDGPAGAEPPRAH-YNIVTECC 59
Db	1 MHGKKPTIRDLVLMQPEPRSLTNCQGL-DSSDSDEAEQPRQDDQVNLQYRVVTECT 59
Oy	60 KCDSTLRLCVOSTHVDITRTLEDDLMGLTGIYXPICS 95
Db	60 SCLCVIRLVQCSDSDIKRLDLLGLTKIVCPCT 95

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RESULT 77
09QN6 HPV18
ID ID Q9QNP6_HPV18 PRELIMINARY; PRT: 105 AA.
AC Q9QNP6;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 07-FEB-2006, entry version 14.
DE E7 protein.
OS Human papillomavirus type 18.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=3333761;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Laastri M., Gulko L., Vinokurova S., Kisseljova N., Velko V.,
RT Kisseljev F.;
RT "Cloning of E6 and E7 Genes of Human Papilloma Virus Type 18 and
RT Transformation Potential of E7 Gene and its Mutants.";
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Velko V.P.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
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CC -----
CC EMBL, Y18492; CAB53098.1; -, Genomic_DNA.
DR GO: GO:0005622; C:intracellular; IEA.
DR GO: GO:0003700; P:transcription factor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR000148; PapiV_E7.
DR Pfam: PF00527; E7; 1.
SQ SEQUENCE 105 AA; 12009 MW; C4979555DADA960 CRC64;

Query Match      38.0%; Score 196.5; DB 2; Length 105;
Best Local Similarity 39.6%; Pred. No. 7e-15;
Matches 42; Conservative 19; Mismatches 34; Indels 11; Gaps 3;

QY 1 MHGCTPTLHRYMDLQPET---TDLYXXQLNDSSEEDETDG-----PAGQAEPPRAH 51
   ||| || | :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 1 MHGKATLQNLVLHLHPENRIPVDLLCHEQLSDSEENDSIDGVNHQHLPARRAEPQR-- 58

QY 52 YNIITFCCKDSTRLCYQSTHVDIRLTLEDLMTGLGTIVXPICSOK 97
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 59 HTMLCMCKCEARIELLVESADDLRAFQQLFLTLTSLFVCPCWCA SQ 104

RESULT 78
081965 HPV59
ID ID O81965_HPV59 PRELIMINARY; PRT: 107 AA.
AC O81965;
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
```

```

DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 21.
DE ORF putative E7 protein.
GN Name=ORF putative E7;
OS Human papillomavirus type 59.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=37115;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=94303229; PubMed=8030272;
RA Rho J., Roy-Burman A., Kim H., de Villiers E.-M., Matsukura T.,
RA Choe J.;
RT "Nucleotide sequence and phylogenetic classification of human
RT papillomavirus type 59."
RL Virology 203:158-161(1994) .
CC -----
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CC -----
CC EMBL; X77858; CAAS4850.1; -, Genomic DNA.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000148; Papv1_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 107 AA; 12042 MW; A6F2B6973D727163 CRC64;

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Query Match 37.8%; Score 195.5; DB 2; Length 107;
Best Local Similarity 43.4%; Pred. No. 9.4e-15;
Matches 46; Conservative 17; Mismatches 30; Indels 13; Gaps 4

Qy 1 MHGDTPTLHEYMALDLP---ETTDLYXXYXQL--NDSSEDEIDGP-----ACQAEPR 49
Db 1 MHGKATLCIDVILDEPQNYEEVDLVACYEQLPDSDESEKDEPPGVNPLLLARAEPR 60
      :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 50 AHNVIVTFCCCKDSTLRLCVQSTHVDRTLEDLMGTGLGYXPCIS 95
Db 61 --HNIVCCCKCNQQLDVLVETSQDGLRALQQLFMDTLTSFVCPICA 104
      :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 79
VE7_PCPV1 STANDARD; PRT; 98 AA.
AC Q02272;
DT 01-APR-1993, integrated into UniProtKB/Swiss-Prot.
DT 01-APR-1993, sequence version 1.
DT 07-FEB-2006, entry version 34.
DE Protein E7.
DE Name=E7;
OS Pygmy chimpanzee papillomavirus type 1.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=10576;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=92391075; PubMed=13256977.
RA van Ransst W., Fuse A., Fiten F., Beuken E., Pfister H., Burk R.D.,
RA Opendakker G.;
RT "Human papillomavirus type 13 and pygmy chimpanzee papillomavirus type
RT 1: comparison of the genome organizations."
RL Virology 190:587-596(1992).
CC -!- FUNCTION. E7 protein has both transforming and trans-activating
CC activities8.
CC -!- SIMILARITY: Belongs to the papillomaviruses E7 protein family.
CC -----
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CC -----
CC EMBL, X62844; CAA44656.1; -; Genomic_DNA.
DR InterPro, IPR000148; Papv1_E7.
DR Pfam, PF00527; E7; 1.
DR Dfam-binding; Early protein; Oncogene; Transcription;

```

KW Transcription regulation.  
 FT CHAIN 1 98 Protein E7.  
 FT MOTIF 58 /FTid=PRO\_0000133464.  
 FT MOTIF 91 C-XX-C motif-1.  
 FT MOTIF 94 C-XX-C motif-2.  
 SQ SEQUENCE 98 AA; 10742 MW; E67165CF8D7BAFA6 CRC64;

Query Match 37.5%; Score 194; DB 1; Length 98;  
 Best Local Similarity 46.4%; Pred. No. 1.3e-14;  
 Matches 45; Conservative 13; Mismatches 35; Indels 4; Gaps 2;

QY 1 MHGDTPLHEHYMDLOPETDLYXXYXQLNDSSEEDIDGPAQAEPRD--RAHNYITFC 58  
 DB 1 MHGKTTTLKDIVDLSPDVGKHCNEQLD--SSEEDVEDQATQATQTOTHTQIVTCC 58  
 59 GQCDSTLRLCVQSTHVDIRLTEDLLMGLGIYXPCIS 95

QY 59 CKCDSTLRLCVQSTHVDIRLTEDLLMGLGIYXPCIS 95  
 DB 59 GQCDSTLRLCVQSTHVDIRLTEDLLMGLGIYXPCIS 95

RESULT 80  
 Q8V9K9 HPV18 PRELIMINARY; PRT; 105 AA.  
 AC Q8V9K9;  
 DT 01-MAR-2002, integrated into UniProtKB/TrEMBL.  
 DT 07-FEB-2006, entry version 11.  
 DE E7 protein.  
 GN Name=E7;  
 OS Human Papillomavirus type 18.  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 OC Alphapapillomavirus.  
 OX NCBI\_TaxID=333761;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=21568387; PubMed=11711624;  
 RX DOI=10.1128/JVI.75.24.12339-12346.2001;  
 RA Shera K.A., Shera C.A., McDougall J.K.;  
 RT "Small Tumor Virus Genomes Are Integrated near Nuclear Matrix  
 Attachment Regions in Transformed Cells.";  
 RT J. Virol. 75:12339-12346(2001).  
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DR EMBL; AF39137; AL34455.1; -; Genomic DNA.  
 DR GO; GO:0005622; C:intracellular; IEA.  
 DR GO; GO:0003700; F:transcription factor activity; IEA.  
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro; IPR000148; Papv1\_E7.  
 DR Pfam; PF00527; E7; 1.  
 SQ SEQUENCE 105 AA; 12036 MW; 2528DEA165850C71 CRC64;

Query Match 37.2%; Score 192.5; DB 2; Length 105;  
 Best Local Similarity 38.7%; Pred. No. 2.1e-14;  
 Matches 41; Conservative 21; Mismatches 33; Indels 11; Gaps 3;

QY 1 MHGDTPLHEHYMDLOPET--TDLYXXYXQLNDSSEEDIDG-----PAGQAEPRAH 51  
 DB 1 MYGPKATLQIIVLHLEPQNEIPVDLCHQQLSDSEEDNDIDGNNHGLPRARAEPR-- 58  
 52 YNIVTFCCKCDSTLRLCVQSTHVDIRLTEDLLMGLGIYXPCISQK 97  
 DB 59 HTMLCMCKCEARIELVLESSADDLRAFOQLFKTLSEFVCPWCASQ 104

RESULT 81  
 Q8B5X6 HPV54 PRELIMINARY; PRT; 95 AA.  
 AC Q8B5X6;  
 DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.  
 DT 01-MAR-2003, sequence version 1.  
 DT 07-FEB-2006, entry version 11.

DE Putative transforming protein E7.  
 GN Name=E7;  
 OS Human Papillomavirus type 54.  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 OC Alphapapillomavirus.  
 OX NCBI\_TaxID=333766;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX PubMed=16306621; DOI=10.1128/JVI.79.24.15503-15510.2005;  
 RA Narechanla A., Chen Z., Desalle R., Burk R.D.;  
 RT "Phylogenetic Incongruence among Oncogenic Genital Alpha Human  
 Papillomaviruses.";  
 RT J. Virol. 79:15503-15510(2005).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Terai M., Burk R.D.;  
 RT "Cervical HPV in Evolution; Genomic sequence of A89, a subtype of  
 HPV54.";  
 RT Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

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DR EMBL; AF36129; AA015449.1; -; Genomic DNA.  
 DR GO; GO:0005622; C:intracellular; IEA.  
 DR GO; GO:0003700; F:transcription factor activity; IEA.  
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro; IPR000148; Papv1\_E7.  
 DR Pfam; PF00527; E7; 1.  
 SQ SEQUENCE 95 AA; 10433 MW; 2B18F84E1BD4D3C8 CRC64;

Query Match 37.0%; Score 191.5; DB 2; Length 95;  
 Best Local Similarity 40.8%; Pred. No. 2.4e-14;  
 Matches 42; Conservative 17; Mismatches 31; Indels 13; Gaps 4;

QY 1 MHGDTPLHEHYMDLOPETDLYXXYXQLNDSSEEDIDGPAQAEPRAHNYITV---- 56  
 DB 1 MHGKTTTLKDIVDLSPDVGKHCNEQLD--SSEEDVEDQATQATQTOTHTQIVTCC 58  
 57 FCCKCDSTLRLCVQSTHVDIRLTEDLLMGLGIYXPCISQK 98  
 DB 56 VCCK--TVRLCVYSTHTGIRVLQELHGLALIEVCPCTASRP 95

RESULT 82  
 Q8QNP5 HPV18 PRELIMINARY; PRT; 105 AA.  
 AC Q8QNP5;  
 DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.  
 DT 07-FEB-2006, entry version 14.  
 DE E7 protein.  
 OS Human papillomavirus type 18.  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 OC Alphapapillomavirus.  
 OX NCBI\_TaxID=333761;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Laessli M., Gul'ko L., Vinokurova S., Kisseljova N., Veiko V.,  
 RA Kisseljev F.;  
 RT "Cloning of E6 and E7 Genes of Human Papilloma Virus Type 18 and  
 RT Transformation Potential of E7 Gene and Its Mutants.";  
 RT Virus Genes 18:2139-149(1999).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Veiko V.P.;  
 RT Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.

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DR EMBL; Y18493; CAB53099.1; -; Genomic DNA.  
 DR GO; GO:0005622; C:intracellular; IEA.

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DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR000148; Papv1_E7.
DR Pfam: PF00527; E7; 1.1952 MW; 247BF448A6BB4FA CRC64;
SQ SEQUENCE 105 AA; 11952 MW; 247BF448A6BB4FA CRC64;

Query Match 37.0%; Score 191.5; DB 2; Length 105;
Best Local Similarity 38.7%; Pred. No. 2.7e-14;
Matches 41; Conservative 20; Mismatches 34; Indels 11; Gaps 3;

QY 1 MHGDTPTLHEHYMLDLOPETTDLYXXYXQLNDSSEEDIDGPAQOAEPRRAH 51
DB 1 MHGKATLQDVLVLEPQNEIPVGLCHCEQLSDSEEDIDGVNHQHLPRARAPQR-- 58

QY 52 YNITPCCDSTLRLCVQSTHVDIRLTEDLLMGTLGIYXPICSQK 97
DB 59 HTMLCKCKCEARIELVVESSADDIRAFQQLFLTLSTVCWCASQ 104

RESULT 83
Q8UTG7_9PAPI PRELIMINARY; PRT; 98 AA.
AC Q8UTG7_9PAPI
DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2002, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE E7.
OS Human papillomavirus - cand91.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxId=20252;
RN [1]
RP NCLECTIDE SEQUENCE.
RX MEDLINE=2079881; PubMed=12085327; DOI=10.1086/340824;
RA Terai M., Burk R.D.;
RT "Identification and characterization of 3 novel genital human
RT papillomaviruses by overlapping polymerase chain reaction: candHPV89,
RT candHPV90, and candHPV91."
RL J. Infect. Dis. 185:1794-1797(2002).
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CC -----
EMBL: AF419318; AAM89131.1; -; Genomic_DNA.
DR GO: GO:0005622; C:intracellular; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR000148; Papv1_E7.
DR Pfam: PF00527; E7; 1.
SQ SEQUENCE 98 AA; 11055 MW; E6874FAE881797E4 CRC64;

Query Match 36.9%; Score 191; DB 2; Length 98;
Best Local Similarity 45.8%; Pred. No. 2.9e-14;
Matches 44; Conservative 16; Mismatches 34; Indels 2; Gaps 2;

QY 1 MHGDTPTLHEHYMLDLOPETTDLYXXYXQLNDSSEEDIDGPAQOAEPRRAH 59
DB 1 MYGKEPTLRDVLVLTQEPESRLTCDEQL-DSSEDEDESGTQDDQVDLVYKVTCT 59

QY 60 KCDSTLRLCVQSTHVDIRLTEDLLMGTLGIYXPIC 95
DB 60 SCYCSIRLVKVCSSDIKTELLGLTLQIVCPDCT 95

RESULT 84
Q212S3_HPV13 PRELIMINARY; PRT; 98 AA.
AC Q212S3_HPV13
DT 07-MAR-2006, integrated into UniProtKB/TrEMBL.
DT 07-MAR-2006, sequence version 1.
DT 07-MAR-2006, entry version 1.
DE E7.
GN Name=E7;

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OS Human papillomavirus type 13.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxId=10573;
RN [1]
RP NCLECTIDE SEQUENCE.
RA Borborema-Santos C.M., Santos P.J.B., Talhari S., Ascolfi-Filho S.;
RT "Sequencing and genome analysis of HPV type 13 isolated in the
RT Amazon."
RL Submitted (DEC-2005) to the EMBL/GenBank/DBJ databases.
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CC -----
EMBL: DQ344807; ABC79058.1; -; Genomic_DNA.
SQ SEQUENCE 98 AA; 10738 MW; 97D6627C57CF896D CRC64;

Query Match 36.8%; Score 190; DB 2; Length 98;
Best Local Similarity 45.0%; Pred. No. 3.8e-14;
Matches 45; Conservative 12; Mismatches 37; Indels 6; Gaps 2;

QY 1 MHGDTPTLHEHYMLDLOPETTDLYXXYXQLNDSSEEDIDGPAQOAEPRRA--HYNIVTF 57
DB 1 MHGQYTLKQIVLDLPTDPVGLCHCEQLSDS---EDVDQAQTQHTSLTLCYQILTS 57

QY 58 CCKCDSTLRLCVQSTHVDIRLTEDLLMGTLGIYXPICSQK 97
DB 58 CSKCSNVRLVVECTGPDHLDLGLTLNIVCPDCAPK 97

RESULT 85
Q98005_9PAPI PRELIMINARY; PRT; 96 AA.
AC Q98005_9PAPI
DT 01-FEB-1997, integrated into UniProtKB/TrEMBL.
DT 01-FEB-1997, sequence version 1.
DT 07-FEB-2006, entry version 20.
DE E7 protein.
OS Human papillomavirus type 74.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxId=44028;
RN [1]
RP NCLECTIDE SEQUENCE.
RX MEDLINE=96379050; PubMed=8784613;
RA Longuet M., Cassemonet P., Orh G.;
RT "A novel genital human papillomavirus (HPV), HPV type 74, found in
RT immunosuppressed patients."
RL J. Clin. Microbiol. 34:1859-1862(1996).
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CC -----
EMBL: U40822; AAC55128.1; -; Genomic_DNA.
DR GO: GO:0005622; C:intracellular; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR000148; Papv1_E7.
DR Pfam: PF00527; E7; 1.
SQ SEQUENCE 96 AA; 10522 MW; 8DF8480CE5CECA3 CRC64;

Query Match 36.6%; Score 189; DB 2; Length 96;
Best Local Similarity 45.9%; Pred. No. 4.8e-14;
Matches 45; Conservative 12; Mismatches 37; Indels 4; Gaps 2;

QY 1 MHGDTPTLHEHYMLDLOPETTDLYXXYXQLNDSSEEDIDGPAQOAEPRRAH-YNIVTFCC 59
DB 1 MHGKYSTLKEIVLELQDPVGLCHCEQLSDSSEEDIDGPAQOAEPRRAH-YNIVTFCCG 57

QY 60 KCDSTLRLCVQSTHVDIRLTEDLLMGTLGIYXPICSQK 97
DB 58 VCNRSIRLVVQCTGPDHLDLGLTLNIVCPDCAPK 95

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RESULT 86
VE7_HPV28      STANDARD;      PRT;      87 AA.
AC P50783;
DT 01-OCT-1996, integrated into UniProtKB/Swiss-Prot.
DT 01-OCT-1996, sequence version 1.
DT 07-FEB-2006, entry version 28.
DE Protein E7.
GN Name=E7;
OS Human papillomavirus type 28.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
NCBI_TaxId=37111;
RN NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RA Delius H.;
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: E7 protein has both transforming and trans-activating
CC activities.
CC -1- SIMILARITY: Belongs to the papillomaviruses E7 protein family.
CC -----
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CC -----
DR EMBL: U31783; AAA79423.1; -, Genomic_DNA.
DR InterPro: IPR000148; Papv1_E7.
DR Pfam: PF00527; E7; 1.
KM DNA-binding; Early protein; Oncogene; Transcription;
KW Transcription regulation.
FT CHAIN 1 87 Protein E7.
FT MOTIF 50 53 /FTId=PRO_0000133426.
FT MOTIF 83 86 C-XX-C motif-1.
FT MOTIF 83 86 C-XX-C motif-2.
SQ SEQUENCE 87 AA; 9625 MW; 4A3692CED16BCD60 CRC64;

Query Match 36.0%; Score 186; DB 1; Length 87;
Best Local Similarity 44.8%; Pred. No. 9.7e-14;
Matches 43; Conservative 11; Mismatches 30; Indels 12; Gaps 3;

OY 1 MGGDTPLHEHMDLPETTDLYXXQLNDSSEED--SIDGPAQAEPDRAHYNIYVTF 58
DB 1 MGGHPRVNDKIELSLAEDVPV---QCVOQDDEEDTNNVEPAQA-----YRVVTL 50
1 MGGHPRVNDKIELSLAEDVPV---QCVOQDDEEDTNNVEPAQA-----YRVVTL 50

OY 59 CCKDSTLRVCVSTHVDIRLTEDLMGTGIVXPIC 94
DB 51 PKCSSPLRLVVECSHADIRALEQLLGLTVVCPRC 86

RESULT 87
VE7_HPV42      STANDARD;      PRT;      93 AA.
AC P27231;
DT 01-APR-1992, integrated into UniProtKB/Swiss-Prot.
DT 01-APR-1992, sequence version 1.
DT 07-FEB-2006, entry version 31.
DE Protein E7.
GN Name=E7;
OS Human papillomavirus type 42.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
NCBI_TaxId=10590;
RN NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RA MEDLINE:92087479; PubMed:1309278;
RA Philipp M., Honore N., Sapp M., Cole S.T., Streeck R.E.;
RT "Human papillomavirus type 42: new sequences, conserved genome
RT organization";
RL Virology 186:331-334 (1992).
CC -1- FUNCTION: E7 protein has both transforming and trans-activating
CC activities.
CC -1- SIMILARITY: Belongs to the papillomaviruses E7 protein family.
CC -----

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CC -----
DR EMBL: M73236; AAA47042.1; ALT_INIT; Genomic_DNA.
DR PIR: F39451; W7M142.
DR InterPro: IPR000148; Papv1_E7.
DR Pfam: PF00527; E7; 1.
KM DNA-binding; Early protein; Oncogene; Transcription;
KW Transcription regulation.
FT CHAIN 1 93 Protein E7.
FT MOTIF 53 56 /FTId=PRO_0000133440.
FT MOTIF 86 89 C-XX-C motif-1.
FT MOTIF 86 89 C-XX-C motif-2.
SQ SEQUENCE 93 AA; 10679 MW; 829D1E24071F7A53 CRC64;

Query Match 35.5%; Score 183.5; DB 1; Length 93;
Best Local Similarity 44.4%; Pred. No. 2.1e-13;
Matches 44; Conservative 17; Mismatches 27; Indels 11; Gaps 4;

OY 1 MGGDTPLHEHMDLP--ET-TDLYXXQLNDSSEEDSIDGPAQAEPDRAHYNIYVTF 57
DB 1 MGGHPRVNDKIELSLAEDVPV---QCVOQDDEEDTNNVEPAQA-----YRVVTL 50
1 MGGHPRVNDKIELSLAEDVPV---QCVOQDDEEDTNNVEPAQA-----YRVVTL 50

OY 58 CCKDSTLRVCVSTHVDIRLTEDLMGTGIVXPIC 96
DB 53 CTQCKSVKLVQCTEADIRNLQOMLGTIDVCPICAR 91

RESULT 88
VE7_HPV66      STANDARD;      PRT;      105 AA.
AC Q80956;
DT 15-JUL-1998, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 30.
DE Protein E7.
GN Name=E7;
OS Human papillomavirus type 66.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
NCBI_TaxId=37119;
RN NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RA PubMed:1663515;
RA Tawheed A.R., Beaudenon S., Favre M., Orth G.;
RT "Characterization of human papillomavirus type 66 from an invasive
RT carcinoma of the uterine cervix.";
RL J. Clin. Microbiol. 29:2656-2660 (1991).
[2]
RN NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RP Delius H.;
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: E7 protein has both transforming and trans-activating
CC activities.
CC -1- SIMILARITY: Belongs to the papillomaviruses E7 protein family.
CC -----
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CC -----
DR EMBL: M75123; -, NOT ANNOTATED CDS; Genomic_DNA.
DR EMBL: U31794; AAA79500.1; -, Genomic_DNA.
DR PIR: B44890; B44890.
DR InterPro: IPR000148; Papv1_E7.
DR Pfam: PF00527; E7; 1.
KM DNA-binding; Early protein; Oncogene; Transcription;
KW Transcription regulation.
FT CHAIN 1 105 Protein E7.
FT MOTIF 66 69 /FTId=PRO_0000133459.
FT MOTIF 98 101 C-XX-C motif-1.
FT MOTIF 98 101 C-XX-C motif-2.
SQ SEQUENCE 105 AA; 11912 MW; C09339FA2F62AFA CRC64;

Query Match 35.5%; Score 183.5; DB 1; Length 105;

```

Best Local Similarity 42.7%; Pred. No. 2.4e-13;  
Matches 44; Conservative 17; Mismatches 33; Indels 9; Gaps 4;

QY 1 MHGPTPLHEMYMLDLPET-EDLYXXYXQNDN-SEEEEDID-----CPAGQAEPRAHY 52  
DB 1 MHGVPPLQEVILELAPQETIDLCNEQLDSSSEDEDEDEHLLERPOQAQAEQHKC-Y 59  
QY 53 NIVTFCCCKDSTLRCLVOSTHVDIRTEEDLLMGTIGIYXPICS 95  
DB 60 LIHPPCKCKELVQDIDISTKEELRVVQQLMGALTYTCPLCA 102

## RESULT 89

037386 CCPV1 PRELIMINARY; PRT; 99 AA.

AC 037386,  
DT 01-JAN-1998, integrated into UniProtKB/TrEMBL.  
DT 01-JAN-1998, sequence version 1.  
DE 07-FEB-2006, entry version 20.

OS Common chimpanzee papillomavirus type 1.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Unclassified Papillomaviridae; primate papillomaviruses;  
OC Common chimpanzee papillomavirus.  
OX NCBI\_TaxID=66261;

NP NUCLEOTIDE SEQUENCE.

RA Schinzel-F. Soza I., Brasky K.M., Hilliard J.K.;  
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.

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DR EMBL: AF020905; AAB71705.1; -; Genomic\_DNA.

DR GO: GO:0005622; C:intracellular; IEA.

DR GO: GO:0003700; F:transcription factor activity; IEA.

DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

DR InterPro: IPR000148; Papv1\_E7.

DR Pfam: PF00527; E7; 1.

SQ SEQUENCE 99 AA; 10856 MW; 7365003547E87AFE CRC64;

Query Match 34.9%; Score 180.5; DB 2; Length 99;  
Best Local Similarity 42.4%; Pred. No. 5e-13;  
Matches 42; Conservative 18; Mismatches 32; Indels 7; Gaps 2;

QY 1 MHGPTPLHEMYMLDLPETTDLYXXYXQNDN-SEEEEDIDGAPAGQAEPRAHY 56  
DB 1 MHGVPPLQEVILELAPQETIDLCNEQLDSSSEDEDEDEHLLERPOQAQAEQHKC-Y 57

QY 57 FCCCKDSTLRCLVOSTHVDIRTEEDLLMGTIGIYXPICS 95

DB 58 SCGHGNNTVRLVVECTGPDIDHNLNLLGSLNIVCPICA 96

## RESULT 90

VE7\_HPV54 STANDARD; PRT; 95 AA.

AC 081019,  
DT 15-JUN-1998, integrated into UniProtKB/Swiss-Prot.  
DT 01-NOV-1996, sequence version 1.  
DT 07-FEB-2006, entry version 30.

DE Protein E7.

GN Name=E7;

OS Human papillomavirus type 54.

OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC AlphaPapillomavirus.

OX NCBI\_TaxID=333766;

NP NUCLEOTIDE SEQUENCE (GENOMIC DNA).

RP Delius H.;

RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: E7 protein has both transforming and trans-activating activities.

CC -!- SIMILARITY: Belongs to the papillomaviruses E7 protein family.

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DR EMBL: U37486; AAA79186.1; -; Genomic\_DNA.

DR InterPro: IPR000148; Papv1\_E7.

DR Pfam: PF00527; E7; 1.

KW DNA-binding; Early protein; Oncogene; Transcription;

KW Transcription regulation.

FT CHAIN 1 95 Protein E7.

FT MOTIF 88 91 /FTID=PRO\_0000133450.

FT SQ SEQUENCE 95 AA; 10565 MW; 6A543269F2561891 CRC64;

Query Match 34.7%; Score 179.5; DB 1; Length 95;  
Best Local Similarity 39.2%; Pred. No. 6.3e-13;  
Matches 40; Conservative 18; Mismatches 31; Indels 13; Gaps 4;

QY 1 MHGPTPLHEMYMLDLPETTDLYXXYXQNDN-SEEEEDIDGAPAGQAEPRAHY 56  
DB 1 MHGVPPLQEVILELAPQETIDLCNEQLDSSSEDEDEDEHLLERPOQAQAEQHKC-Y 55

QY 57 FCCCKDSTLRCLVOSTHVDIRTEEDLLMGTIGIYXPICS 97  
DB 56 VCCCKDSTLRCLVOSTHVDIRTEEDLLMGTIGIYXPICS 94

## RESULT 91

VE7\_HPV70 STANDARD; PRT; 109 AA.

AC P50785;  
DT 01-OCT-1996, integrated into UniProtKB/Swiss-Prot.  
DT 01-OCT-1996, sequence version 1.  
DT 07-FEB-2006, entry version 28.

DE Protein E7.

GN Name=E7;

OS Human papillomavirus type 70.

OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC AlphaPapillomavirus.

OX NCBI\_TaxID=39457;

NP NUCLEOTIDE SEQUENCE (GENOMIC DNA).

RP MEDLINE=96249586; PubMed=8815087;

RA Forslund O., Hansson B.G.;

RT "Human papillomavirus type 70 genome cloned from overlapping PCR products: complete nucleotide sequence and genomic organization.";

RT J. Clin. Microbiol. 34:802-809 (1996).

RN [2]

NP NUCLEOTIDE SEQUENCE (GENOMIC DNA).

RP MEDLINE=97060129; PubMed=8904450;

RA Longuet M., Beaudenon S., Orh G.;

RT "Two novel genital human papillomavirus (HPV) types, HPV68 and HPV70,

RT related to the potentially oncogenic HPV39.";

RT J. Clin. Microbiol. 34:738-744 (1996).

CC -!- FUNCTION: E7 protein has both transforming and trans-activating

CC activities.

CC -!- SIMILARITY: Belongs to the papillomaviruses E7 protein family.

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DR EMBL: U21941; AAC54851.1; -; Genomic\_DNA.

DR EMBL: U22461; AAC54881.1; -; Genomic\_DNA.

DR InterPro: IPR000148; Papv1\_E7.

DR Pfam: PF00527; E7; 1.

DR DNA-binding; Early protein; Oncogene; Transcription;

KW Transcription regulation.

FT CHAIN 1 109 Protein E7.

FT MOTIF 66 69 /FTID=PRO\_0000133462.

FT MOTIF 101 104 C-XX-C motif-1.

FT MOTIF 109 104 C-XX-C motif-2.

SQ SEQUENCE 109 AA; 12657 MW; 2FD3C643DFAF891 CRC64;

Query Match 34.6%; Score 179; DB 1; Length 109;  
 Best Local Similarity 40.8%; Pred. No. 8.5e-13;  
 Matches 43; Conservative 14; Mismatches 36; Indels 14; Gaps 3;

QY 1 MHGDTPLHEMYMDLPQ---ETTDLYXXYQLNDSSEEDIDGP-----AGQAEPD 48  
 DB 1 MHGPRPTLQIVLDLYPYNEIQPVLDVCHQLEDSDNETEPHVNHHQQLARREPFQ 60

QY 49 RAHNYIVTFCCCDSTLRCLCVQSTHVDIRLTEDLLMGTGIVXPIC 95  
 DB 61 R-HKICQWCKCKNTTLHLVVEASQENLRSLQLFMETLSFVCPWCA 105

RESULT 92  
 VE7\_HPV57 STANDARD; PRT; 92 AA.  
 AC P22160;  
 DT 01-AUG-1991, integrated into UniProtKB/Swiss-Prot.  
 DT 07-FEB-2006, entry version 1.  
 DE Protein E7.  
 GN Name=E7;  
 OS Human papillomavirus type 57.  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 OC Alphapapillomavirus.  
 NCBI\_TaxID=333753;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
 RX MEDLINE=1188699; PubMed=1964523; DOI=10.1016/0168-1702(90)90091-O;  
 RA Hirsch-Behnam A., Dellus H., de Villiers E.M.;  
 RT "A comparative sequence analysis of two human papillomavirus (HPV)  
 types 2a and 57.";  
 RL Virus Res. 18:81-98(1990).  
 CC -I- FUNCTION: E7 protein has both transforming and trans-activating  
 activities.  
 CC -I- SIMILARITY: Belongs to the papillomaviruses E7 proteins family.  
 CC -----  
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 CC -----  
 CC EMBL: X55965; CA39431.1; -; Genomic\_DNA.  
 CC DR PIR: S15622; S15622.  
 DR InterPro: IPR000148; Papv1\_E7.  
 DR Pfam: PF00527; E7; 1.  
 KW DNA-binding; Early protein; Oncogene; Transcription;  
 KM Transcription regulation.  
 FT CHAIN 1 92 Protein E7.  
 FT MOTIF 55 58 /FTID=PRO\_0000133453.  
 FT MOTIF 88 91 C-XX-C motif-2.  
 FT MOTIF 91 C-XX-C motif-2.  
 SQ SEQUENCE 92 AA; 10376 MW; DB56C16916257B13 CRC64;

Query Match 34.5%; Score 178.5; DB 1; Length 92;  
 Best Local Similarity 43.3%; Pred. No. 7.9e-13;  
 Matches 42; Conservative 15; Mismatches 31; Indels 9; Gaps 3;

QY 1 MHGDTPLHEMYMDLPQ---ETTDLYXXYQLNDSSEEDIDGPAGQAEPRAHNYIVTF 57  
 DB 1 MHGPRPTLQIVLDLYPYNEIQPVLDVCHQLEDSDNETEPHVNHHQQLARREPFQ 60

QY 58 CCKCDSTLRCLCVQSTHVDIRLTEDLLMGTGIVXPIC 94  
 DB 55 CCKCHSTVRLVVEGAGADIRHLEQLFLNTLTIVCPRC 91

RESULT 93  
 VE7\_HPV56 STANDARD; PRT; 105 AA.  
 AC P36833;  
 DT 01-JUN-1994, integrated into UniProtKB/Swiss-Prot.  
 DT 01-JUN-1994, sequence version 1.  
 DT 07-FEB-2006, entry version 31.

DE Protein E7.  
 GN Name=E7;  
 OS Human papillomavirus type 56.  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 OC Alphapapillomavirus.  
 NCBI\_TaxID=10596;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
 RX MEDLINE=94265501; PubMed=8205838;  
 RA Dellus H., Hofmann B.;  
 RT "Primer-directed sequencing of human papillomavirus types.";  
 RL Curr. Top. Microbiol. Immunol. 186:13-31(1994).  
 CC -I- FUNCTION: E7 protein has both transforming and trans-activating  
 activities.  
 CC -I- SIMILARITY: Belongs to the papillomaviruses E7 protein family.  
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 CC -----  
 CC EMBL: X74463; CA52597.1; -; Genomic\_DNA.  
 CC DR PIR: S36580; S36580.  
 DR InterPro: IPR000148; Papv1\_E7.  
 DR Pfam: PF00527; E7; 1.  
 KW DNA-binding; Early protein; Oncogene; Transcription;  
 KM Transcription regulation.  
 FT CHAIN 1 105 Protein E7.  
 FT MOTIF 65 68 /FTID=PRO\_0000133452.  
 FT MOTIF 98 101 C-XX-C motif-1.  
 FT MOTIF 101 C-XX-C motif-2.  
 SQ SEQUENCE 105 AA; 11892 MW; 35424B643B4E0183 CRC64;

Query Match 34.5%; Score 178.5; DB 1; Length 105;  
 Best Local Similarity 40.8%; Pred. No. 9.3e-13;  
 Matches 42; Conservative 17; Mismatches 35; Indels 9; Gaps 3;

QY 1 MHGDTPLHEMYMDLPQ---ETTDLYXXYQLNDSSEEDIDGPAGQAEPRAHNYIVTF 52  
 DB 1 MHGPRPTLQIVLDLYPYNEIQPVLDVCHQLEDSDNETEPHVNHHQQLARREPFQ 59

QY 53 NIVTFCCCDSTLRCLCVQSTHVDIRLTEDLLMGTGIVXPIC 95  
 DB 60 LIHVPCCEKFFVQLDIQSTKEDLRVQQLMGTGIVTCTPCA 102

RESULT 94  
 VE7\_HPV07 STANDARD; PRT; 111 AA.  
 AC P36816;  
 DT 01-JUN-1994, integrated into UniProtKB/Swiss-Prot.  
 DT 01-JUN-1994, sequence version 1.  
 DT 07-FEB-2006, entry version 31.  
 DE Protein E7.  
 GN Name=E7;  
 OS Human papillomavirus type 7.  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 OC Alphapapillomavirus.  
 NCBI\_TaxID=10620;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
 RX MEDLINE=94265501; PubMed=8205838;  
 RA Dellus H., Hofmann B.;  
 RT "Primer-directed sequencing of human papillomavirus types.";  
 RL Curr. Top. Microbiol. Immunol. 186:13-31(1994).  
 CC -I- FUNCTION: E7 protein has both transforming and trans-activating  
 activities.  
 CC -I- SIMILARITY: Belongs to the papillomaviruses E7 protein family.  
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 CC -----  
 CC EMBL: X74463; CA52477.1; -; Genomic\_DNA.  
 CC DR PIR: S36585; S36585.  
 DR InterPro: IPR000148; Papv1\_E7.

DR Pfam; PF00527; E7; 1.  
 KM DNA-binding; Early protein; Oncogene; Transcription;  
 KM Transcription regulation.  
 FT CHAIN 1 111 Protein E7.  
 FT MOTIF 71 74 /FTid=PRO\_0000133406.  
 FT MOTIF 104 107 C-XX-C motif-1.  
 FT MOTIF 107 C-XX-C motif-2.  
 SQ SEQUENCE 111 AA; 12460 MW; 830ADCA5F912BF1A CRC64;

Query Match 34.5%; Score 178.5; DB 1; Length 111;  
 Best Local Similarity 39.8%; Pred. No. 9.9e-13;  
 Matches 45; Conservative 12; Mismatches 33; Indels 23; Gaps 3;

Qy 1 MHGDPPTLHEVMDLPETDLYXXQVNDSSSEEDFIDGPAQAEPPRAH-----YNIY 51  
 Db 1 MHGERTIGDVLVDQPEPVLSCEQL-DSSDSDDHE-----QDQDSSNRREQPTQ 55

Qy 52 -----YNIYTFCKCSDTLRLCVOSTHVDIRFTLEDLLMGTIGVXPICS 95  
 Db 56 QDLQVNIQSPKIVTHCVFCHGLVRLVHACTATDIRQVQLMGTINIVCPNCA 108

## RESULT 95

VE7\_HPV51 STANDARD; PRT; 101 AA.  
 AC P26558;  
 DT 01-AUG-1992, integrated into UniProtKB/Swiss-Prot.  
 DT 01-AUG-1992, sequence version 1.  
 DT 07-FEB-2006, entry version 31.  
 DE Protein E7.  
 GN Name=E7;  
 OS Human Papillomavirus type 51.  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 OC Alphapapillomavirus.  
 OX NCBI\_TaxId=10595;

NP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
 RX MEDLINE=91303675; PubMed=1649326;  
 RA Lungu O., Crum C.P., Silverstein S.J.;

RT "Biologic properties and nucleotide sequence analysis of human  
 papillomavirus type 51.";

RL J. Virol. 65:4216-4225(1991).  
 CC -1- FUNCTION: E7 protein has both transforming and trans-activating  
 activities.

CC -1- SIMILARITY: Belongs to the papillomaviruses E7 protein family.  
 CC -----

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DR EMBL; M62877; -; NOT\_ANNOTATED\_CDS; Genomic\_DNA.  
 DR PIR; F40415; W7M151.  
 DR InterPro; IPR000148; Papv1\_E7.

DR Pfam; PF00527; E7; 1.  
 KM DNA-binding; Early protein; Oncogene; Transcription;  
 KM Transcription regulation.

KW CHAIN 1 101 Protein E7.  
 FT MOTIF 62 65 /FTid=PRO\_0000133447.  
 FT MOTIF 95 98 C-XX-C motif-1.  
 FT MOTIF 98 C-XX-C motif-2.

SQ SEQUENCE 101 AA; 11339 MW; 65E85C554099801A CRC64;

Query Match 34.4%; Score 178; DB 1; Length 101;  
 Best Local Similarity 41.0%; Pred. No. 1e-12;  
 Matches 41; Conservative 16; Mismatches 37; Indels 6; Gaps 3;

Qy 1 MHGDPPTLHEVMDLPETDLYXXQVNDSSSEEDFIDGPAQAEPPRAH-----YNIY 55  
 Db 1 MRGNVPLKIDVHLIRPTEIDLCYEQF-DSSSEEDVDNMRQQLPERRAQAATCYRIE 59

Qy 56 TFCCKCDSTLRLCVOSTHVDIRFTLEDLLMGTIGVXPICS 95  
 Db 60 APCRCSSVVOQLAVSSGDTLRVVOQLMGLSLVCPNCA 99

Qy 56 TFCCKCDSTLRLCVOSTHVDIRFTLEDLLMGTIGVXPICS 95  
 Db 60 APCRCSSVVOQLAVSSGDTLRVVOQLMGLSLVCPNCA 99

RESULT 96  
 VE7\_HPV55 STANDARD; PRT; 97 AA.  
 AC Q80935;  
 DT 15-JUL-1998, integrated into UniProtKB/Swiss-Prot.  
 DT 01-NOV-1996, sequence version 1.  
 DT 07-FEB-2006, entry version 30.  
 DE Protein E7.  
 GN Name=E7;  
 OS Human Papillomavirus type 55.  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 OC Alphapapillomavirus.  
 OX NCBI\_TaxId=37114;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
 RA Delius H.;

RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: E7 protein has both transforming and trans-activating  
 activities.  
 CC -1- SIMILARITY: Belongs to the papillomaviruses E7 protein family.  
 CC -----

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DR EMBL; U31791; AAA79479.1; -; Genomic\_DNA.  
 DR InterPro; IPR000148; Papv1\_E7.

DR Pfam; PF00527; E7; 1.  
 KM DNA-binding; Early protein; Oncogene; Transcription;  
 KM Transcription regulation.

KW CHAIN 1 97 Protein E7.  
 FT MOTIF 57 60 /FTid=PRO\_0000133451.  
 FT MOTIF 90 93 C-XX-C motif-1.  
 FT MOTIF 93 C-XX-C motif-2.

SQ SEQUENCE 97 AA; 10621 MW; E2997616BC647D42 CRC64;

Query Match 34.1%; Score 176.5; DB 1; Length 97;  
 Best Local Similarity 44.4%; Pred. No. 1.5e-12;  
 Matches 44; Conservative 14; Mismatches 36; Indels 5; Gaps 3;

Qy 1 MHGDPPTLHEVMDLPETDLYXXQVNDSSSEEDFIDGPAQAEPPRAH-YNIYTF 58  
 Db 1 MHGVTPLKEIVELDPDPVGLHCNEQLDSS--EBEVDLATQATQDTQPYQIVTTC 57

Qy 59 CKCDSTLRLCVOSTHVDIRFTLEDLLMGTIGVXPICSOK 97  
 Db 58 GTCNRNRYLVVQCTGTDICQHLTLGLSLVCPNCA 96

Qy 59 CKCDSTLRLCVOSTHVDIRFTLEDLLMGTIGVXPICSOK 97  
 Db 58 GTCNRNRYLVVQCTGTDICQHLTLGLSLVCPNCA 96

RESULT 97  
 VE7\_HPV2A STANDARD; PRT; 92 AA.  
 AC P25485;  
 DT 01-MAY-1992, integrated into UniProtKB/Swiss-Prot.  
 DT 01-MAY-1992, sequence version 1.  
 DT 07-FEB-2006, entry version 32.  
 DE Protein E7.  
 GN Name=E7;  
 OS Human Papillomavirus type 2a.  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 OC Alphapapillomavirus.  
 OX NCBI\_TaxId=10584;  
 RN [1]

RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
 RX MEDLINE=91188699; PubMed=1964523; DOI=10.1016/0168-1702(90)90091-O;  
 RA Hirsch-Behnam A., Delius H., de Villiers E.M.;

RT "A comparative sequence analysis of two human papillomavirus (HPV)  
 types 2a and 57.";

RL Virus Res. 18:81-98(1990).  
 CC -1- FUNCTION: E7 protein has both transforming and trans-activating  
 activities.  
 CC -1- SIMILARITY: Belongs to the papillomaviruses E7 protein family.  
 CC -----

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DR EMBL; U31791; AAA79479.1; -; Genomic\_DNA.  
 DR InterPro; IPR000148; Papv1\_E7.

DR Pfam; PF00527; E7; 1.  
 KM DNA-binding; Early protein; Oncogene; Transcription;  
 KM Transcription regulation.

KW CHAIN 1 92 Protein E7.  
 FT MOTIF 57 60 /FTid=PRO\_0000133451.  
 FT MOTIF 90 93 C-XX-C motif-1.  
 FT MOTIF 93 C-XX-C motif-2.

SQ SEQUENCE 92 AA; 10621 MW; E2997616BC647D42 CRC64;

Query Match 34.1%; Score 176.5; DB 1; Length 97;  
 Best Local Similarity 44.4%; Pred. No. 1.5e-12;  
 Matches 44; Conservative 14; Mismatches 36; Indels 5; Gaps 3;

Qy 1 MHGDPPTLHEVMDLPETDLYXXQVNDSSSEEDFIDGPAQAEPPRAH-YNIYTF 58  
 Db 1 MHGVTPLKEIVELDPDPVGLHCNEQLDSS--EBEVDLATQATQDTQPYQIVTTC 57

Qy 59 CKCDSTLRLCVOSTHVDIRFTLEDLLMGTIGVXPICSOK 97  
 Db 58 GTCNRNRYLVVQCTGTDICQHLTLGLSLVCPNCA 96

Qy 59 CKCDSTLRLCVOSTHVDIRFTLEDLLMGTIGVXPICSOK 97  
 Db 58 GTCNRNRYLVVQCTGTDICQHLTLGLSLVCPNCA 96

Qy 59 CKCDSTLRLCVOSTHVDIRFTLEDLLMGTIGVXPICSOK 97  
 Db 58 GTCNRNRYLVVQCTGTDICQHLTLGLSLVCPNCA 96

Qy 59 CKCDSTLRLCVOSTHVDIRFTLEDLLMGTIGVXPICSOK 97  
 Db 58 GTCNRNRYLVVQCTGTDICQHLTLGLSLVCPNCA 96

Qy 59 CKCDSTLRLCVOSTHVDIRFTLEDLLMGTIGVXPICSOK 97  
 Db 58 GTCNRNRYLVVQCTGTDICQHLTLGLSLVCPNCA 96

Qy 59 CKCDSTLRLCVOSTHVDIRFTLEDLLMGTIGVXPICSOK 97  
 Db 58 GTCNRNRYLVVQCTGTDICQHLTLGLSLVCPNCA 96

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 CC -----  
 DR EMBL; X55964; -; NOT\_ANNOTATED\_CDS; Genomic\_DNA.  
 DR PIR; S15615; S15615.  
 DR InterPro; IPR000148; Papyl\_E7.  
 DR Pfam; PF00527; E7; 1.  
 DR DNA-binding; Early protein; Oncogene; Transcription;  
 KM Transcription regulation.  
 FT CHAIN 1 92  
 FT Protein E7.  
 FT /FRID=PRO\_0000133400.  
 FT MOTIF 55 58  
 FT MOTIF 88 91 C-XX-C motif-1.  
 FT C-XX-C motif-2.  
 SQ SEQUENCE 92 AA; 10369 MW; 0C4412D9C7A9EBA CRC64;  
 Query Match 33.9%; Score 175.5; DB 1; Length 92;  
 Best Local Similarity 43.3%; Pred. No. 1.8e-12;  
 Matches 42; Conservative 13; Mismatches 35; Indels 7; Gaps 3;  
 QY 1 MGGDTPTLH--YMDLPETTDLYXXQLNDSSSEEDIDGAGQAEPPRAHNYITFC 58  
 DB 1 MGGNPSLMDITLIDELIPEIVDLHCDEQF--DSSSEENHQ---LTPDVQAYGVVTC 55  
 QY 59 CKCDSTLRLCVQSTHVDIRTELDLMTGLTGIYXPICS 95  
 DB 56 CKCGRTLRVLCVQSTHVDIRTELDLMTGLTGIYXPICS 92

RESULT 98  
 Q9IR58 HPV82 PRELIMINARY; PRT; 100 AA.  
 AC Q9IR58;  
 DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.  
 DT 01-OCT-2000, sequence version 1.  
 DT 07-FEB-2006, entry version 15.  
 DE E7 protein.  
 OS Human papillomavirus type 82.  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 OC Alphapapillomavirus.  
 OC NCBI\_TaxID=129724;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=20087389; PubMed=10618284;  
 RA Kuno N., Sato T., Sato Y., Sugase M., Matsukura T.;  
 RT "Molecular cloning and nucleotide sequence analysis of a novel human  
 RT papillomavirus (type 82) associated with vaginal intraepithelial  
 RT neoplasia.";  
 RL Clin. Diagn. Lab. Immunol. 7:91-95(2000).  
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 CC -----  
 DR EMBL; AB027021; BAA90736.1; -; Genomic\_DNA.  
 DR GO; GO:0005622; C:intracellular; IEA.  
 DR GO; GO:0003700; R:transcription factor activity; IEA.  
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro; IPR000148; Papyl\_E7.  
 DR Pfam; PF00527; E7; 1.  
 SQ SEQUENCE 100 AA; 11325 MW; 47E8C0D0F67A81D CRC64;

Query Match 33.9%; Score 175.5; DB 2; Length 100;  
 Best Local Similarity 40.0%; Pred. No. 2e-12;  
 Matches 40; Conservative 18; Mismatches 35; Indels 7; Gaps 4;  
 QY 1 MGGDTPTLH--YMDLPETTDLYXXQLNDSSSEEDIDG---PAGQAEPPRAHNYITFC 55  
 DB 1 MGGNPSLMDITLIDELIPEIVDLHCDEQF--DSSSEENHQ---LTPDVQAYGVVTC 55  
 QY 56 CKCDSTLRLCVQSTHVDIRTELDLMTGLTGIYXPICS 95  
 DB 59 CKCGRTLRVLCVQSTHVDIRTELDLMTGLTGIYXPICS 92

RESULT 99  
 Q2VJB9 9PAPI PRELIMINARY; PRT; 96 AA.  
 ID Q2VJB9;  
 AC Q2VJB9;  
 DT 10-JAN-2006, integrated into UniProtKB/TrEMBL.  
 DT 10-JAN-2006, sequence version 1.  
 DT 07-FEB-2006, entry version 3.  
 DE E7 protein.  
 OS Human papillomavirus type 102.  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 OC Alphapapillomavirus.  
 OC NCBI\_TaxID=338327;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=QV340771;  
 RX PubMed=16306621; DOI=10.1128/JVI.79.24.15503-15510.2005;  
 RA Narechantha A., Chen Z., Desalle R., Burk R.D.;  
 RT "Phylogenetic incongruence among Oncogenic Genital Alpha Human  
 RT Papillomaviruses";  
 RL J. Virol. 79:15503-15510(2005).  
 CC -----  
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
 CC Distributed under the Creative Commons Attribution-NoDerivs License  
 CC -----  
 DR EMBL; DQ080083; AAZ39521.1; -; Genomic\_DNA.  
 SQ SEQUENCE 96 AA; 10594 MW; E791B4A9BA8B85F CRC64;  
 Query Match 33.8%; Score 174.5; DB 2; Length 96;  
 Best Local Similarity 42.7%; Pred. No. 2.5e-12;  
 Matches 41; Conservative 13; Mismatches 41; Indels 1; Gaps 1;  
 QY 1 MGGDTPTLH--YMDLPETTDLYXXQLNDSSSEEDIDGAGQAEPPRAHNYITFC 59  
 DB 1 MGGNPSLMDITLIDELIPEIVDLHCDEQF--DSSSEENHQ---LTPDVQAYGVVTC 55  
 QY 60 KCDSTLRLCVQSTHVDIRTELDLMTGLTGIYXPICS 95  
 DB 61 MCGQSTLRVLCVQSTHVDIRTELDLMTGLTGIYXPICS 96

RESULT 100  
 VE7 HPV10 STANDARD; PRT; 86 AA.  
 ID VE7 HPV10  
 AC P36818;  
 DT 01-JUN-1994, integrated into UniProtKB/Swiss-Prot.  
 DT 01-JUN-1994, sequence version 1.  
 DT 07-FEB-2006, entry version 32.  
 DE Protein E7.  
 GN Name=E7;  
 OS Human papillomavirus type 10.  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 OC Alphapapillomavirus.  
 OC NCBI\_TaxID=333759;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
 RX MEDLINE=94265501; PubMed=8205838;  
 RA Delius H., Hofmann B.;  
 RT "Primer-directed sequencing of human papillomavirus types.";  
 RL Curr. Top. Microbiol. Immunol. 186:13-31(1994).  
 CC -1- FUNCTION: E7 protein has both transforming and trans-activating  
 CC activities.  
 CC -1- SIMILARITY: Belongs to the papillomaviruses E7 protein family.  
 CC -----  
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
 CC Distributed under the Creative Commons Attribution-NoDerivs License  
 CC -----  
 DR EMBL; X74465; CA52490.1; -; Genomic\_DNA.  
 DR PIR; S36533; S36533.  
 DR InterPro; IPR000148; Papyl\_E7.  
 DR Pfam; PF00527; E7; 1.  
 DR DNA-binding; Early protein; Oncogene; Transcription;  
 KM Transcription regulation.  
 FT CHAIN 1 86  
 FT Protein E7.

FT	MOTIF	49	52	/FTId=PRO_0000133409.
FT	MOTIF	82	85	C-XX-C motif-1.
FT	MOTIF	82	85	C-XX-C motif-2.
SO	SEQUENCE	86 AA;	9541 MW;	E557B8952A125090 CRC64

Query Match	33.6%	Score 173.5	DB 1	Length 86
Best Local Similarity	42.6%	Pred. No. 2.8e12		
Matches 40	Conservative 10	Mismatches 35	Indels 9	Gaps 2

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Db      1 MHGGHPFVKDOIELSLAPEDIPIV-----CNVQLDBEDYTDA----VEBPQAQRNVVTCEKK 51
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Search completed: May 27, 2006, 05:16:26  
Job time : 154.133 secs

GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

## OM protein - protein search, using sw model

Run on: May 27, 2006, 05:16:46 ; Search time 28.7309 Seconds

(without alignments)  
298.563 Million cell updates/sec

Title: US-10-530-253-14ED

Perfect score: 517  
Sequence: 1 MHGDTPTLHXYMDLQPEPT.....LEDULMGTGLVPRICQKP 98Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 100 summaries

Database :

Issued Patents AA:\*

1: /EMC\_Ceitera\_SIDS3/prodata/2/iaa/5 COMB.pep:\*

2: /EMC\_Ceitera\_SIDS3/prodata/2/iaa/6 COMB.pep:\*

3: /EMC\_Ceitera\_SIDS3/prodata/2/iaa/7 COMB.pep:\*

4: /EMC\_Ceitera\_SIDS3/prodata/2/iaa/H COMB.pep:\*

5: /EMC\_Ceitera\_SIDS3/prodata/2/iaa/PCUS COMB.pep:\*

6: /EMC\_Ceitera\_SIDS3/prodata/2/iaa/PC COMB.pep:\*

7: /EMC\_Ceitera\_SIDS3/prodata/2/iaa/bactfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	513	99.2	220	2	US-09-485-885-8
2	512	99.0	98	1	US-08-406-248-6
3	512	99.0	98	2	US-08-075-541D-42
4	512	99.0	98	2	US-09-382-616A-1
5	512	99.0	98	2	US-08-944-368A-4
6	512	99.0	98	2	US-09-820-764-4
7	512	99.0	98	2	US-09-986-118A-4
8	512	99.0	98	2	US-09-728-466-1
9	512	99.0	98	2	US-09-824-017-4
10	512	99.0	98	2	US-09-637-746-3
11	512	99.0	98	2	US-09-501-097A-7
12	512	99.0	98	2	US-09-980-523A-12
13	512	99.0	121	2	US-10-267-311-12
14	512	99.0	121	2	US-10-267-311-12
15	512	99.0	198	2	US-09-613-303-35
16	512	99.0	198	2	US-10-267-311-35
17	512	99.0	220	2	US-10-485-885-1
18	512	99.0	239	2	US-09-485-885-12
19	512	99.0	253	1	US-08-459-818-20
20	512	99.0	253	1	US-08-889-666-20
21	512	99.0	253	1	US-08-466-078-20
22	512	99.0	253	1	US-08-725-776-20
23	512	99.0	263	1	US-08-488-062-20
24	512	99.0	266	2	US-08-117-083-9
25	512	99.0	266	2	US-08-860-165-10
26	512	99.0	266	2	US-09-359-382-10
27	512	99.0	266	2	US-09-367-309A-1
28	512	99.0	287	2	US-09-501-097A-25
29	512	99.0	295	2	US-09-613-303-33
30	512	99.0	295	2	US-10-267-311-33
31	512	99.0	324	2	US-09-613-303-25
32	512	99.0	324	2	US-10-267-311-25
33	512	99.0	371	2	US-09-485-885-6
34	512	99.0	390	2	US-09-485-885-14
35	512	99.0	493	2	US-09-613-303-19
36	512	99.0	493	2	US-10-267-311-19
37	512	99.0	639	2	US-09-613-303-17
38	512	99.0	641	2	US-10-267-311-17
39	512	99.0	641	2	US-09-613-303-15
40	512	99.0	641	2	US-10-267-311-15
41	512	99.0	647	2	US-09-613-303-53
42	512	99.0	647	2	US-10-267-311-53
43	507	98.1	98	2	US-09-566-420-19
44	507	98.1	98	2	US-10-201-764-19
45	503	97.3	98	2	US-09-613-303-8
46	503	97.3	98	2	US-10-267-311-8
47	503	97.3	648	2	US-09-613-303-29
48	503	97.3	648	2	US-10-267-311-29
49	503	97.3	711	2	US-09-613-303-41
50	503	97.3	711	2	US-10-267-311-41
51	503	97.3	724	2	US-09-613-303-45
52	503	97.3	724	2	US-10-267-311-45
53	500	96.7	420	2	US-09-501-097A-22
54	500	96.7	723	2	US-09-501-097A-20
55	478	92.5	185	2	US-09-462-993-2
56	353	68.3	172	2	US-08-860-165-12
57	353	68.3	172	2	US-09-359-382-12
58	345	66.7	172	2	US-08-860-165-14
59	345	66.7	172	2	US-09-359-382-14
60	247	47.8	601	1	US-08-606-288-7
61	247	47.8	601	1	US-08-606-288-10
62	247	47.8	601	2	US-09-347-483-7
63	247	47.8	601	2	US-09-347-483-10
64	243	47.0	1587	2	US-09-000-094-46
65	243	47.0	1587	2	US-10-011-749-46
66	240	46.4	375	2	US-09-000-094-42
67	240	46.4	375	2	US-10-011-749-42
68	240	46.4	465	2	US-09-000-094-44
69	240	46.4	465	2	US-10-011-749-44
70	209	40.4	38	2	US-09-501-097A-6
71	201.5	39.0	227	2	US-09-485-885-19
72	200.5	38.8	372	1	US-08-117-083-13
73	200.5	38.8	281	2	US-09-485-885-23
74	192.5	37.2	227	2	US-09-485-885-16
75	171	33.1	30	1	US-08-934-915-52
76	171	33.1	30	2	US-09-486-394-3
77	162	31.3	30	1	US-08-934-915-53
78	154	29.8	30	2	US-09-486-394-1
79	153	29.6	30	1	US-08-934-915-51
80	153	29.6	30	2	US-09-486-394-4
81	150.5	29.1	32	2	US-08-075-541D-7
82	148	28.6	30	2	US-09-828-645-7
83	147	28.4	30	1	US-08-363-586-1
84	147	28.4	30	2	US-09-828-645-3
85	146	28.2	30	1	US-08-934-915-54
86	145	28.0	30	2	US-09-486-394-2
87	143	27.7	25	2	US-08-075-541D-47
88	137	26.5	28	2	US-09-486-394-5
89	136	26.3	25	1	US-08-363-586-2
90	126	24.4	26	2	US-08-075-541D-40
91	122	23.6	30	1	US-08-934-915-71
92	121	23.4	23	2	US-09-980-523A-14
93	120	23.2	20	2	US-08-075-541D-10
94	118	22.8	20	1	US-08-934-915-48
95	118	22.8	20	2	US-09-980-177A-73
96	116	22.4	20	2	US-09-980-177A-74
97	114	22.1	19	2	US-08-075-541D-3
98	113	21.9	20	1	US-08-934-915-46
99	112	21.7	20	2	US-08-075-541D-43

100 112 21.7 20 2 US-09-980-177A-69

Sequence 69, Appl

## ALIGNMENTS

## RESULT 1

US-09-485-885-8  
; Sequence 8, Application US/09485885  
; Patent No. 6342224  
; GENERAL INFORMATION:  
; APPLICANT: Bruck, Claudine  
; APPLICANT: Cabezon Silva, Teresa  
; APPLICANT: Delisse, Anne-Marie Eva Fernande  
; APPLICANT: Gerard, Catherine Marie Ghislaine  
; APPLICANT: Lombardo-Bencheikh, Angela  
; TITLE OF INVENTION: Vaccine  
; FILE REFERENCE: B45107  
; CURRENT APPLICATION NUMBER: US/09/485,885  
; CURRENT FILING DATE: 2000-02-18  
; PRIOR APPLICATION NUMBER: PCT/EP98/05285  
; PRIOR FILING DATE: 1998-08-17  
; PRIOR APPLICATION NUMBER: GB 9717953.5  
; PRIOR FILING DATE: 1997-08-22  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO: 8  
; LENGTH: 220  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-09-485-885-8

Query Match 99.2%; Score 513; DB 2; Length 220;

Best Local Similarity 96.9%; Pred. No. 1.8e-59; Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEYMLDLPETTDLYXXYXQINDSSEEDIDGPAQAEPDRAHNYITVFCK 60  
Db 114 MHGDTPLHEYMLDLPETTDLYXXYXQINDSSEEDIDGPAQAEPDRAHNYITVFCK 173  
Qy 61 CDSTRLCVOSTHVDIRLTEDLMTGLGIYVPICSQKP 98  
Db 174 CDSTRLCVOSTHVDIRLTEDLMTGLGIYVPICSQKP 211

## RESULT 2

US-08-406-248-6  
; Sequence 6, Application US/08406248  
; Patent No. 5736318  
; GENERAL INFORMATION:  
; APPLICANT: Munger, Karl  
; APPLICANT: Jones, D. Leanne  
; TITLE OF INVENTION: METHOD AND KIT FOR EVALUATING  
; TITLE OF INVENTION: TRANSFORMED CELLS  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Ann-Louise Kerner, Ph.D., Lappin & Kusmer  
; STREET: 200 State Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/406,248  
; FILING DATE:  
; CLASSIFICATION: 436  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McDanielis, Patricia A.

; REGISTRATION NUMBER: 33,194  
; REFERENCE/DOCKET NUMBER: HAZ-011  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-330-1300  
; TELEFAX: 617-330-1311  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 98 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-406-248-6

Query Match 99.0%; Score 512; DB 1; Length 98;

Best Local Similarity 96.9%; Pred. No. 8e-60; Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEYMLDLPETTDLYXXYXQINDSSEEDIDGPAQAEPDRAHNYITVFCK 60  
Db 1 MHGDTPLHEYMLDLPETTDLYCYEQINDSSEEDIDGPAQAEPDRAHNYITVFCK 60  
Qy 61 CDSTRLCVOSTHVDIRLTEDLMTGLGIYVPICSQKP 98  
Db 61 CDSTRLCVOSTHVDIRLTEDLMTGLGIYVPICSQKP 98

## RESULT 3

US-08-075-541D-42  
; Sequence 42, Application US/08075541D  
; Patent No. 6183745  
; GENERAL INFORMATION:  
; APPLICANT: TINDLE, ROBERT  
; APPLICANT: FERNANDO, GERMAIN  
; APPLICANT: FRAZER, IAN  
; TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND  
; TITLE OF INVENTION: PEPTIDES FOR USE THEREIN  
; NUMBER OF SEQUENCES: 56  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.  
; STREET: 1601 MARKET STREET, 36TH FLOOR  
; CITY: PHILADELPHIA  
; STATE: PENNSYLVANIA  
; COUNTRY: USA  
; ZIP: 19103-2398  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/075,541D  
; FILING DATE: 10-JUN-1993  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: AU Pk 3876  
; FILING DATE: 12-DEC-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/au91/00575  
; FILING DATE: 12-DEC-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: NADEL, ALAN S  
; REGISTRATION NUMBER: 27,363  
; REFERENCE/DOCKET NUMBER: 8795-4  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-567-2020  
; TELEFAX: 215-567-2991  
; INFORMATION FOR SEQ ID NO: 42:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 98 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide

US-08-075-541D-42

Query Match 99.0%; Score 512; DB 2; Length 98;  
Best Local Similarity 96.9%; Pred. No. 8e-60;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDPPTLHEHYMDLQPEETDLYXXYXQUNDSEEDIEDGPAQAEPPRAHYNIVTFCK 60  
DB 1 MHGDPPTLHEHYMDLQPEETDLYCYEQUNDSEEDIEDGPAQAEPPRAHYNIVTFCK 60

QY 61 CDSTLRVCVOSTHVDIRTLIEDLMTGTLGIVXPICSOX 98  
DB 61 CDSTLRVCVOSTHVDIRTLIEDLMTGTLGIVXPICSOX 98

RESULT 4  
US-09-382-616A-1

Sequence 1, Application US/09382616A  
Patent No. 6200746  
GENERAL INFORMATION:

APPLICANT: Fisher, Christopher

APPLICANT: He, Wanxia

TITLE OF INVENTION: Methods to Identify Anti-Viral Agents

FILE REFERENCE: 28341/6216

CURRENT APPLICATION NUMBER: US/09/382,616A

PRIOR FILING DATE: 1999-08-25

PRIOR APPLICATION NUMBER: 09/382,616

NUMBER OF SEQ ID NOS: 43

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 1

LENGTH: 98

TYPE: PRT

ORGANISM: Papillomavirus sylvilagi

US-09-382-616A-1

Query Match 99.0%; Score 512; DB 2; Length 98;  
Best Local Similarity 96.9%; Pred. No. 8e-60;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDPPTLHEHYMDLQPEETDLYXXYXQUNDSEEDIEDGPAQAEPPRAHYNIVTFCK 60  
DB 1 MHGDPPTLHEHYMDLQPEETDLYCYEQUNDSEEDIEDGPAQAEPPRAHYNIVTFCK 60

QY 61 CDSTLRVCVOSTHVDIRTLIEDLMTGTLGIVXPICSOX 98  
DB 61 CDSTLRVCVOSTHVDIRTLIEDLMTGTLGIVXPICSOX 98

RESULT 5  
US-08-944-368A-4

Sequence 4, Application US/08944368A  
Patent No. 6228368  
GENERAL INFORMATION:

APPLICANT: Giesman, et al

TITLE OF INVENTION: Papilloma Virus Capsomere Vaccine

TITLE OF INVENTION: Formulations and Methods of Use

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &amp;

STREET: 233 South Wacker Drive, 6300 Sears Tower

CITY: Chicago

STATE: Illinois

COUNTRY: United States of America

ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/944,368A

FILING DATE:

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Williams Jr., Joseph A.

REGISTRATION NUMBER: 38,659

REFERENCE/DOCKET NUMBER: 27013/34028

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-474-6300

TELEFAX: 312-474-0448

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 98 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-944-368A-4

Query Match 99.0%; Score 512; DB 2; Length 98;  
Best Local Similarity 96.9%; Pred. No. 8e-60;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDPPTLHEHYMDLQPEETDLYXXYXQUNDSEEDIEDGPAQAEPPRAHYNIVTFCK 60  
DB 1 MHGDPPTLHEHYMDLQPEETDLYCYEQUNDSEEDIEDGPAQAEPPRAHYNIVTFCK 60

QY 61 CDSTLRVCVOSTHVDIRTLIEDLMTGTLGIVXPICSOX 98  
DB 61 CDSTLRVCVOSTHVDIRTLIEDLMTGTLGIVXPICSOX 98

RESULT 6  
US-09-820-764-4

Sequence 4, Application US/09820764  
Patent No. 6352696  
GENERAL INFORMATION:

APPLICANT: BURGER, Alexander

APPLICANT: HALEK, Michael

TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE

TITLE OF INVENTION: FORMULATIONS AND METHODS OF USE

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESSES:

ADDRESSEE: FOLEY &amp; LARDNER

STREET: 3000 K Street, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/820,764

FILING DATE: 30-Mar-2001

CLASSIFICATION: &lt;Unknown&gt;

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/026,896

FILING DATE: 20-FEB-1998

ATTORNEY/AGENT INFORMATION:

NAME: Sandercock, Colin G.

REGISTRATION NUMBER: 31,298

REFERENCE/DOCKET NUMBER: 37067/102

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 672-5300

TELEFAX: (202) 672-5399

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 98 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-820-764-4

Query Match 99.0%; Score 512; DB 2; Length 98;  
Best Local Similarity 96.9%; Pred. No. 8e-60;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDPPTLHEYMALDQPEPTDLYXXQXNDSSSEDEIDGPAGQAEPPRAHNYIVTFCK 60  
Db 1 MHGDPPTLHEYMALDQPEPTDLYXXQXNDSSSEDEIDGPAGQAEPPRAHNYIVTFCK 60  
Qy 61 CDSTRLCVOSTHVDIRLTEDLMLGTLGIYXPCISQKP 98  
Db 61 CDSTRLCVOSTHVDIRLTEDLMLGTLGIYXPCISQKP 98

RESULT 7

US-09-986-118A-4  
; Sequence 4, Application US/09986118A  
; Patent No. 6562351  
; GENERAL INFORMATION:

APPLICANT: BURGER, Alexander

TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE

FORMULATIONS AND METHODS OF USE

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESS: FOLEY &amp; LARDNER

STREET: 3000 K Street, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/986,118A

FILING DATE: 07-No. 6562351-2001

CLASSIFICATION: &lt;Unknown&gt;

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/026,896

FILING DATE: &lt;Unknown&gt;

ATTORNEY/AGENT INFORMATION:

NAME: Sandercock, Colin G.

REGISTRATION NUMBER: 31,298

REFERENCE/DOCKET NUMBER: 37067/102

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 672-5300

TELEFAX: (202) 672-5399

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 98 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-986-118A-4

Query Match 99.0%; Score 512; DB 2; Length 98;  
Best Local Similarity 96.9%; Pred. No. 8e-60;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDPPTLHEYMALDQPEPTDLYXXQXNDSSSEDEIDGPAGQAEPPRAHNYIVTFCK 60  
Db 1 MHGDPPTLHEYMALDQPEPTDLYXXQXNDSSSEDEIDGPAGQAEPPRAHNYIVTFCK 60  
Qy 61 CDSTRLCVOSTHVDIRLTEDLMLGTLGIYXPCISQKP 98  
Db 61 CDSTRLCVOSTHVDIRLTEDLMLGTLGIYXPCISQKP 98

RESULT 8

US-09-728-466-1

; Sequence 1, Application US/09728466

; Patent No. 6641994

; GENERAL INFORMATION:

APPLICANT: Fisher, Christopher

TITLE OF INVENTION: Methods to Identify Anti-Viral Agents

FILE REFERENCE: 26341/6216

CURRENT APPLICATION NUMBER: US/09/728,466

CURRENT FILING DATE: 2000-12-01

PRIOR APPLICATION NUMBER: 09/382,616

PRIOR FILING DATE: 1999-08-25

NUMBER OF SEQ ID NOS: 43

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 1

LENGTH: 98

TYPE: PRT

ORGANISM: Papillomavirus sv1v1lag1

US-09-728-466-1

Query Match 99.0%; Score 512; DB 2; Length 98;  
Best Local Similarity 96.9%; Pred. No. 8e-60;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDPPTLHEYMALDQPEPTDLYXXQXNDSSSEDEIDGPAGQAEPPRAHNYIVTFCK 60  
Db 1 MHGDPPTLHEYMALDQPEPTDLYXXQXNDSSSEDEIDGPAGQAEPPRAHNYIVTFCK 60  
Qy 61 CDSTRLCVOSTHVDIRLTEDLMLGTLGIYXPCISQKP 98  
Db 61 CDSTRLCVOSTHVDIRLTEDLMLGTLGIYXPCISQKP 98

RESULT 9

US-09-824-017-4

; Sequence 4, Application US/09824017

; Patent No. 6649167

; GENERAL INFORMATION:

APPLICANT: BURGER, Alexander

TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE

FORMULATIONS AND METHODS OF USE

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESS: FOLEY &amp; LARDNER

STREET: 3000 K Street, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/824,017

FILING DATE: 03-Apr-2001

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/026,896

FILING DATE: 1998-02-20

ATTORNEY/AGENT INFORMATION:

NAME: Sandercock, Colin G.

REGISTRATION NUMBER: 31,298

REFERENCE/DOCKET NUMBER: 37067/102

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 672-5300

TELEFAX: (202) 672-5399

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 98 amino acids

TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 4  
US-09-824-017-4

Query Match 99.0%; Score 512; DB 2; Length 98;  
Best Local Similarity 96.9%; Pred. No. 8e-60; 3; Indels 0; Gaps 0;  
Matches 95; Conservative 0; Mismatches 3;

QY 1 MHGDTPLHEHYMDLQPEETDLYXXQNDSSSEDEIDGPAGAEPPRAHYNIVTFCK 60  
|||||  
DB 1 MHGDTPLHEHYMDLQPEETDLYCYEQNDSSSEDEIDGPAGAEPPRAHYNIVTFCK 60  
|||||

QY 61 CDSTLRVCVOSTHYDRTLEDLMGTGIVXPICQKP 98  
|||||  
DB 61 CDSTLRVCVOSTHYDRTLEDLMGTGIVCPICQKP 98  
|||||

RESULT 10  
US-09-637-746-3  
Sequence 3, Application US/09637746  
Patent No. 6727079  
GENERAL INFORMATION:  
APPLICANT: Thorgelsson, Snorri S.  
APPLICANT: Moltach, Joseph T.  
TITLE OF INVENTION: CDNA ENCODING A GENE BOG (BST OVER-EXPRESSED GENE) AND ITS PROTEIN  
FILE REFERENCE: 11613.29USW1  
CURRENT APPLICATION NUMBER: US/09/637,746  
CURRENT FILING DATE: 2000-08-11  
PRIOR APPLICATION NUMBER: PCT/US99/04142  
PRIOR FILING DATE: 1999-02-25  
PRIOR APPLICATION NUMBER: US 60/079,567  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: US 60/075,922  
PRIOR FILING DATE: 1998-02-25  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 3  
LENGTH: 98  
TYPE: PRT  
ORGANISM: Human papillomavirus  
US-09-637-746-3

Query Match 99.0%; Score 512; DB 2; Length 98;  
Best Local Similarity 96.9%; Pred. No. 8e-60; 3; Indels 0; Gaps 0;  
Matches 95; Conservative 0; Mismatches 3;

QY 1 MHGDTPLHEHYMDLQPEETDLYXXQNDSSSEDEIDGPAGAEPPRAHYNIVTFCK 60  
|||||  
DB 1 MHGDTPLHEHYMDLQPEETDLYCYEQNDSSSEDEIDGPAGAEPPRAHYNIVTFCK 60  
|||||

QY 61 CDSTLRVCVOSTHYDRTLEDLMGTGIVXPICQKP 98  
|||||  
DB 61 CDSTLRVCVOSTHYDRTLEDLMGTGIVCPICQKP 98  
|||||

RESULT 11  
US-09-501-097A-7  
Sequence 7, Application US/09501097A  
Patent No. 6734173  
GENERAL INFORMATION:  
APPLICANT: Tzzy-Chou Wu  
APPLICANT: Chien-Pou Hung  
TITLE OF INVENTION: IMPROVED HSP DNA VACCINES  
FILE REFERENCE: 2240-169349  
CURRENT APPLICATION NUMBER: US/09/501,097A  
CURRENT FILING DATE: 2000-02-09  
NUMBER OF SEQ ID NOS: 25  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 7

LENGTH: 98  
TYPE: PRT  
ORGANISM: human papillomavirus  
US-09-501-097A-7

Query Match 99.0%; Score 512; DB 2; Length 98;  
Best Local Similarity 96.9%; Pred. No. 8e-60; 3; Indels 0; Gaps 0;  
Matches 95; Conservative 0; Mismatches 3;

QY 1 MHGDTPLHEHYMDLQPEETDLYXXQNDSSSEDEIDGPAGAEPPRAHYNIVTFCK 60  
|||||  
DB 1 MHGDTPLHEHYMDLQPEETDLYCYEQNDSSSEDEIDGPAGAEPPRAHYNIVTFCK 60  
|||||

QY 61 CDSTLRVCVOSTHYDRTLEDLMGTGIVXPICQKP 98  
|||||  
DB 61 CDSTLRVCVOSTHYDRTLEDLMGTGIVCPICQKP 98  
|||||

RESULT 12  
US-09-980-523A-12  
Sequence 12, Application US/09980523A  
Patent No. 6783763  
GENERAL INFORMATION:  
APPLICANT: CHOPPIN, JEANNINE  
APPLICANT: BOURGAULT VILLADA, ISABELLE  
APPLICANT: GUILLET, JEAN-GERARD  
APPLICANT: CONNAN, FRANCINE  
APPLICANT: FERRIS, ESTELLE  
TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 AND E7  
TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE  
TITLE OF INVENTION: PARTICULARLY IN VACCINATION  
FILE REFERENCE: WO1 A0 INS  
CURRENT APPLICATION NUMBER: US/09/980,523A  
CURRENT FILING DATE: 2002-04-29  
PRIOR APPLICATION NUMBER: PCT/FR00/01513  
PRIOR FILING DATE: 2000-05-31  
PRIOR APPLICATION NUMBER: FR 99/07012  
PRIOR FILING DATE: 1999-06-03  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 12  
LENGTH: 98  
TYPE: PRT  
ORGANISM: Human Papillomavirus  
US-09-980-523A-12

Query Match 99.0%; Score 512; DB 2; Length 98;  
Best Local Similarity 96.9%; Pred. No. 8e-60; 3; Indels 0; Gaps 0;  
Matches 95; Conservative 0; Mismatches 3;

QY 1 MHGDTPLHEHYMDLQPEETDLYXXQNDSSSEDEIDGPAGAEPPRAHYNIVTFCK 60  
|||||  
DB 1 MHGDTPLHEHYMDLQPEETDLYCYEQNDSSSEDEIDGPAGAEPPRAHYNIVTFCK 60  
|||||

QY 61 CDSTLRVCVOSTHYDRTLEDLMGTGIVXPICQKP 98  
|||||  
DB 61 CDSTLRVCVOSTHYDRTLEDLMGTGIVCPICQKP 98  
|||||

RESULT 13  
US-09-613-303-12  
Sequence 12, Application US/09613303  
Patent No. 6495347  
GENERAL INFORMATION:  
APPLICANT: Siegel, Marvin  
APPLICANT: Chu, N. Randall  
APPLICANT: Mizen, Lee A.  
TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO  
FILE REFERENCE: 12071/002001  
CURRENT APPLICATION NUMBER: US/09/613,303  
CURRENT FILING DATE: 2000-07-10  
PRIOR APPLICATION NUMBER: US 60/143,757  
PRIOR FILING DATE: 1999-07-08

```
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
US-09-613-303-12
```

```
Query Match          99.0%; Score 512; DB 2; Length 121;
Best Local Similarity 96.9%; Pred. No. 1.1e-59;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy 1 MHGDTPTLHEWMLDQPEPTTDLXXYXQUNDSESEDEIDGPAGQAEPPRAHYNIVTFCK 60
    |||||||
Db 24 MHGDTPTLHEWMLDQPEPTTDLXXYXQUNDSESEDEIDGPAGQAEPPRAHYNIVTFCK 83
    |||||||

Qy 61 CDSTRLCVOGTHVDIRLTEDLMGTGIVXPCISQKP 98
    |||||||
Db 84 CDSTRLCVOGTHVDIRLTEDLMGTGIVXPCISQKP 121
    |||||||
```

```
RESULT 14
US-10-267-311-12
; Sequence 12, Application US/10267311
; Patent No. 6657055
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
US-10-267-311-12
```

```
Query Match          99.0%; Score 512; DB 2; Length 121;
Best Local Similarity 96.9%; Pred. No. 1.1e-59;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy 1 MHGDTPTLHEWMLDQPEPTTDLXXYXQUNDSESEDEIDGPAGQAEPPRAHYNIVTFCK 60
    |||||||
Db 24 MHGDTPTLHEWMLDQPEPTTDLXXYXQUNDSESEDEIDGPAGQAEPPRAHYNIVTFCK 83
    |||||||

Qy 61 CDSTRLCVOGTHVDIRLTEDLMGTGIVXPCISQKP 98
    |||||||
Db 84 CDSTRLCVOGTHVDIRLTEDLMGTGIVXPCISQKP 121
    |||||||
```

```
RESULT 15
US-09-613-303-35
; Sequence 35, Application US/09613303
; Patent No. 6495347
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/09/613,303
```

```
; CURRENT FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
US-09-613-303-35
```

```
Query Match          99.0%; Score 512; DB 2; Length 198;
Best Local Similarity 96.9%; Pred. No. 2.1e-59;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy 1 MHGDTPTLHEWMLDQPEPTTDLXXYXQUNDSESEDEIDGPAGQAEPPRAHYNIVTFCK 60
    |||||||
Db 101 MHGDTPTLHEWMLDQPEPTTDLXXYXQUNDSESEDEIDGPAGQAEPPRAHYNIVTFCK 160
    |||||||

Qy 61 CDSTRLCVOGTHVDIRLTEDLMGTGIVXPCISQKP 98
    |||||||
Db 161 CDSTRLCVOGTHVDIRLTEDLMGTGIVXPCISQKP 198
    |||||||
```

```
RESULT 16
US-10-267-311-35
; Sequence 35, Application US/10267311
; Patent No. 6657055
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
US-10-267-311-35
```

```
Query Match          99.0%; Score 512; DB 2; Length 198;
Best Local Similarity 96.9%; Pred. No. 2.1e-59;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy 1 MHGDTPTLHEWMLDQPEPTTDLXXYXQUNDSESEDEIDGPAGQAEPPRAHYNIVTFCK 60
    |||||||
Db 101 MHGDTPTLHEWMLDQPEPTTDLXXYXQUNDSESEDEIDGPAGQAEPPRAHYNIVTFCK 160
    |||||||

Qy 61 CDSTRLCVOGTHVDIRLTEDLMGTGIVXPCISQKP 98
    |||||||
Db 161 CDSTRLCVOGTHVDIRLTEDLMGTGIVXPCISQKP 198
    |||||||
```

```
RESULT 17
US-09-485-885-1
; Sequence 1, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cadezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
```



MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/889,666  
FILING DATE: 08-JUL-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/375390  
FILING DATE: 18-JAN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Adriano, Sarah B.  
REGISTRATION NUMBER: 34,470  
REFERENCE/DOCKET NUMBER: 30436-35US01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 310-445-1140  
TELEFAX: 310-445-9031  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 253 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-889-666-20

Query Match 99.0%; Score 512; DB 1; Length 253;  
Best Local Similarity 96.9%; Pred. No. 2.9e-59;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDPPTHHEVMDLPQPTTDLVYXXQLNDSSEDEIDGPAGQAEPPRAHNYITVFCCK 60  
Db 156 MHGDPPTHHEVMDLPQPTTDLVYXXQLNDSSEDEIDGPAGQAEPPRAHNYITVFCCK 215  
Qy 61 CDSTRLCVQSTHVDIRLTLEDLMGTGIVXPICQKP 98  
Db 216 CDSTRLCVQSTHVDIRLTLEDLMGTGIVXPICQKP 253

RESULT 21  
US-08-465-078-20  
Sequence 20, Application US/08465078  
Patent No. 5885796  
GENERAL INFORMATION:  
APPLICANT: Linsley, Peter S.  
APPLICANT: Ledbetter, Jeffrey A.  
APPLICANT: Dame, Nitin K.  
APPLICANT: Brady, William  
APPLICANT: Kienert, Peter A.  
TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merchant & Gould  
STREET: 1150 Santa Monica Blvd., Suite 400  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90025  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/465,078  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/375390  
FILING DATE: 18-JAN-1995  
ATTORNEY/AGENT INFORMATION:

NAME: Adriano, Sarah B.  
REGISTRATION NUMBER: 34,470  
REFERENCE/DOCKET NUMBER: 30436-35US01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 310-445-1140  
TELEFAX: 310-445-9031  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 253 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-465-078-20

Query Match 99.0%; Score 512; DB 1; Length 253;  
Best Local Similarity 96.9%; Pred. No. 2.9e-59;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDPPTHHEVMDLPQPTTDLVYXXQLNDSSEDEIDGPAGQAEPPRAHNYITVFCCK 60  
Db 156 MHGDPPTHHEVMDLPQPTTDLVYXXQLNDSSEDEIDGPAGQAEPPRAHNYITVFCCK 215  
Qy 61 CDSTRLCVQSTHVDIRLTLEDLMGTGIVXPICQKP 98  
Db 216 CDSTRLCVQSTHVDIRLTLEDLMGTGIVXPICQKP 253

RESULT 22  
US-08-725-776-20  
Sequence 20, Application US/08725776  
Patent No. 5968510  
GENERAL INFORMATION:  
APPLICANT: Linsley, Peter S.  
APPLICANT: Ledbetter, Jeffrey A.  
APPLICANT: Dame, Nitin K.  
APPLICANT: Brady, William  
APPLICANT: Kienert, Peter A.  
TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merchant & Gould  
STREET: 1150 Santa Monica Blvd., Suite 400  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90025  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/725,776  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/375390  
FILING DATE: 18-JAN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Adriano, Sarah B.  
REGISTRATION NUMBER: 34,470  
REFERENCE/DOCKET NUMBER: 30436-35US01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 310-445-1140  
TELEFAX: 310-445-9031  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 253 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein

US-08-725-776-20

Query Match 99.0%; Score 512; DB 1; Length 253;

Best Local Similarity 96.9%; Pred. No. 2.9e-59;

Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MGGDTPLHRYMDLQPETTDLYXXQNDSSSEDEIDDPAGQAEPRAHYNIIVTFCK 60  
Db 156 MGGDTPLHRYMDLQPETTDLYCYEQNDSSSEDEIDDPAGQAEPRAHYNIIVTFCK 215

Qy 61 CDSTLRICVOSTHVDIRTELDLMGTIGIYXPCISQKP 98  
Db 216 CDSTLRICVOSTHVDIRTELDLMGTIGIYXPCISQKP 253

RESULT 23

US-08-488-062-20

Sequence 20, Application US/08488062

Patent No. 5977318

GENERAL INFORMATION:

APPLICANT: Linsley, Peter S.

APPLICANT: Ledbetter, Jeffrey A.

APPLICANT: Dangle, Nitin K.

APPLICANT: Brady, William

APPLICANT: Kiener, Peter A.

TITLE OF INVENTION: CT1a4 Receptor and Uses Thereof

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: Merchant &amp; Gould

STREET: 11150 Santa Monica Blvd., Suite 400

CITY: Los Angeles

STATE: California

COUNTRY: USA

ZIP: 90025

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/488,062

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/375390

FILING DATE: 18-JAN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Adriano, Sarah B.

REGISTRATION NUMBER: 34,470

REFERENCE/DOCKET NUMBER: 30436-35US01

TELECOMMUNICATION INFORMATION:

TELEPHONE: 310-445-1140

TELEFAX: 310-445-9031

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 253 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-488-062-20

Query Match 99.0%; Score 512; DB 1; Length 253;

Best Local Similarity 96.9%; Pred. No. 2.9e-59;

Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MGGDTPLHRYMDLQPETTDLYXXQNDSSSEDEIDDPAGQAEPRAHYNIIVTFCK 60  
Db 156 MGGDTPLHRYMDLQPETTDLYCYEQNDSSSEDEIDDPAGQAEPRAHYNIIVTFCK 215

Qy 61 CDSTLRICVOSTHVDIRTELDLMGTIGIYXPCISQKP 98  
Db 216 CDSTLRICVOSTHVDIRTELDLMGTIGIYXPCISQKP 253

RESULT 24

US-08-117-083-9

Sequence 9, Application US/08117083

Patent No. 5719054

GENERAL INFORMATION:

APPLICANT: Bourisnell, Michael E.

APPLICANT: Inglis, Stephen C.

APPLICANT: Munro, Alan J.

TITLE OF INVENTION: Recombinant Virus Vectors Encoding Human

NUMBER OF SEQUENCES: 70

CORRESPONDENCE ADDRESS:

ADDRESSEE: Walter H. Dreger

STREET: 4 Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/117,083

FILING DATE: 10-SEP-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Dreger, Walter H.

REGISTRATION NUMBER: 24,190

REFERENCE/DOCKET NUMBER: A-58783

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-781-1989

TELEFAX: 415-398-3249

TELE: 910 277299

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 263 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

FEATURES:

NAME/KEY: Protein

LOCATION: 1..263

OTHER INFORMATION: /note= "Xaa refers to stop codon in

OTHER INFORMATION: the open reading frame."

US-08-117-083-9

Query Match 99.0%; Score 512; DB 1; Length 263;

Best Local Similarity 96.9%; Pred. No. 3.1e-59;

Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MGGDTPLHRYMDLQPETTDLYXXQNDSSSEDEIDDPAGQAEPRAHYNIIVTFCK 60  
Db 162 MGGDTPLHRYMDLQPETTDLYCYEQNDSSSEDEIDDPAGQAEPRAHYNIIVTFCK 221

Qy 61 CDSTLRICVOSTHVDIRTELDLMGTIGIYXPCISQKP 98  
Db 222 CDSTLRICVOSTHVDIRTELDLMGTIGIYXPCISQKP 259

RESULT 25

US-08-860-165-10

Sequence 10, Application US/08860165A

Patent No. 6004557

GENERAL INFORMATION:

APPLICANT: EDWARDS, Stirling John

APPLICANT: COX, John Cooper

APPLICANT: WEBB, Elizabeth Ann

APPLICANT: FRAZER, Ian

TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS  
FILE REFERENCE: 17227/130  
CURRENT APPLICATION NUMBER: US/08/860,165A  
CURRENT FILING DATE: 1997-09-22  
EARLIER APPLICATION NUMBER: PCT/AU95/00868  
EARLIER FILING DATE: 1995-12-20  
EARLIER APPLICATION NUMBER: AU PN0157  
EARLIER FILING DATE: 1994-12-20  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: Patentn Ver. 2.0  
SEQ ID NO 10  
LENGTH: 266  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion  
US-08-860-165-10

Query Match 99.0%; Score 512; DB 2; Length 266;  
Best Local Similarity 96.9%; Pred. No. 3.2e-59;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEYMDLQPEETDLYXXQLNDSSEEDIDGPAGAEPRRAHYNIVTFCK 60  
Db 161 MHGDTPLHEYMDLQPEETDLYCYEQLNDSSEEDIDGPAGAEPRRAHYNIVTFCK 220  
Qy 61 CDSTLRICVOSTHVDIRTELDLMGTIGIYPCISQKP 98  
Db 221 CDSTLRICVOSTHVDIRTELDLMGTIGIYPCISQKP 258

RESULT 26  
US-09-359-382-10  
Sequence 10, Application US/09359382  
Patent No. 6306397  
GENERAL INFORMATION:  
APPLICANT: EDWARDS, Scitling John  
APPLICANT: COX, John Cooper  
APPLICANT: WEBB, Elizabeth Ann  
APPLICANT: FRATER, Ian  
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS  
FILE REFERENCE: 017227/0148  
CURRENT APPLICATION NUMBER: US/09/359,382  
CURRENT FILING DATE: 1999-07-23  
EARLIER APPLICATION NUMBER: US 08/860,165  
EARLIER FILING DATE: 1997-09-22  
EARLIER APPLICATION NUMBER: PCT/AU95/00868  
EARLIER FILING DATE: 1995-12-20  
EARLIER APPLICATION NUMBER: AU PN0157/94  
EARLIER FILING DATE: 1994-12-20  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: Patentn Ver. 2.0  
SEQ ID NO 10  
LENGTH: 266  
TYPE: PRT  
ORGANISM: Human papillomavirus type 16  
US-09-359-382-10

Query Match 99.0%; Score 512; DB 2; Length 266;  
Best Local Similarity 96.9%; Pred. No. 3.2e-59;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEYMDLQPEETDLYXXQLNDSSEEDIDGPAGAEPRRAHYNIVTFCK 60  
Db 161 MHGDTPLHEYMDLQPEETDLYCYEQLNDSSEEDIDGPAGAEPRRAHYNIVTFCK 220  
Qy 61 CDSTLRICVOSTHVDIRTELDLMGTIGIYPCISQKP 98  
Db 221 CDSTLRICVOSTHVDIRTELDLMGTIGIYPCISQKP 258

RESULT 27  
US-09-367-309A-1

Sequence 1, Application US/09367309A  
Patent No. 6428807  
GENERAL INFORMATION:  
APPLICANT: MACFARLAN, RODERICK I.  
APPLICANT: MALLIKOS, JIM  
TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES  
FILE REFERENCE: 017227/0149  
CURRENT APPLICATION NUMBER: US/09/367,309A  
CURRENT FILING DATE: 1999-08-11  
PRIOR APPLICATION NUMBER: PCT/AU98/00080  
PRIOR FILING DATE: 1998-02-13  
PRIOR APPLICATION NUMBER: AU PO 5178  
PRIOR FILING DATE: 1997-02-19  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: Patentn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 266  
TYPE: PRT  
ORGANISM: Human papillomavirus type 16  
US-09-367-309A-1

Query Match 99.0%; Score 512; DB 2; Length 266;  
Best Local Similarity 96.9%; Pred. No. 3.2e-59;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEYMDLQPEETDLYXXQLNDSSEEDIDGPAGAEPRRAHYNIVTFCK 60  
Db 161 MHGDTPLHEYMDLQPEETDLYCYEQLNDSSEEDIDGPAGAEPRRAHYNIVTFCK 220  
Qy 61 CDSTLRICVOSTHVDIRTELDLMGTIGIYPCISQKP 98  
Db 221 CDSTLRICVOSTHVDIRTELDLMGTIGIYPCISQKP 258

RESULT 28  
US-09-501-097A-25  
Sequence 25, Application US/09501097A  
Patent No. 6734173  
GENERAL INFORMATION:  
APPLICANT: Tzyy-Chou Wu  
APPLICANT: Chien-Fu Hung  
TITLE OF INVENTION: IMPROVED HSP DNA VACCINES  
FILE REFERENCE: 2240-169349  
CURRENT APPLICATION NUMBER: US/09/501,097A  
CURRENT FILING DATE: 2000-02-09  
NUMBER OF SEQ ID NOS: 25  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 25  
LENGTH: 287  
TYPE: PRT  
ORGANISM: Human papillomavirus/Mouse  
US-09-501-097A-25

Query Match 99.0%; Score 512; DB 2; Length 287;  
Best Local Similarity 96.9%; Pred. No. 3.5e-59;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEYMDLQPEETDLYXXQLNDSSEEDIDGPAGAEPRRAHYNIVTFCK 60  
Db 190 MHGDTPLHEYMDLQPEETDLYCYEQLNDSSEEDIDGPAGAEPRRAHYNIVTFCK 249  
Qy 61 CDSTLRICVOSTHVDIRTELDLMGTIGIYPCISQKP 98  
Db 250 CDSTLRICVOSTHVDIRTELDLMGTIGIYPCISQKP 287

RESULT 29  
US-09-613-303-33  
Sequence 33, Application US/09613303  
Patent No. 6495347  
GENERAL INFORMATION:  
APPLICANT: Siegel, Marvin  
APPLICANT: Chu, N. Randall

APPLICANT: Mizzen, Lee A.  
TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO  
FILE REFERENCE: 12071/002001  
CURRENT APPLICATION NUMBER: US/09/613,303  
CURRENT FILING DATE: 2000-07-10  
PRIOR APPLICATION NUMBER: US 60/143,757  
PRIOR FILING DATE: 1999-07-08  
NUMBER OF SEQ ID NOS: 55  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 33  
LENGTH: 295  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: fusion sequence  
US-09-613-303-33

Query Match 99.0%; Score 512; DB 2; Length 295;  
Best Local Similarity 96.9%; Pred. No. 3,6e-59;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGGDTPLHRYMLDLQPETTDLYXXQLNDSSEEDSIDGPAGAEPPRAHYNIVTFCK 60  
DB 198 MGGDTPLHRYMLDLQPETTDLYCYEQLNDSSEEDSIDGPAGAEPPRAHYNIVTFCK 257  
QY 61 CDSTLRICVOSTHVDIRTLIEDLMGTLGIYCPICSQKP 98  
DB 258 CDSTLRICVOSTHVDIRTLIEDLMGTLGIYCPICSQKP 295

RESULT 30  
US-10-267-311-33  
Sequence 33; Application US/10267311  
Patent No. 6657055  
GENERAL INFORMATION:  
APPLICANT: Siegel, Marvin  
APPLICANT: Chu, N. Randall  
APPLICANT: Mizzen, Lee A.  
TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO  
FILE REFERENCE: 12071/002001  
CURRENT APPLICATION NUMBER: US/10/267,311  
CURRENT FILING DATE: 2002-10-09  
PRIOR APPLICATION NUMBER: US/09/613,303  
PRIOR FILING DATE: 2000-07-10  
PRIOR APPLICATION NUMBER: US 60/143,757  
PRIOR FILING DATE: 1999-07-08  
NUMBER OF SEQ ID NOS: 55  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 33  
LENGTH: 295  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: fusion sequence  
US-10-267-311-33

Query Match 99.0%; Score 512; DB 2; Length 295;  
Best Local Similarity 96.9%; Pred. No. 3,6e-59;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGGDTPLHRYMLDLQPETTDLYXXQLNDSSEEDSIDGPAGAEPPRAHYNIVTFCK 60  
DB 198 MGGDTPLHRYMLDLQPETTDLYCYEQLNDSSEEDSIDGPAGAEPPRAHYNIVTFCK 257  
QY 61 CDSTLRICVOSTHVDIRTLIEDLMGTLGIYCPICSQKP 98  
DB 258 CDSTLRICVOSTHVDIRTLIEDLMGTLGIYCPICSQKP 295

RESULT 31  
US-09-613-303-25  
Sequence 25; Application US/09613303  
Patent No. 6495347

GENERAL INFORMATION:  
APPLICANT: Siegel, Marvin  
APPLICANT: Chu, N. Randall  
APPLICANT: Mizzen, Lee A.  
TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO  
FILE REFERENCE: 12071/002001  
CURRENT APPLICATION NUMBER: US/09/613,303  
CURRENT FILING DATE: 2000-07-10  
PRIOR APPLICATION NUMBER: US 60/143,757  
PRIOR FILING DATE: 1999-07-08  
NUMBER OF SEQ ID NOS: 55  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 25  
LENGTH: 324  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: fusion sequence  
US-09-613-303-25

Query Match 99.0%; Score 512; DB 2; Length 324;  
Best Local Similarity 96.9%; Pred. No. 4,1e-59;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGGDTPLHRYMLDLQPETTDLYXXQLNDSSEEDSIDGPAGAEPPRAHYNIVTFCK 60  
DB 227 MGGDTPLHRYMLDLQPETTDLYCYEQLNDSSEEDSIDGPAGAEPPRAHYNIVTFCK 286  
QY 61 CDSTLRICVOSTHVDIRTLIEDLMGTLGIYCPICSQKP 98  
DB 287 CDSTLRICVOSTHVDIRTLIEDLMGTLGIYCPICSQKP 324

RESULT 32  
US-10-267-311-25  
Sequence 25; Application US/10267311  
Patent No. 6657055  
GENERAL INFORMATION:  
APPLICANT: Siegel, Marvin  
APPLICANT: Chu, N. Randall  
APPLICANT: Mizzen, Lee A.  
TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO  
FILE REFERENCE: 12071/002001  
CURRENT APPLICATION NUMBER: US/10/267,311  
CURRENT FILING DATE: 2002-10-09  
PRIOR APPLICATION NUMBER: US/09/613,303  
PRIOR FILING DATE: 2000-07-10  
PRIOR APPLICATION NUMBER: US 60/143,757  
PRIOR FILING DATE: 1999-07-08  
NUMBER OF SEQ ID NOS: 55  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 25  
LENGTH: 324  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: fusion sequence  
US-10-267-311-25

Query Match 99.0%; Score 512; DB 2; Length 324;  
Best Local Similarity 96.9%; Pred. No. 4,1e-59;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGGDTPLHRYMLDLQPETTDLYXXQLNDSSEEDSIDGPAGAEPPRAHYNIVTFCK 60  
DB 227 MGGDTPLHRYMLDLQPETTDLYCYEQLNDSSEEDSIDGPAGAEPPRAHYNIVTFCK 286  
QY 61 CDSTLRICVOSTHVDIRTLIEDLMGTLGIYCPICSQKP 98  
DB 287 CDSTLRICVOSTHVDIRTLIEDLMGTLGIYCPICSQKP 324

RESULT 33

```
US-09-485-885-6
; Sequence 6, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485, 885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9711953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-6

Query Match          99.0%; Score 512; DB 2; Length 371;
Best Local Similarity 96.9%; Pred. No. 5e-59;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDPPTLHEXMDLQPEPTDLYXXQLNDSSEDEIDGPAGQAEPRAHYNIIVTFCK 60
DB 265 MHGDPPTLHEXMDLQPEPTDLYCYEQUNDSEDEIDGPAGQAEPRAHYNIIVTFCK 324

QY 61 CDSTLRFCVOSTHVDIRTLIEDLMLGTIGIVPCISQRP 98
DB 325 CDSTLRFCVOSTHVDIRTLIEDLMLGTIGIVPCISQRP 362

RESULT 34
US-09-485-885-14
; Sequence 14, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485, 885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9711953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-14

Query Match          99.0%; Score 512; DB 2; Length 390;
Best Local Similarity 96.9%; Pred. No. 5.4e-59;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDPPTLHEXMDLQPEPTDLYXXQLNDSSEDEIDGPAGQAEPRAHYNIIVTFCK 60
DB 284 MHGDPPTLHEXMDLQPEPTDLYCYEQUNDSEDEIDGPAGQAEPRAHYNIIVTFCK 343

QY 61 CDSTLRFCVOSTHVDIRTLIEDLMLGTIGIVPCISQRP 98
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DB 344 CDSTLRFCVOSTHVDIRTLIEDLMLGTIGIVPCISQRP 381

RESULT 35
US-09-613-303-19
; Sequence 19, Application US/09613303
; Patent No. 6495347
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A THI-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/09/613,303
; CURRENT FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 493
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
US-09-613-303-19

Query Match          99.0%; Score 512; DB 2; Length 493;
Best Local Similarity 96.9%; Pred. No. 7.4e-59;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDPPTLHEXMDLQPEPTDLYXXQLNDSSEDEIDGPAGQAEPRAHYNIIVTFCK 60
DB 396 MHGDPPTLHEXMDLQPEPTDLYCYEQUNDSEDEIDGPAGQAEPRAHYNIIVTFCK 455

QY 61 CDSTLRFCVOSTHVDIRTLIEDLMLGTIGIVPCISQRP 98
DB 456 CDSTLRFCVOSTHVDIRTLIEDLMLGTIGIVPCISQRP 493

RESULT 36
US-10-267-311-19
; Sequence 19, Application US/10267311
; Patent No. 6657055
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A THI-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 493
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
US-10-267-311-19

Query Match          99.0%; Score 512; DB 2; Length 493;
Best Local Similarity 96.9%; Pred. No. 7.4e-59;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDPPTLHEXMDLQPEPTDLYXXQLNDSSEDEIDGPAGQAEPRAHYNIIVTFCK 60
```

```
Db      396 MHGDTPLHEHYMDLQPETTDLYCYEQNDSSSEDEIDGPAGQAEPPRAHYNIVTFCK 455
Qy      61 CDSTLRICVOSTHVDIRTLIEDLIMGTLGIVXPCISQKP 98
Db      456 CDSTLRICVOSTHVDIRTLIEDLIMGTLGIVCPCISQKP 493

RESULT 37
US-09-613-303-17
; Sequence 17, Application US/09613303
; Patent No. 6495347
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 639
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
US-09-613-303-17

Query Match      99.0%; Score 512; DB 2; Length 639;
Best Local Similarity 96.9%; Pred. No. 1,1e-58;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 MHGDTPLHEHYMDLQPETTDLYCYEQNDSSSEDEIDGPAGQAEPPRAHYNIVTFCK 60
Db      542 MHGDTPLHEHYMDLQPETTDLYCYEQNDSSSEDEIDGPAGQAEPPRAHYNIVTFCK 601

Qy      61 CDSTLRICVOSTHVDIRTLIEDLIMGTLGIVXPCISQKP 98
Db      602 CDSTLRICVOSTHVDIRTLIEDLIMGTLGIVCPCISQKP 639

RESULT 38
US-10-267-311-17
; Sequence 17, Application US/10267311
; Patent No. 6657055
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 639
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
US-10-267-311-17

Query Match      99.0%; Score 512; DB 2; Length 639;
Best Local Similarity 96.9%; Pred. No. 1,1e-58;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy      1 MHGDTPLHEHYMDLQPETTDLYCYEQNDSSSEDEIDGPAGQAEPPRAHYNIVTFCK 60
Db      542 MHGDTPLHEHYMDLQPETTDLYCYEQNDSSSEDEIDGPAGQAEPPRAHYNIVTFCK 601

Qy      61 CDSTLRICVOSTHVDIRTLIEDLIMGTLGIVXPCISQKP 98
Db      602 CDSTLRICVOSTHVDIRTLIEDLIMGTLGIVCPCISQKP 639

RESULT 39
US-09-613-303-51
; Sequence 51, Application US/09613303
; Patent No. 6495347
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
US-09-613-303-51

Query Match      99.0%; Score 512; DB 2; Length 641;
Best Local Similarity 96.9%; Pred. No. 1,1e-58;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 MHGDTPLHEHYMDLQPETTDLYCYEQNDSSSEDEIDGPAGQAEPPRAHYNIVTFCK 60
Db      544 MHGDTPLHEHYMDLQPETTDLYCYEQNDSSSEDEIDGPAGQAEPPRAHYNIVTFCK 603

Qy      61 CDSTLRICVOSTHVDIRTLIEDLIMGTLGIVXPCISQKP 98
Db      604 CDSTLRICVOSTHVDIRTLIEDLIMGTLGIVCPCISQKP 641

RESULT 40
US-10-267-311-51
; Sequence 51, Application US/10267311
; Patent No. 6657055
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
US-10-267-311-51
```

```
Query Match          99.0%; Score 512; DB 2; Length 641;
Best Local Similarity 96.9%; Pred. No. 1.1e-58;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 MHGDTPLHEHYMLDLOPETTDLYXXQLNDSSEDEIDGPAGQAEPRAHYNIYTFCK 60
Db      544 MHGDTPLHEHYMLDLOPETTDLYCYEQINDSSEDEIDGPAGQAEPRAHYNIYTFCK 603

Qy      61 CDSTRLCVOSTHYDITLEDLMGTIGIYXPCSQKP 98
Db      604 CDSTRLCVOSTHYDITLEDLMGTIGIYXPCSQKP 641

RESULT 41
US-09-613-303-53
; Sequence 53, Application US/09613303
; Patent No. 6495347
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mitzel, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/09/613,303
; CURRENT FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 647
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; US-09-613-303-53

Query Match          99.0%; Score 512; DB 2; Length 647;
Best Local Similarity 96.9%; Pred. No. 1.1e-58;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 MHGDTPLHEHYMLDLOPETTDLYXXQLNDSSEDEIDGPAGQAEPRAHYNIYTFCK 60
Db      550 MHGDTPLHEHYMLDLOPETTDLYCYEQINDSSEDEIDGPAGQAEPRAHYNIYTFCK 609

Qy      61 CDSTRLCVOSTHYDITLEDLMGTIGIYXPCSQKP 98
Db      610 CDSTRLCVOSTHYDITLEDLMGTIGIYXPCSQKP 647

RESULT 42
US-10-267-311-53
; Sequence 53, Application US/10267311
; Patent No. 6657055
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mitzel, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 647
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
```

```
; OTHER INFORMATION: fusion sequence
US-10-267-311-53

Query Match          99.0%; Score 512; DB 2; Length 647;
Best Local Similarity 96.9%; Pred. No. 1.1e-58;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 MHGDTPLHEHYMLDLOPETTDLYXXQLNDSSEDEIDGPAGQAEPRAHYNIYTFCK 60
Db      550 MHGDTPLHEHYMLDLOPETTDLYCYEQINDSSEDEIDGPAGQAEPRAHYNIYTFCK 609

Qy      61 CDSTRLCVOSTHYDITLEDLMGTIGIYXPCSQKP 98
Db      610 CDSTRLCVOSTHYDITLEDLMGTIGIYXPCSQKP 647

RESULT 43
US-09-566-420-19
; Sequence 19, Application US/09566420
; Patent No. 6500641
; GENERAL INFORMATION:
; APPLICANT: CHEN, SI-YI AND ZHAOYANG, YOU
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANTIGENS WHICH ELICIT AN
; FILE REFERENCE: TBA
; CURRENT APPLICATION NUMBER: US/09/566,420
; CURRENT FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/132,752
; PRIOR FILING DATE: 1999-05-06
; PRIOR APPLICATION NUMBER: 60/132,750
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Human papillomavirus type E7
; US-09-566-420-19

Query Match          98.1%; Score 507; DB 2; Length 98;
Best Local Similarity 95.9%; Pred. No. 3.7e-59;
Matches 94; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy      1 MHGDTPLHEHYMLDLOPETTDLYXXQLNDSSEDEIDGPAGQAEPRAHYNIYTFCK 60
Db      1 MHGDTPLHEHYMLDLOPETTDLYCYEQINDSSEDEIDGPAGQAEPRAHYNIYTFCK 60

Qy      61 CDSTRLCVOSTHYDITLEDLMGTIGIYXPCSQKP 98
Db      61 CDSTRLCVOSTHYDITLEDLMGTIGIYXPCSQKP 98

RESULT 44
US-10-201-764-19
; Sequence 19, Application US/10201764
; Patent No. 6716623
; GENERAL INFORMATION:
; APPLICANT: CHEN, SI-YI AND ZHAOYANG, YOU
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANTIGENS WHICH ELICIT AN
; FILE REFERENCE: TBA
; CURRENT APPLICATION NUMBER: US/10/201,764
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/566,420
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/132,752
; PRIOR FILING DATE: 1999-05-06
; PRIOR APPLICATION NUMBER: 60/132,750
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 98
```

```
; TYPE: PRT
; ORGANISM: Human papillomavirus type E7
US-10-201-764-19

Query Match          98.1%; Score 507; DB 2; Length 98;
Best Local Similarity 95.9%; Pred. No. 3,7e-59;
Matches 94; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MGGDTPLHEHYMDLQPEETDLYXXQNLNDSSEEDIDGPAGQAEPPDRAHYNIVTFCK 60
Db 1 MGGDTPLHEHYMDLQPEETDLYCYEQNLNDSSEEDIDGPAGQAEPPDRAHYNIVTFCK 60

Qy 61 CDSTLRLCVOSTHVDIRTLIEDLIMGTLGIYXPCISQKP 98
Db 61 CDSTLRLCVOSTHVDIRTLIEDLIMGTLGIYXPCISQKP 98

RESULT 45
US-09-613-303-8
; Sequence 8, Application US/09613303
; Patent No. 6495347
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/09/613,303
; CURRENT FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
US-09-613-303-8

Query Match          97.3%; Score 503; DB 2; Length 98;
Best Local Similarity 95.9%; Pred. No. 1,2e-58;
Matches 94; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MGGDTPLHEHYMDLQPEETDLYXXQNLNDSSEEDIDGPAGQAEPPDRAHYNIVTFCK 60
Db 1 MGGDTPLHEHYMDLQPEETDLYCYEQNLNDSSEEDIDGPAGQAEPPDRAHYNIVTFCK 60

Qy 61 CDSTLRLCVOSTHVDIRTLIEDLIMGTLGIYXPCISQKP 98
Db 61 CDSTLRLCVOSTHVDIRTLIEDLIMGTLGIYXPCISQKP 98

RESULT 46
US-10-267-311-8
; Sequence 8, Application US/10267311
; Patent No. 6657055
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
```

```
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
US-10-267-311-8

Query Match          97.3%; Score 503; DB 2; Length 98;
Best Local Similarity 95.9%; Pred. No. 1,2e-58;
Matches 94; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MGGDTPLHEHYMDLQPEETDLYXXQNLNDSSEEDIDGPAGQAEPPDRAHYNIVTFCK 60
Db 1 MGGDTPLHEHYMDLQPEETDLYCYEQNLNDSSEEDIDGPAGQAEPPDRAHYNIVTFCK 60

Qy 61 CDSTLRLCVOSTHVDIRTLIEDLIMGTLGIYXPCISQKP 98
Db 61 CDSTLRLCVOSTHVDIRTLIEDLIMGTLGIYXPCISQKP 98

RESULT 47
US-09-613-303-29
; Sequence 29, Application US/09613303
; Patent No. 6495347
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/09/613,303
; CURRENT FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 648
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
US-09-613-303-29

Query Match          97.3%; Score 503; DB 2; Length 648;
Best Local Similarity 95.9%; Pred. No. 1,7e-57;
Matches 94; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MGGDTPLHEHYMDLQPEETDLYXXQNLNDSSEEDIDGPAGQAEPPDRAHYNIVTFCK 60
Db 1 MGGDTPLHEHYMDLQPEETDLYCYEQNLNDSSEEDIDGPAGQAEPPDRAHYNIVTFCK 60

Qy 61 CDSTLRLCVOSTHVDIRTLIEDLIMGTLGIYXPCISQKP 98
Db 61 CDSTLRLCVOSTHVDIRTLIEDLIMGTLGIYXPCISQKP 98

RESULT 48
US-10-267-311-29
; Sequence 29, Application US/10267311
; Patent No. 6657055
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
```

```
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 648
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
US-10-267-311-29
```

```
Query Match          97.3%; Score 503; DB 2; Length 648;
Best Local Similarity 95.9%; Pred. No. 1.7e-57;
Matches 94; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy 1 MHGDTPLHEYMLDLOPETTDLYXXYXOLNDSSEBEDIQPAQAEPDRAHYNIVTFCK 60
Db 1 MDGDTPLHEYMLDLOPETTDLYCYEQNLNDSSEBEDIQPAQAEPDRAHYNIVTFCK 60
```

```
Qy 61 CDSTLRVCVOSTHVDIRTLBLLMGTLGIYXPCISQKP 98
Db 61 CDSTLRVCVOSTHVDIRTLBLLMGTLGIYXPCISQKP 98
```

```
RESULT 49
US-09-613-303-41
; Sequence 41, Application US/09613303
; Patent No. 6495347
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 711
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
US-09-613-303-41
```

```
Query Match          97.3%; Score 503; DB 2; Length 711;
Best Local Similarity 95.9%; Pred. No. 1.9e-57;
Matches 94; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy 1 MHGDTPLHEYMLDLOPETTDLYXXYXOLNDSSEBEDIQPAQAEPDRAHYNIVTFCK 60
Db 1 MDGDTPLHEYMLDLOPETTDLYCYEQNLNDSSEBEDIQPAQAEPDRAHYNIVTFCK 60
```

```
Qy 61 CDSTLRVCVOSTHVDIRTLBLLMGTLGIYXPCISQKP 98
Db 61 CDSTLRVCVOSTHVDIRTLBLLMGTLGIYXPCISQKP 98
```

```
RESULT 50
US-10-267-311-41
; Sequence 41, Application US/10267311
; Patent No. 6657055
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
```

```
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 711
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
US-10-267-311-41
```

```
Query Match          97.3%; Score 503; DB 2; Length 711;
Best Local Similarity 95.9%; Pred. No. 1.9e-57;
Matches 94; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy 1 MHGDTPLHEYMLDLOPETTDLYXXYXOLNDSSEBEDIQPAQAEPDRAHYNIVTFCK 60
Db 1 MDGDTPLHEYMLDLOPETTDLYCYEQNLNDSSEBEDIQPAQAEPDRAHYNIVTFCK 60
```

```
Qy 61 CDSTLRVCVOSTHVDIRTLBLLMGTLGIYXPCISQKP 98
Db 61 CDSTLRVCVOSTHVDIRTLBLLMGTLGIYXPCISQKP 98
```

```
RESULT 51
US-09-613-303-45
; Sequence 45, Application US/09613303
; Patent No. 6495347
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 724
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
US-09-613-303-45
```

```
Query Match          97.3%; Score 503; DB 2; Length 724;
Best Local Similarity 95.9%; Pred. No. 1.9e-57;
Matches 94; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy 1 MHGDTPLHEYMLDLOPETTDLYXXYXOLNDSSEBEDIQPAQAEPDRAHYNIVTFCK 60
Db 1 MDGDTPLHEYMLDLOPETTDLYCYEQNLNDSSEBEDIQPAQAEPDRAHYNIVTFCK 60
```

```
Qy 61 CDSTLRVCVOSTHVDIRTLBLLMGTLGIYXPCISQKP 98
Db 61 CDSTLRVCVOSTHVDIRTLBLLMGTLGIYXPCISQKP 98
```

```
RESULT 52
US-10-267-311-45
; Sequence 45, Application US/10267311
; Patent No. 6657055
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
```

```
; CURRENT APPLICATION NUMBER: US/10/267,311
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 724
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
US-10-267-311-45
```

```
Query Match          97.3%; Score 503; DB 2; Length 724;
Best Local Similarity 95.9%; Pred. No. 1,9e-57;
Matches 94; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 1 MGGDTPLHEHYMDLQPEETDLYXXYQNDSSSEDEIDGPAGAEPPRAHYNIVTFCK 60
DB 1 MGGDTPLHEHYMDLQPEETDLYCYEQNDSSSEDEIDGPAGAEPPRAHYNIVTFCK 60
QY 61 CDSTLRICVQSTHVDIRLTEDLMGTGIVXCQKP 98
DB 61 CDSTLRICVQSTHVDIRLTEDLMGTGIVCPCSQP 98
```

```
RESULT 53
US-09-501-097A-22
; Sequence 22, Application US/09501097A
; Patent No. 6734173
; GENERAL INFORMATION:
; APPLICANT: Tzyy-Chou Wu
; APPLICANT: Chien-Fu Hung
; TITLE OF INVENTION: IMPROVED HSP DNA VACCINES
; FILE REFERENCE: 2240-169349
; CURRENT APPLICATION NUMBER: US/09/501,097A
; CURRENT FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Mouse/Pseudomonas
US-09-501-097A-22
```

```
Query Match          96.7%; Score 500; DB 2; Length 420;
Best Local Similarity 96.9%; Pred. No. 2,3e-57;
Matches 93; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1 MGGDTPLHEHYMDLQPEETDLYXXYQNDSSSEDEIDGPAGAEPPRAHYNIVTFCK 60
DB 317 MGGDTPLHEHYMDLQPEETDLYCYEQNDSSSEDEIDGPAGAEPPRAHYNIVTFCK 376
QY 61 CDSTLRICVQSTHVDIRLTEDLMGTGIVXCQKP 96
DB 377 CDSTLRICVQSTHVDIRLTEDLMGTGIVCPCSQ 412
```

```
RESULT 54
US-09-501-097A-20
; Sequence 20, Application US/09501097A
; Patent No. 6734173
; GENERAL INFORMATION:
; APPLICANT: Tzyy-Chou Wu
; APPLICANT: Chien-Fu Hung
; TITLE OF INVENTION: IMPROVED HSP DNA VACCINES
; FILE REFERENCE: 2240-169349
; CURRENT APPLICATION NUMBER: US/09/501,097A
; CURRENT FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 25
```

```
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 723
; TYPE: PRT
; ORGANISM: human papillomavirus/mycobacterium tuberculosis
US-09-501-097A-20
```

```
Query Match          96.7%; Score 500; DB 2; Length 723;
Best Local Similarity 96.9%; Pred. No. 4,8e-57;
Matches 93; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1 MGGDTPLHEHYMDLQPEETDLYXXYQNDSSSEDEIDGPAGAEPPRAHYNIVTFCK 60
DB 1 MGGDTPLHEHYMDLQPEETDLYCYEQNDSSSEDEIDGPAGAEPPRAHYNIVTFCK 60
QY 61 CDSTLRICVQSTHVDIRLTEDLMGTGIVXCQKP 96
DB 61 CDSTLRICVQSTHVDIRLTEDLMGTGIVCPCSQ 96
```

```
RESULT 55
US-09-462-993-2
; Sequence 2, Application US/09462993
; Patent No. 6884786
; GENERAL INFORMATION:
; APPLICANT: KIENY, Marie-Paule
; APPLICANT: BALLOUL, Jean-Marc
; APPLICANT: BIZOUARNE, Nadine
; TITLE OF INVENTION: ANTITUMORAL COMPOSITION BASED ON IMMUNOGENIC
; FILE REFERENCE: 01753-122
; CURRENT APPLICATION NUMBER: US/09/462,993
; CURRENT FILING DATE: 2000-04-17
; PRIOR APPLICATION NUMBER: PCT/FR98/01576
; PRIOR FILING DATE: 1998-07-17
; PRIOR APPLICATION NUMBER: FR 97/09152
; PRIOR FILING DATE: 1997-07-18
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patentin Ver. 2.2
; SEQ ID NO 2
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Derived from human papillomavirus, strain
; OTHER INFORMATION: HPV-16, E7 fusion signals of the rabies
; OTHER INFORMATION: glycoprotein, clone E7*TMR.
US-09-462-993-2
```

```
Query Match          92.5%; Score 478; DB 2; Length 185;
Best Local Similarity 92.9%; Pred. No. 6e-55;
Matches 91; Conservative 0; Mismatches 1; Indels 6; Gaps 1;
```

```
QY 1 MGGDTPLHEHYMDLQPEETDLYXXYQNDSSSEDEIDGPAGAEPPRAHYNIVTFCK 60
DB 26 MGGDTPLHEHYMDLQPEETDLYCYEQNDSSSEDEIDGPAGAEPPRAHYNIVTFCK 79
QY 61 CDSTLRICVQSTHVDIRLTEDLMGTGIVXCQKP 98
DB 80 CDSTLRICVQSTHVDIRLTEDLMGTGIVCPCSQP 117
```

```
RESULT 56
US-08-860-165-12
; Sequence 12, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
```

```
; CURRENT APPLICATION NUMBER: US/08/860.165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU P0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-12

Query Match          66.3%; Score 353; DB 2; Length 172;
Best Local Similarity 97.0%; Pred. No. 1.8e-38;
Matches 64; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGGDTPLHEXMDLQPEETDLYXXYXOLNDSSEEDSIDGPAGQAEPRRAHYNIVTFCK 60
    |||||
Db 99 MGGDTPLHEXMDLQPEETDLYCYEQUNDSSEEDSIDGPAGQAEPRRAHYNIVTFCK 158

QY 61 CDSTLR 66
    |||||
Db 159 CDSTLR 164

RESULT 57
US-09-359-382-12
; Sequence 12, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU P0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-12

Query Match          68.3%; Score 353; DB 2; Length 172;
Best Local Similarity 97.0%; Pred. No. 1.8e-38;
Matches 64; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGGDTPLHEXMDLQPEETDLYXXYXOLNDSSEEDSIDGPAGQAEPRRAHYNIVTFCK 60
    |||||
Db 99 MGGDTPLHEXMDLQPEETDLYCYEQUNDSSEEDSIDGPAGQAEPRRAHYNIVTFCK 158

QY 61 CDSTLR 66
    |||||
Db 159 CDSTLR 164

RESULT 58
US-08-860-165-14
; Sequence 14, Application US/08860165A
; Patent No. 6004557
```

```
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860.165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU P0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-14

Query Match          66.7%; Score 345; DB 2; Length 172;
Best Local Similarity 98.5%; Pred. No. 2e-37;
Matches 64; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 34 EDEIDGPAGQAEPRRAHYNIVTFCKCDSTLRVCQSTHVDIRTEEDLMGTGIVXPI 93
    |||||
Db 2 EDEIDGPAGQAEPRRAHYNIVTFCKCDSTLRVCQSTHVDIRTEEDLMGTGIVCPI 61

QY 94 CSQKP 98
    |||||
Db 62 CSQKP 66

RESULT 59
US-09-359-382-14
; Sequence 14, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU P0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-14

Query Match          66.7%; Score 345; DB 2; Length 172;
Best Local Similarity 98.5%; Pred. No. 2e-37;
Matches 64; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 34 EDEIDGPAGQAEPRRAHYNIVTFCKCDSTLRVCQSTHVDIRTEEDLMGTGIVXPI 93
    |||||
Db 2 EDEIDGPAGQAEPRRAHYNIVTFCKCDSTLRVCQSTHVDIRTEEDLMGTGIVCPI 61

QY 94 CSQKP 98
    |||||
```

Db 62 CSQKP 66

RESULT 60

US-08-606-288-7

Sequence 7, Application US/08606288

Patent No. 5955087

GENERAL INFORMATION:

APPLICANT: Whittle, N.R.

APPLICANT: Carmichael, J.P.

APPLICANT: Connor, S.E.

APPLICANT: Thompson, H.S.G.

APPLICANT: Wilson, M.J.

TITLE OF INVENTION: Polypeptides Useful as Immunotherapeutic

TITLE OF INVENTION: Agents, and Methods of Polypeptide Preparation

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert

STREET: Suite 3400, Four Embarcadero Center

CITY: San Francisco

STATE: California

COUNTRY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/606,288

FILING DATE: 23-FEB-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9503786.7

FILING DATE: 24-FEB-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/000034

FILING DATE: 08-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9515478.7

FILING DATE: 28-JUL-1995

ATTORNEY/AGENT INFORMATION:

NAME: Walter H. Dregger

REGISTRATION NUMBER: 24,190

REFERENCE/DOCKET NUMBER: A-63284/WHD

TELEPHONE: (415) 781-1989

TELEFAX: (415) 398-3249

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 601 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-606-288-7

Query Match 47.8%; Score 247; DB 1; Length 601;

Best Local Similarity 53.5%; Pred. No. 1e-23;

Matches 53; Conservative 14; Mismatches 28; Indels 4; Gaps 3;

Qy 1 MHSPTLHEHYMLDQ-PETTDLYXXYQLNDSSEER-DEIDGPAQAEPRAHNYITFC 58

Db 493 MGRHVTLKDIIVDLQPPDVGHLHCEQLVDSSEDEVVDGQ--DSQPLKHQYITCC 550

Qy 59 CKKDSIRLCVOSTHVDIRITLEDLMGTGLGVXPIGSQK 97

Db 551 CGCDSNVRLVVOCTETDIRVQQLLGLTNIIVCPICAPK 589

RESULT 61

US-08-606-288-10

Sequence 10, Application US/08606288

Patent No. 5955087

GENERAL INFORMATION:

APPLICANT: Whittle, N.R.

APPLICANT: Carmichael, J.P.

APPLICANT: Connor, S.E.

APPLICANT: Thompson, H.S.G.

APPLICANT: Wilson, M.J.

TITLE OF INVENTION: Polypeptides Useful as Immunotherapeutic

TITLE OF INVENTION: Agents, and Methods of Polypeptide Preparation

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert

STREET: Suite 3400, Four Embarcadero Center

CITY: San Francisco

STATE: California

COUNTRY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/606,288

FILING DATE: 23-FEB-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9503786.7

FILING DATE: 24-FEB-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/000034

FILING DATE: 08-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9515478.7

FILING DATE: 28-JUL-1995

ATTORNEY/AGENT INFORMATION:

NAME: Walter H. Dregger

REGISTRATION NUMBER: 24,190

REFERENCE/DOCKET NUMBER: A-63284/WHD

TELEPHONE: (415) 781-1989

TELEFAX: (415) 398-3249

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 601 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHEICAL: NO

ANTI-SENSE: NO

US-08-606-288-10

Query Match 47.8%; Score 247; DB 1; Length 601;

Best Local Similarity 53.5%; Pred. No. 1e-23;

Matches 53; Conservative 14; Mismatches 28; Indels 4; Gaps 3;

Qy 1 MHSPTLHEHYMLDQ-PETTDLYXXYQLNDSSEER-DEIDGPAQAEPRAHNYITFC 58

Db 493 MGRHVTLKDIIVDLQPPDVGHLHCEQLVDSSEDEVVDGQ--DSQPLKHQYITCC 550

Qy 59 CKKDSIRLCVOSTHVDIRITLEDLMGTGLGVXPIGSQK 97

Db 551 CGCDSNVRLVVOCTETDIRVQQLLGLTNIIVCPICAPK 589

RESULT 62

US-09-347-483-7

Sequence 7, Application US/09347483

Patent No. 6123948

GENERAL INFORMATION:

APPLICANT: Whittle, N.R.

APPLICANT: Carmichael, J.P.

APPLICANT: Connor, S.E.

APPLICANT: Thompson, H.S.G.

APPLICANT: Wilson, M.J.

TITLE OF INVENTION: Polypeptides Useful as Immunotherapeutic

TITLE OF INVENTION: Agents, and Methods of Polypeptide Preparation

NUMBER OF SEQUENCES: 10

;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert  
;; STREET: Suite 3400, Four Embarcadero Center  
;; CITY: San Francisco  
;; STATE: California  
;; COUNTRY: USA  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/347,483  
;; FILING DATE:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/606,288  
;; FILING DATE:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 60/000034  
;; FILING DATE: 08-JUN-1995  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: GB 9515478.7  
;; FILING DATE: 28-JUL-1995  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Walter H. Dreyer  
;; REGISTRATION NUMBER: 24,190  
;; REFERENCE/DOCKET NUMBER: A-63284/WHD  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (415) 781-1989  
;; TELEFAX: (415) 398-3249  
;; INFORMATION FOR SEQ ID NO: 7:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 601 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; US-09-347-483-7

Query Match 47.8%; Score 247; DB 2; Length 601;  
Best Local Similarity 53.5%; Pred. No. 1e-23;  
Matches 53; Conservative 14; Mismatches 28; Indels 4; Gaps 3;

Qy 1 MHGDTPTLHEXYMLDQ-PETTDLYXXYQQLNDSSEEE-DEIDGPAQAEPDRAHNYITFC 58  
Db 493 MHGHRVTLKDIIVDLQPPDPVGLHCYEQVLVSSSEDEVVDGQ--DSQPLKQHYQVITCC 550

Qy 59 CKCDSTRLCVQSTHVDIRLTEDLMGTGLGVPICSOK 97  
Db 551 CGCDSNVRLVVOCTETDIRREVQQLLGLTINIVCPICAPK 589

RESULT 63  
US-09-347-483-10  
; Sequence 10, Application US/09347483  
; Patent No. 6123948  
; GENERAL INFORMATION:  
; APPLICANT: Whittle, N.R.  
; APPLICANT: Carmichael, J.P.  
; APPLICANT: Connor, S.E.  
; APPLICANT: Thompson, H.S.G.  
; APPLICANT: Wilson, M.J.  
; TITLE OF INVENTION: Polypeptides Useful as Immunotherapeutic  
; TITLE OF INVENTION: Agents, and Methods of Polypeptide Preparation  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert  
; STREET: Suite 3400, Four Embarcadero Center  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/347,483  
;; FILING DATE:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/606,288  
;; FILING DATE:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 60/000034  
;; FILING DATE: 08-JUN-1995  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: GB 9515478.7  
;; FILING DATE: 28-JUL-1995  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Walter H. Dreyer  
;; REGISTRATION NUMBER: 24,190  
;; REFERENCE/DOCKET NUMBER: A-63284/WHD  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (415) 781-1989  
;; TELEFAX: (415) 398-3249  
;; INFORMATION FOR SEQ ID NO: 10:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 601 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; HYPOTHETICAL: NO  
;; ANTI-SENSE: NO  
;; US-09-347-483-10

Query Match 47.8%; Score 247; DB 2; Length 601;  
Best Local Similarity 53.5%; Pred. No. 1e-23;  
Matches 53; Conservative 14; Mismatches 28; Indels 4; Gaps 3;

Qy 1 MHGDTPTLHEXYMLDQ-PETTDLYXXYQQLNDSSEEE-DEIDGPAQAEPDRAHNYITFC 58  
Db 493 MHGHRVTLKDIIVDLQPPDPVGLHCYEQVLVSSSEDEVVDGQ--DSQPLKQHYQVITCC 550

Qy 59 CKCDSTRLCVQSTHVDIRLTEDLMGTGLGVPICSOK 97  
Db 551 CGCDSNVRLVVOCTETDIRREVQQLLGLTINIVCPICAPK 589

RESULT 64  
US-09-000-094-46  
; Sequence 46, Application US/09000094  
; Patent No. 6365160  
; GENERAL INFORMATION:  
; APPLICANT: WEBB, Elizabeth Ann  
; MARGRETT, Mary Brigid  
; COX, John Cooper  
; FRAZER, Ian  
; MCWILLIAN, Nigel Alan John  
; WILLIAMS, Mark Philip  
; MOLONEY, Margaret Bridget  
; HOLLAND  
; EDWARDS, Stirling John  
; TITLE OF INVENTION: PAPILLOMAVIRUS POLYPEPTIDE CONSTRUCTS  
; NUMBER OF SEQUENCES: 50  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: FOLEY & LARDNER  
; STREET: 3000 K Street, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/000,094  
FILING DATE: 21-Apr-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/AU96/00473  
FILING DATE: 26-JUL-1996  
APPLICATION NUMBER: AU PN 4439/95  
FILING DATE: 27-JUL-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 017227/0137  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1587 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 46:  
US-09-000-094-46

Query Match 47.0%; Score 243; DB 2; Length 1587;  
Best Local Similarity 52.5%; Pred. No. 1.3e-22;  
Matches 52; Conservative 15; Mismatches 28; Indels 4; Gaps 3;

Qy 1 MHGDTPIHEVM-DLQ-PETTDLYXXKQLNDSEEE-DEIDGPAGAEPPRAHNYITFC 58  
Db 839 MGRHVTLKQIVLDLPDPVGLHCYQLVDSSEDEVYDQ--DSQPLKHQIVTCC 896

Qy 59 CKCDSTRLCVGOSTHVDIRLTEDLTMGLTGIYXPCSQK 97  
Db 897 CGCDSNRLVVOCTETDIRVQQLLTGTLNIVCPICAPK 935

RESULT 65  
US-10-011-749-46  
Sequence 46, Application US/10011749  
Patent No. 6726912  
GENERAL INFORMATION:  
APPLICANT: WEBB, Elizabeth Ann  
MARGETS, Mary Brigid  
COX, John Cooper  
FRAZER, Ian  
MCMTILAN, Nigel Alan John  
WILLIAMS, Mark Philip  
MOLONEY, Margaret Bridget  
Holland  
EDWARDS, Scitling John  
TITLE OF INVENTION: PAPILLOMAVIRUS POLYPROTEIN CONSTRUCTS  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FOLEY & LARDNER  
STREET: 3000 K Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/011,749  
FILING DATE: 11-Dec-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/000,094  
FILING DATE: 21-Apr-1998  
APPLICATION NUMBER: WO PCT/AU96/00473

FILING DATE: 26-JUL-1996  
APPLICATION NUMBER: AU PN 4439/95  
FILING DATE: 27-JUL-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 017227/0137  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1587 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 46:  
US-10-011-749-46

Query Match 47.0%; Score 243; DB 2; Length 1587;  
Best Local Similarity 52.5%; Pred. No. 1.3e-22;  
Matches 52; Conservative 15; Mismatches 28; Indels 4; Gaps 3;

Qy 1 MHGDTPIHEVM-DLQ-PETTDLYXXKQLNDSEEE-DEIDGPAGAEPPRAHNYITFC 58  
Db 839 MGRHVTLKQIVLDLPDPVGLHCYQLVDSSEDEVYDQ--DSQPLKHQIVTCC 896

Qy 59 CKCDSTRLCVGOSTHVDIRLTEDLTMGLTGIYXPCSQK 97  
Db 897 CGCDSNRLVVOCTETDIRVQQLLTGTLNIVCPICAPK 935

RESULT 66  
US-09-000-094-22  
Sequence 22, Application US/09000094  
Patent No. 6365160  
GENERAL INFORMATION:  
APPLICANT: WEBB, Elizabeth Ann  
MARGETS, Mary Brigid  
COX, John Cooper  
FRAZER, Ian  
MCMTILAN, Nigel Alan John  
WILLIAMS, Mark Philip  
MOLONEY, Margaret Bridget  
Holland  
EDWARDS, Scitling John  
TITLE OF INVENTION: PAPILLOMAVIRUS POLYPROTEIN CONSTRUCTS  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FOLEY & LARDNER  
STREET: 3000 K Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/000,094  
FILING DATE: 21-Apr-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/AU96/00473  
FILING DATE: 26-JUL-1996  
APPLICATION NUMBER: AU PN 4439/95  
FILING DATE: 27-JUL-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 017227/0137



Query Match 46.4%; Score 240; DB 2; Length 465;  
Best Local Similarity 51.5%; Pred. No. 6.1e-23;  
Matches 51; Conservative 16; Mismatches 28; Indels 4; Gaps 3;  
Db 152 LHGRHTLKNIDIVDLQPPDPVGLHCYEQVLDSSSEDEVDGQ--DSQPLKQHFIYTCC 209  
Qy 1 MHGDTPLHEMYMDLQ-PETTDLYXXQXNDSSSE-DEIDGPAQAPRAHNIYVFC 58  
152 LHGRHTLKNIDIVDLQPPDPVGLHCYEQVLDSSSEDEVDGQ--DSQPLKQHFIYTCC 209  
Db 59 CKCDSTLRCLCVGSTHVDIRTEEDLLMGTGIVXPICSQK 97  
210 CGCDSNVRLVQCTETDIRREVQQLLGTINIVCPICAPK 248  
Qy 59 CKCDSTLRCLCVGSTHVDIRTEEDLLMGTGIVXPICSQK 97  
210 CGCDSNVRLVQCTETDIRREVQQLLGTINIVCPICAPK 248  
Db 210 CGCDSNVRLVQCTETDIRREVQQLLGTINIVCPICAPK 248  
RESULT 69  
US-10-011-749-24  
; Sequence 24, Application US/10011749  
; Patent No. 6726912  
; GENERAL INFORMATION:  
; APPLICANT: WEBB, Elizabeth Ann  
; MARGETTS, Mary Bridgid  
; COX, John Cooper  
; FRAZER, Ian  
; MCWILLIAM, Nigel Alan John  
; WILLIAMS, Mark Philip  
; MOLONEY, Margaret Bridget  
; Holland  
; EDWARDS, Scirling John  
; TITLE OF INVENTION: PAPILLOMAVIRUS POLYPEPTIDE CONSTRUCTS  
; NUMBER OF SEQUENCES: 50  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FOLEY & LARDNER  
; STREET: 3000 K Street, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/011.749  
; FILING DATE: 11-Dec-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/000.094  
; FILING DATE: 21-Apr-1998  
; APPLICATION NUMBER: WO PCT/AU96/00473  
; FILING DATE: 26-JUL-1996  
; APPLICATION NUMBER: AU PN 4439/95  
; FILING DATE: 27-JUL-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BENT, Stephen A.  
; REGISTRATION NUMBER: 29,768  
; REFERENCE/DOCKET NUMBER: 017227/0137  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 672-5300  
; TELEFAX: (202) 672-5399  
; INFORMATION FOR SEQ ID NO: 24:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 465 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 24:  
US-10-011-749-24  
Query Match 46.4%; Score 240; DB 2; Length 465;  
Best Local Similarity 51.5%; Pred. No. 6.1e-23;  
Matches 51; Conservative 16; Mismatches 28; Indels 4; Gaps 3;  
Qy 1 MHGDTPLHEMYMDLQ-PETTDLYXXQXNDSSSE-DEIDGPAQAPRAHNIYVFC 58  
152 LHGRHTLKNIDIVDLQPPDPVGLHCYEQVLDSSSEDEVDGQ--DSQPLKQHFIYTCC 209  
Db 59 CKCDSTLRCLCVGSTHVDIRTEEDLLMGTGIVXPICSQK 97  
210 CGCDSNVRLVQCTETDIRREVQQLLGTINIVCPICAPK 248

Query Match 40.4%; Score 209; DB 2; Length 38;  
Best Local Similarity 100.0%; Pred. No. 2.4e-20;  
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 30 DSSEDEIDGPAQAPRAHNIYVFCCKCDSTLR 67  
1 DSSEDEIDGPAQAPRAHNIYVFCCKCDSTLR 38  
Db 152 LHGRHTLKNIDIVDLQPPDPVGLHCYEQVLDSSSEDEVDGQ--DSQPLKQHFIYTCC 209  
Qy 59 CKCDSTLRCLCVGSTHVDIRTEEDLLMGTGIVXPICSQK 97  
210 CGCDSNVRLVQCTETDIRREVQQLLGTINIVCPICAPK 248  
Db 210 CGCDSNVRLVQCTETDIRREVQQLLGTINIVCPICAPK 248  
RESULT 70  
US-09-501-097A-6  
; Sequence 6, Application US/09501097A  
; Patent No. 6734173  
; GENERAL INFORMATION:  
; APPLICANT: Tzyy-Chou Wu  
; APPLICANT: Chien-Fu Hung  
; TITLE OF INVENTION: IMPROVED HSP DNA VACCINES  
; FILE REFERENCE: 2240-169349  
; CURRENT APPLICATION NUMBER: US/09/501,097A  
; CURRENT FILING DATE: 2000-02-09  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 38  
; TYPE: PRT  
; ORGANISM: human papillomavirus  
US-09-501-097A-6  
Query Match 40.4%; Score 209; DB 2; Length 38;  
Best Local Similarity 100.0%; Pred. No. 2.4e-20;  
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 30 DSSEDEIDGPAQAPRAHNIYVFCCKCDSTLR 67  
1 DSSEDEIDGPAQAPRAHNIYVFCCKCDSTLR 38  
Db 152 LHGRHTLKNIDIVDLQPPDPVGLHCYEQVLDSSSEDEVDGQ--DSQPLKQHFIYTCC 209  
Qy 59 CKCDSTLRCLCVGSTHVDIRTEEDLLMGTGIVXPICSQK 97  
210 CGCDSNVRLVQCTETDIRREVQQLLGTINIVCPICAPK 248  
Db 210 CGCDSNVRLVQCTETDIRREVQQLLGTINIVCPICAPK 248  
RESULT 71  
US-09-485-885-19  
; Sequence 19, Application US/09485885  
; Patent No. 6342224  
; GENERAL INFORMATION:  
; APPLICANT: Bruck, Claudine  
; APPLICANT: Cabezon Silva, Teresa  
; APPLICANT: Delisse, Anne-Marie Eva Bernande  
; APPLICANT: Gerard, Catherine Marie Ghislaine  
; APPLICANT: Lombardo-Bencheikh, Angela  
; TITLE OF INVENTION: Vaccine  
; FILE REFERENCE: B45107  
; CURRENT APPLICATION NUMBER: US/09/485,885  
; CURRENT FILING DATE: 2000-02-18  
; PRIOR APPLICATION NUMBER: PCT/EP98/05285  
; PRIOR FILING DATE: 1998-08-17  
; PRIOR APPLICATION NUMBER: GB 9717953.5  
; PRIOR FILING DATE: 1997-08-22  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 19  
; LENGTH: 227  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-09-485-885-19  
Query Match 39.0%; Score 201.5; DB 2; Length 227;  
Best Local Similarity 39.6%; Pred. No. 2.0e-18;  
Matches 42; Conservative 20; Mismatches 33; Indels 11; Gaps 3;  
Qy 1 MHGDTPLHEMYMDLQ-PETTDLYXXQXNDSSSE-DEIDGPAQAPRAHNIYVFC 58  
152 LHGRHTLKNIDIVDLQPPDPVGLHCYEQVLDSSSEDEVDGQ--DSQPLKQHFIYTCC 209  
Db 114 MHGKATLQDIVVHLEPQNEIPVLLGHQQLSDSEENDEIDGVNHQLPARRAEPOR-- 171  
Qy 52 YNIYTFCCCKDSTLRCLCVGSTHVDIRTEEDLLMGTGIVXPICSQK 97  
172 HTMLCMCKCKEARIELVYESSADDLRAFOQLFNTLSFVCPWCASQ 217  
Db 172 HTMLCMCKCKEARIELVYESSADDLRAFOQLFNTLSFVCPWCASQ 217



```

; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; APPLICANT: DILLNER, LENA
; APPLICANT: CHENG, HWEE-MING
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
; NUMBER OF SEQUENCES: 193
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: MASON & ASSOCIATES, P. A.
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
; CITY: CLEARWATER
; STATE: FLORIDA
; COUNTRY: U.S.A.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 3.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,915
; FILING DATE: 22-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/949,836
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: LOUISE A. FOUTCH
; REGISTRATION NUMBER: 37,133
; REFERENCE/DOCKET NUMBER: 1946.6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 813-538-3800
; TELEFAX: 813-538-3820
; TELEX:
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-934-915-52

Query Match      33.1%; Score 171; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.8e-15;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      44 QAEPRAHYNIYVFCCCKDSTLRCLVQSTH 73
DB      1 QAEPRAHYNIYVFCCCKDSTLRCLVQSTH 30

RESULT 76
US-09-486-394-3
; Sequence 3, Application US/09486394
; Patent No. 6478749
; GENERAL INFORMATION:
; APPLICANT: Hopfl, Reinhard
; TITLE OF INVENTION: Diagnostic Kit for Skin Tests, and Method
; FILE REFERENCE: 032929-001
; CURRENT APPLICATION NUMBER: US/09/486,394
; CURRENT FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/04773
; PRIOR FILING DATE: 1998-07-30
; PRIOR APPLICATION NUMBER: DE 197 37 409.3
; PRIOR FILING DATE: 1997-08-27
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
```

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; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(30)
; OTHER INFORMATION: E7 peptide.
; US-09-486-394-3

Query Match      33.1%; Score 171; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.8e-15;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      41 PQAQEPDRAHYNIYVFCCCKDSTLRCLVQ 70
DB      1 PQAQEPDRAHYNIYVFCCCKDSTLRCLVQ 30

RESULT 77
US-08-934-915-53
; Sequence 53, Application US/08934915
; Patent No. 5932412
; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; APPLICANT: DILLNER, LENA
; APPLICANT: CHENG, HWEE-MING
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
; NUMBER OF SEQUENCES: 193
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: MASON & ASSOCIATES, P. A.
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
; CITY: CLEARWATER
; STATE: FLORIDA
; COUNTRY: U.S.A.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 3.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,915
; FILING DATE: 22-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/949,836
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: LOUISE A. FOUTCH
; REGISTRATION NUMBER: 37,133
; REFERENCE/DOCKET NUMBER: 1946.6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 813-538-3800
; TELEFAX: 813-538-3820
; TELEX:
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-934-915-53

Query Match      31.3%; Score 162; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.8e-14;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      58 CCKCDSTLRCLVQSTHYDITLTLDMGTL 87
DB      1 CCKCDSTLRCLVQSTHYDITLTLDMGTL 30

RESULT 78
```

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US-09-486-394-1
; Sequence 1, Application US/09486394
; Patent No. 6478749
; GENERAL INFORMATION:
; APPLICANT: Hopfl, Reinhard
; TITLE OF INVENTION: Diagnostic Kit for Skin Tests, and Method
; FILE REFERENCE: 032929-001
; CURRENT APPLICATION NUMBER: US/09/486,394
; CURRENT FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/04773
; PRIOR FILING DATE: 1998-07-30
; PRIOR APPLICATION NUMBER: DE 197 37 409.3
; PRIOR FILING DATE: 1997-08-27
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(30)
; OTHER INFORMATION: E7 peptide.
US-09-486-394-1

Query Match          29.8%; Score 154; DB 2; Length 30;
Best Local Similarity 93.3%; Pred. No. 3,2e-13;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 MHGDTPLHEYMLDLQPETTDLYXXQLND 30
Db      1 MHGDTPLHEYMLDLQPETTDLYCYEQIND 30

RESULT 79
US-08-934-915-51
; Sequence 51, Application US/08934915
; Patent No. 5932412
; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; APPLICANT: DILLNER, LENA
; APPLICANT: CHENG, HWEI-MING
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
; NUMBER OF SEQUENCES: 193
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MASON & ASSOCIATES, P.A.
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
; CITY: CLEARWATER
; STATE: FLORIDA
; COUNTRY: U.S.A.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 3.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,915
; FILING DATE: 22-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/949,836
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: LOUISE A. Foutch
; REGISTRATION NUMBER: 37,133
; REFERENCE/DOCKET NUMBER: 1946.6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 813-538-3800
; TELEFAX: 813-538-3820
```

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TELEX:
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-934-915-51

Query Match          29.6%; Score 153; DB 1; Length 30;
Best Local Similarity 93.3%; Pred. No. 4.4e-13;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2 HGDPTLHEYMLDLQPETTDLYXXQLNDS 31
Db      1 HGDPTLHEYMLDLQPETTDLYCYEQINDS 30

RESULT 80
US-09-486-394-4
; Sequence 4, Application US/09486394
; Patent No. 6478749
; GENERAL INFORMATION:
; APPLICANT: Hopfl, Reinhard
; TITLE OF INVENTION: Diagnostic Kit for Skin Tests, and Method
; FILE REFERENCE: 032929-001
; CURRENT APPLICATION NUMBER: US/09/486,394
; CURRENT FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/04773
; PRIOR FILING DATE: 1998-07-30
; PRIOR APPLICATION NUMBER: DE 197 37 409.3
; PRIOR FILING DATE: 1997-08-27
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(30)
; OTHER INFORMATION: E7 peptide.
US-09-486-394-4

Query Match          29.6%; Score 153; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 4.4e-13;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      61 CDSTLRICVOSTHYDITLEDLMTGLGIV 90
Db      1 CDSTLRICVOSTHYDITLEDLMTGLGIV 30

RESULT 81
US-08-075-541D-7
; Sequence 7, Application US/0807541D
; Patent No. 6183745
; GENERAL INFORMATION:
; APPLICANT: TINDLE, ROBERT
; APPLICANT: FRAZER, IAN
; APPLICANT: FERNANDO, GERMAIN
; TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
; TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: 1601 MARKET STREET, 36TH FLOOR
; CITY: PHILADELPHIA
; STATE: PENNSYLVANIA
; COUNTRY: USA
; ZIP: 19103-2398
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
```

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/075,541D  
FILING DATE: 10-JUN-1993  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: AU pk 3876  
FILING DATE: 12-DEC-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: pcc/au91/00575  
FILING DATE: 12-DEC-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: NADEL, ALAN S  
REGISTRATION NUMBER: 27,363  
REFERENCE/DOCKET NUMBER: 8795-4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-567-2020  
TELEFAX: 215-567-2991  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 32 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-075-541D-7

Query Match 29.1%; Score 150.5; DB 2; Length 32;  
Best Local Similarity 56.6%; Pred. No. 1e-12; 2; Indels 21; Gaps 1;  
Matches 30; Conservative 0; Mismatches 2;

QY 10 EYMLDLPETTDLYXXYQLNDSSEEDIDGPAQAPDRAHYIVTFCCKCD 62  
Db 1 EYMLD-----GIDGPAQAPDRAHYIVTFCCKCD 32

RESULT 82  
US-09-828-645-7  
Sequence 7, Application US/09828645  
Patent No. 6743593  
GENERAL INFORMATION:  
APPLICANT: Hu, Yao Xiong  
TITLE OF INVENTION: Immunological Methodology for Discerning Human Papillomavirus  
FILE REFERENCE: 146-1-002  
CURRENT APPLICATION NUMBER: US/09/828,645  
CURRENT FILING DATE: 2001-04-05  
PRIOR APPLICATION NUMBER: US 60/194,796  
PRIOR FILING DATE: 2000-04-05  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 7  
LENGTH: 30  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Derived from the E7 early region of HPV-16  
NAME/KEY: misc feature  
LOCATION: (19)-(19)  
OTHER INFORMATION: Xaa = L-carboxymethylcysteine  
US-09-828-645-7

Query Match 28.6%; Score 148; DB 2; Length 30;  
Best Local Similarity 96.7%; Pred. No. 2e-12;  
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 PTLHEVMDLPETTDLYXXYQLNDSSEEE 35  
Db 1 PTLHEVMDLPETTDLYXXYQLNDSSEEE 30

RESULT 83

US-08-363-586-1  
Sequence 1, Application US/08363586  
Patent No. 5629161  
GENERAL INFORMATION:  
APPLICANT: Mueller, Martin  
TITLE OF INVENTION: Use of HPV-16 E6 and E7-Gene Derived  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
ADDRESS: Dunner  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/363,586  
FILING DATE: 23-DEC-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/909,296  
FILING DATE: 09-JUL-1992  
APPLICATION NUMBER: EP 91111720.8  
FILING DATE: 13-JUL-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Wadler, Linda A.  
REGISTRATION NUMBER: 33,218  
REFERENCE/DOCKET NUMBER: 02481-1195-00000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 30 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-363-586-1

Query Match 28.4%; Score 147; DB 1; Length 30;  
Best Local Similarity 93.3%; Pred. No. 2.7e-12;  
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 PTLHEVMDLPETTDLYXXYQLNDSSEEE 35  
Db 1 PTLHEVMDLPETTDLYCYEQLNDSSEEE 30

RESULT 84  
US-09-828-645-3  
Sequence 3, Application US/09828645  
Patent No. 6743593  
GENERAL INFORMATION:  
APPLICANT: Hu, Yao Xiong  
TITLE OF INVENTION: Immunological Methodology for Discerning Human Papillomavirus  
FILE REFERENCE: 146-1-002  
CURRENT APPLICATION NUMBER: US/09/828,645  
CURRENT FILING DATE: 2001-04-05  
PRIOR APPLICATION NUMBER: US 60/194,796  
PRIOR FILING DATE: 2000-04-05  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 3  
LENGTH: 30  
TYPE: PRT  
ORGANISM: Artificial Sequence

FEATURE:  
OTHER INFORMATION: Derived from the E7 early region of HPV-16  
US-09-828-645-3

Query Match 28.4%; Score 147; DB 2; Length 30;  
Best Local Similarity 93.3%; Pred. No. 2.7e-12;  
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 6 PTLHEVMDLOPETTDLYXXYQNDSSSEE 35  
DB 1 PTLHEVMDLOPETTDLYXXYQNDSSSEE 30

RESULT 85  
US-08-934-915-54  
Sequence 54, Application US/08934915  
Patent No. 5932412  
GENERAL INFORMATION:  
APPLICANT: DILLNER, JOAKIM  
APPLICANT: DILLNER, LENA  
APPLICANT: CHENG, HWEI-MING  
TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN  
TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,  
TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,  
TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR  
NUMBER OF SEQUENCES: 193  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MASON & ASSOCIATES, P. A.  
STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500  
CITY: CLEARWATER  
STATE: FLORIDA  
COUNTRY: U.S. A.  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Windows 3.0  
SOFTWARE: Microsoft Word 6.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/934,915  
FILING DATE: 22-SEP-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/949,836  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: LOUISE A. Fouch  
REGISTRATION NUMBER: 37,133  
REFERENCE/DOCKET NUMBER: 1946.6  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 813-538-3800  
TELEFAX: 813-538-3820  
TEXT:  
INFORMATION FOR SEQ ID NO: 54:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 30 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-934-915-54

Query Match 28.2%; Score 146; DB 1; Length 30;  
Best Local Similarity 96.7%; Pred. No. 3.7e-12;  
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 69 VOSTHVDIRTLEDLIMGTGLGVXPCISQXP 98  
DB 1 VOSTHVDIRTLEDLIMGTGLGVXPCISQXP 30

RESULT 86  
US-09-486-394-2  
Sequence 2, Application US/09486394

Patent No. 6478749  
GENERAL INFORMATION:  
APPLICANT: Hopfl, Reinhard  
TITLE OF INVENTION: Diagnostic Kit for Skin Tests, and Method  
FILE REFERENCE: 032929-001  
CURRENT APPLICATION NUMBER: US/09/486,394  
CURRENT FILING DATE: 2000-06-20  
PRIOR APPLICATION NUMBER: PCT/EP98/04773  
PRIOR FILING DATE: 1998-07-30  
PRIOR APPLICATION NUMBER: DE 197 37 409.3  
PRIOR FILING DATE: 1997-08-27  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 2  
LENGTH: 30  
TYPE: PRT  
ORGANISM: Human papillomavirus type 16  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (1)..(30)  
OTHER INFORMATION: E7 peptide.  
US-09-486-394-2

Query Match 28.0%; Score 145; DB 2; Length 30;  
Best Local Similarity 93.3%; Pred. No. 5e-12;  
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 21 DLYXXYQNDSSSEEEDIDGPAQAEPPRA 50  
DB 1 DLYCYEQNDSSSEEEDIDGPAQAEPPRA 30

RESULT 87  
US-08-075-541D-47  
Sequence 47, Application US/08075541D  
Patent No. 6183745  
GENERAL INFORMATION:  
APPLICANT: TINDLE, ROBERT  
APPLICANT: FERNANDO, GERMAIN  
APPLICANT: FRAZER, IAN  
TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND  
TITLE OF INVENTION: PEPTIDES FOR USE THEREIN  
NUMBER OF SEQUENCES: 56  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P. C.  
STREET: 1601 MARKET STREET, 36TH FLOOR  
CITY: PHILADELPHIA  
STATE: PENNSYLVANIA  
COUNTRY: USA  
ZIP: 19103-2398  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/075,541D  
FILING DATE: 10-JUN-1993  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: AU pk 3876  
FILING DATE: 12-DEC-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: pct/au91/00575  
FILING DATE: 12-DEC-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: NADEL, ALAN S  
REGISTRATION NUMBER: 27,363  
REFERENCE/DOCKET NUMBER: 8795-4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-567-2020  
TELEFAX: 215-567-2991  
INFORMATION FOR SEQ ID NO: 47:

SEQUENCE CHARACTERISTICS:  
LENGTH: 25 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-075-541D-47

Query Match 27.7%; Score 143; DB 2; Length 25;  
Best Local Similarity 100.0%; Pred. No. 7.2e-12;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 50 AHNYIVTFCCKCDSTLRLCVQSTHV 74  
DB 1 AHNYIVTFCCKCDSTLRLCVQSTHV 25

RESULT 88  
US-09-486-394-5  
Sequence 5, Application US/09486394  
Patent No. 6478749  
GENERAL INFORMATION:  
APPLICANT: Hopfl, Reinhard  
TITLE OF INVENTION: Diagnostic Kit for Skin Tests, and Method  
FILE REFERENCE: 032929-001  
CURRENT APPLICATION NUMBER: US/09/486,394  
CURRENT FILING DATE: 2000-06-20  
PRIOR APPLICATION NUMBER: PCT/EP98/04773  
PRIOR FILING DATE: 1998-07-30  
PRIOR APPLICATION NUMBER: DE 197 37 409.3  
PRIOR FILING DATE: 1997-08-27  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 5  
LENGTH: 28  
TYPE: PRT  
ORGANISM: Human papillomavirus type 16  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (1)..(28)  
OTHER INFORMATION: E7 peptide.  
US-09-486-394-5

Query Match 26.5%; Score 137; DB 2; Length 28;  
Best Local Similarity 96.4%; Pred. No. 5.2e-11;  
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 71 STHYDRTLEDLMGTGLGVXPCISQKP 98  
DB 1 STHYDRTLEDLMGTGLGVXPCISQKP 28

RESULT 89  
US-08-363-586-2  
Sequence 2, Application US/08363586  
Patent No. 5629161  
GENERAL INFORMATION:  
APPLICANT: Mueller, Martin  
APPLICANT: Giesmann, Lutz  
TITLE OF INVENTION: Use of HPV-16 E6 and E7-gene derived  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Flanagan, Henderson, Farabow, Garrett &  
ADDRESSEE: Dunner  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/363,586  
FILING DATE: 23-DEC-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/909,296  
FILING DATE: 09-JUL-1992  
APPLICATION NUMBER: EP 9111720.8  
FILING DATE: 13-JUL-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Wadler, Linda A.  
REGISTRATION NUMBER: 33,218  
REFERENCE/DOCKET NUMBER: 02481-1195-00000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4400  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 25 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-363-586-2

Query Match 26.3%; Score 136; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 6e-11;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 NDSSEDEIDGPAGAEPPRAHYN 53  
DB 1 NDSSEDEIDGPAGAEPPRAHYN 25

RESULT 90  
US-08-075-541D-40  
Sequence 40, Application US/08075541D  
Patent No. 6183745  
GENERAL INFORMATION:  
APPLICANT: TINDLE, ROBERT  
APPLICANT: FERNANDO, GERMAIN  
APPLICANT: FRAZER, IAN  
TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND  
TITLE OF INVENTION: PEPTIDES FOR USE THEREIN  
NUMBER OF SEQUENCES: 56  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PANITCH SCHWARZ JACOBS & NADEL, P.C.  
STREET: 1601 MARKET STREET, 36TH FLOOR  
CITY: PHILADELPHIA  
STATE: PENNSYLVANIA  
COUNTRY: USA  
ZIP: 19103-2398  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/075,541D  
FILING DATE: 10-JUN-1993  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: AU pk 3876  
FILING DATE: 12-DEC-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: pct/au91/00575  
FILING DATE: 12-DEC-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: NADEL, ALAN S  
REGISTRATION NUMBER: 27,363  
REFERENCE/DOCKET NUMBER: 8795-4  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-567-2020  
TELEFAX: 215-567-2991  
INFORMATION FOR SEQ ID NO: 40:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-075-541D-40

Query Match 24.4%; Score 126; DB 2; Length 26;  
Best Local Similarity 96.2%; Pred. No. 1.3e-09;  
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 72 THVDRTLEDLMGTGIVPCISOK 97  
Db 1 THVDRTLEDLMGTGIVPCISOK 26

RESULT 91  
US-08-934-915-71  
Sequence 71, Application US/08934915  
Patent No. 5932412  
GENERAL INFORMATION:  
APPLICANT: DILLNER, JOAKIM  
APPLICANT: DILLNER, LENA  
APPLICANT: CHENG, HWEE-MING  
TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN  
TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,  
TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,  
TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR  
TITLE OF INVENTION: DIAGNOSTIC PURPOSES  
NUMBER OF SEQUENCES: 193  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MASON & ASSOCIATES, P.A.  
STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500  
CITY: CLEARWATER  
STATE: FLORIDA  
COUNTRY: U.S.A.  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Microsoft Word 6.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/934,915  
FILING DATE: 22-SEP-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/949,836  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: LOUISE A. FOUTCH  
REGISTRATION NUMBER: 37,133  
REFERENCE/DOCKET NUMBER: 1946.6  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 813-538-3800  
TELEFAX: 813-538-3820  
TELEX:  
INFORMATION FOR SEQ ID NO: 71:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 30 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-934-915-71

Query Match 23.6%; Score 122; DB 1; Length 30;  
Best Local Similarity 75.9%; Pred. No. 5.5e-09;  
Matches 22; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
QY 58 CCKCDSTLRCLCVOSTHVDRTLEDLMGT 86

Db 1 CCKCDSTLRCLCVOSTHVDRTLEDLMGT 29

RESULT 92  
US-09-980-523A-14  
Sequence 14, Application US/09980523A  
Patent No. 6783763  
GENERAL INFORMATION:  
APPLICANT: CHOIPPIN, JEANNINE  
APPLICANT: BOURGAULT VILLADA, ISABELLE  
APPLICANT: GUILLET, JEAN-GERARD  
APPLICANT: CONNAN, FRANCES  
APPLICANT: FERRIS, ESTELLE  
TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 AND E7  
TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE  
FILE REFERENCE: WO/98/01513  
CURRENT FILING DATE: 2002-04-29  
CURRENT APPLICATION NUMBER: US/09/980,523A  
PRIOR FILING DATE: 2000-05-31  
PRIOR APPLICATION NUMBER: PCT/FR00/01513  
PRIOR FILING DATE: 1999-06-03  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 14  
LENGTH: 23  
TYPE: PRT  
ORGANISM: Human Papillomavirus  
US-09-980-523A-14

Query Match 23.4%; Score 121; DB 2; Length 23;  
Best Local Similarity 95.7%; Pred. No. 5.2e-09;  
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GDTPTLHEVMDLQPETTDLYXY 25  
Db 1 GDTPTLHEVMDLQPETTDLYCY 23

RESULT 93  
US-08-075-541D-10  
Sequence 10, Application US/08075541D  
Patent No. 6183745  
GENERAL INFORMATION:  
APPLICANT: TINDLE, ROBERT  
APPLICANT: FERNANDO, GERMAIN  
APPLICANT: FRAZER, IAN  
TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND  
TITLE OF INVENTION: PEPTIDES FOR USE THEREIN  
NUMBER OF SEQUENCES: 56  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.  
STREET: 1601 MARKET STREET, 36TH FLOOR  
CITY: PHILADELPHIA  
STATE: PENNSYLVANIA  
COUNTRY: USA  
ZIP: 19103-2398  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/075,541D  
FILING DATE: 10-JUN-1993  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: AU pk 3876  
FILING DATE: 12-DEC-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: pct/au91/00575

;; FILING DATE: 12-DEC-1991  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: NADEL, ALAN S  
;; REGISTRATION NUMBER: 27,363  
;; REFERENCE/DOCKET NUMBER: 8795-4  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 215-567-2020  
;; TELEFAX: 215-567-2991  
;; INFORMATION FOR SEQ ID NO: 10:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 20 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
US-08-075-541D-10

Query Match 23.2%; Score 120; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 5.8e-09;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 43 GQAEPRAHYIVTFCKCD 62  
Db 1 GQAEPRAHYIVTFCKCD 20

RESULT 94  
US-08-934-915-48  
; Sequence 48, Application US/08934915  
; Patent No. 5932412  
; GENERAL INFORMATION:  
; APPLICANT: DILNER, JOAKIM  
; APPLICANT: DILNER, LENA  
; APPLICANT: CHENG, HWEI-MING  
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN  
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,  
; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,  
; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR  
; TITLE OF INVENTION: DIAGNOSTIC PURPOSES  
; NUMBER OF SEQUENCES: 193  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MASON & ASSOCIATES, P.A.  
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500  
; CITY: CLEARWATER  
; STATE: FLORIDA  
; COUNTRY: U.S.A.  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: Windows 3.0  
; SOFTWARE: Microsoft Word 6.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/934,915  
; FILING DATE: 22-SEP-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/949,836  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: LOUISE A. FOUTCH  
; REGISTRATION NUMBER: 37,133  
; REFERENCE/DOCKET NUMBER: 1946.6  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 813-538-3800  
; TELEFAX: 813-538-3820  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 48:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-934-915-48

Query Match 22.8%; Score 118; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e-08;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 47 PDRAHYIVTFCKCDSTLR 66  
Db 1 PDRAHYIVTFCKCDSTLR 20

RESULT 95  
US-09-980-177A-73  
; Sequence 73, Application US/09980177A  
; Patent No. 6838084  
; GENERAL INFORMATION:  
; APPLICANT: Jochims, Ingrid  
; APPLICANT: Nieland, John  
; TITLE OF INVENTION: Cytotoxic T-Cell Epitopes of the  
; TITLE OF INVENTION: Papilloma Virus L1-Protein and Use Thereof in Diagnosis and  
; TITLE OF INVENTION: Therapy  
; FILE REFERENCE: 50125/036001  
; CURRENT APPLICATION NUMBER: US/09/980,177A  
; CURRENT FILING DATE: 2001-11-29  
; PRIOR APPLICATION NUMBER: PCT/EP00/05006  
; PRIOR FILING DATE: 2000-05-31  
; PRIOR APPLICATION NUMBER: DE 19925199.1  
; PRIOR FILING DATE: 1999-06-01  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 73  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Human papillomavirus type 16  
US-09-980-177A-73

Query Match 22.8%; Score 118; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e-08;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 45 AEPDRAHYIVTFCKCDST 64  
Db 1 AEPDRAHYIVTFCKCDST 20

RESULT 96  
US-09-980-177A-74  
; Sequence 74, Application US/09980177A  
; Patent No. 6838084  
; GENERAL INFORMATION:  
; APPLICANT: Jochims, Ingrid  
; APPLICANT: Nieland, John  
; TITLE OF INVENTION: Cytotoxic T-Cell Epitopes of the  
; TITLE OF INVENTION: Papilloma Virus L1-Protein and Use Thereof in Diagnosis and  
; TITLE OF INVENTION: Therapy  
; FILE REFERENCE: 50125/036001  
; CURRENT APPLICATION NUMBER: US/09/980,177A  
; CURRENT FILING DATE: 2001-11-29  
; PRIOR APPLICATION NUMBER: PCT/EP00/05006  
; PRIOR FILING DATE: 2000-05-31  
; PRIOR APPLICATION NUMBER: DE 19925199.1  
; PRIOR FILING DATE: 1999-06-01  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 74  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Human papillomavirus type 16  
US-09-980-177A-74

Query Match 22.4%; Score 116; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.9e-08;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	56	TFCKCKDSTLR	CVQSTHVD	75
Db	1	TFCKCKDSTLR	CVQSTHVD	20

RESULT 97  
US-08-075

? Sequence 3, Application US/08075541D  
? Patent No. 6183745  
? GENERAL INFORMATION:  
? APPLICANT: TINDLE, ROBERT  
? APPLICANT: FERNANDO, GERMAIN  
? APPLICANT: FAZER, IAN  
? TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND  
? TITLE OF INVENTION: PEPTIDES FOR USE THEREIN  
? NUMBER OF SEQUENCES: 56  
? CORRESPONDENCE ADDRESS:  
? ADDRESSEE: PAINTCH SCHWARZE JACOBS & NADEL, P.C.  
? STREET: 1601 MARKET STREET, 36TH FLOOR  
? CITY: PHILADELPHIA  
? STATE: PENNSYLVANIA  
? COUNTRY: USA  
? ZIP: 19103-2398  
? COMPUTER READABLE FORM:  
? MEDIUM TYPE: Floppy disk  
? COMPUTER: IBM PC compatible  
? OPERATING SYSTEM: PC-DOS/MS-DOS  
? SOFTWARE: PatentIn Release #1.0, Version #1.25  
? CURRENT APPLICATION DATA:  
? APPLICATION NUMBER: US/08/075,541D  
? FILING DATE: 10-JUN-1993  
? CLASSIFICATION: 424  
? PRIOR APPLICATION DATA:  
? APPLICATION NUMBER: AU pk 3876  
? FILING DATE: 12-DEC-1990  
? PRIOR APPLICATION DATA:  
? APPLICATION NUMBER: pcc/au91/00575  
? FILING DATE: 12-DEC-1991  
? ATTORNEY/AGENT INFORMATION:  
? NAME: NADEL, ALAN S  
? REGISTRATION NUMBER: 27,363  
? REFERENCE/DOCKET NUMBER: 8795-4  
? TELECOMMUNICATION INFORMATION:  
? TELEPHONE: 215-567-2020  
? TELEFAX: 215-567-2991  
? INFORMATION FOR SEQ ID NO: 3:  
? SEQUENCE CHARACTERISTICS:  
? LENGTH: 19 amino acids  
? TYPE: amino acid  
? STRANDEDNESS: single  
? TOPOLOGY: linear  
? MOLECULE TYPE: peptide  
? US-08-075-541D-3

Query Match	22.1%	Score 114	DB 2	Length 19
Best Local Similarity	100.0%	Pred. No. 3,3	3-08	
Matches 19	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	44 QAEPRRAHYNYVTFCCKCD	62		
Db	1 QAEPRRAHYNYVTFCCKCD	19		

RESULT 98  
US-08-934

Sequence 46, Application US/089349A15  
Patent No. 5932412  
GENERAL INFORMATION:  
APPLICANT: DILNER, JOAKIM  
APPLICANT: DILNER, LENA  
APPLICANT: CHENG, HMER-MING  
TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN  
PAPILLOMAVIRUS 1, 5, 6, 8,

```

; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56
; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
; NUMBER OF SEQUENCES: 193

```

CORRESPONDENCE ADDRESS:  
ADDRESSEE: MASON & ASSOCIATES, P.A.  
STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500  
CITY: CLEARWATER  
STATE: FLORIDA  
COUNTRY: U.S.A.  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Windows 3.0  
SOFTWARE: Microsoft Word 6.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/934,915  
FILING DATE: 22-SEP-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/949,836  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: LOUISE A. FOUTCH  
REGISTRATION NUMBER: 37,133  
REFERENCE/DOCKET NUMBER: 1946.6  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 813-538-3800  
TELEFAX: 813-538-3620  
TELEX:  
INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-934-915-46

Query Match	21.9%	Score	113	DB 1	Length	20			
Best Local Similarity	100.0%	Pred. NO.	4.9e-08						
Matches	20	Conservative	0	Mismatches	0	Indels	0	Gaps	0

RESULT 99  
US-08-075-541D-43  
; Sequence 43, Application US/08075541D

APPLICANT: TINDLE, ROBERT  
 APPLICANT: FERNAND, GERMAIN  
 APPLICANT: FAZZER, IAN  
 TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND  
 TITLE OF INVENTION: PEPTIDES FOR USE THEREIN  
 NUMBER OF SEQUENCES: 56  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: PAINTCH SCHWARZE JACOBS & NADEL, P.C.  
 STREET: 1601 MARKET STREET, 36TH FLOOR  
 CITY: PHILADELPHIA  
 STATE: PENNSYLVANIA  
 COUNTRY: USA  
 ZIP: 19103-2398  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/075,541D  
 FILING DATE: 10-JUN-1993

```

; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU pk 3876
; FILING DATE: 12-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: pct/au91/00575
; FILING DATE: 12-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: NADEL, ALAN S
; REGISTRATION NUMBER: 27,363
; REFERENCE/DOCKET NUMBER: 8795-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-567-2020
; TELEFAX: 215-567-2991
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-08-075-541D-43

```

```

Query Match          21.7%; Score 112; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.6e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY      1 MHGDTPTLHEYMULDLPETT 20
        |||||
Db      1 MHGDTPTLHEYMULDLPETT 20

```

```

RESULT 100
US-09-980-177A-69
; Sequence 69, Application US/09980177A
; Patent No. 683084
; GENERAL INFORMATION:
; APPLICANT: Jochmus, Ingrid
; APPLICANT: Nieland, John
; TITLE OF INVENTION: Cytotoxic T-Cell Epitopes of the
; TITLE OF INVENTION: Papilloma Virus L1-Protein and Use Thereof in Diagnosis and
; FILE REFERENCE: 50125/036001
; CURRENT APPLICATION NUMBER: US/09/980,177A
; CURRENT FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: PCT/EP00/05006
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: DE 19925199.1
; PRIOR FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 69
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
;
US-09-980-177A-69

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```

Query Match          21.7%; Score 112; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.6e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY      1 MHGDTPTLHEYMULDLPETT 20
        |||||
Db      1 MHGDTPTLHEYMULDLPETT 20

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Job time : 30.7309 secs

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OM protein - protein search, using sw model

Run on: May 27, 2006, 05:33:17 ; Search time 101.936 Seconds  
(without alignments)  
445.330 Million cell updates/sec

Title: US-10-530-253-14ED  
Perfect score: 517  
Sequence: 1 MHGDTPLHEWMLDLPETT.....LEDLMGTGIVYPCISQKP 98

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214658 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : Published Applications AA Main:\*

- 1: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US07\_PUBCOMB.pep:\*
- 2: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US08\_PUBCOMB.pep:\*
- 3: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US09\_PUBCOMB.pep:\*
- 4: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US10\_PUBCOMB.pep:\*
- 5: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US108\_PUBCOMB.pep:\*
- 6: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	514	99.4	248	5	US-10-530-253-11 Sequence 11, Appl
2	513	99.2	220	4	US-10-000-903-8 Sequence 8, Appl
3	513	99.2	220	5	US-10-899-771-8 Sequence 8, Appl
4	513	99.2	248	5	US-10-530-253-9 Sequence 9, Appl
5	513	99.2	805	4	US-10-367-095-9 Sequence 9, Appl
6	513	99.2	805	4	US-10-368-046-9 Sequence 9, Appl
7	513	99.2	805	4	US-10-367-367-9 Sequence 9, Appl
8	513	99.2	805	4	US-10-918-337-9 Sequence 9, Appl
9	512	99.0	98	3	US-09-728-466-1 Sequence 1, Appl
10	512	99.0	98	3	US-09-820-765-4 Sequence 4, Appl
11	512	99.0	98	3	US-09-824-017-4 Sequence 4, Appl
12	512	99.0	98	3	US-09-986-118A-4 Sequence 4, Appl
13	512	99.0	98	4	US-10-177-390-8 Sequence 8, Appl
14	512	99.0	98	4	US-10-654-129-4 Sequence 4, Appl
15	512	99.0	98	4	US-10-772-988-3 Sequence 3, Appl
16	512	99.0	98	4	US-10-479-541-5 Sequence 5, Appl
17	512	99.0	98	5	US-10-042-526A-4 Sequence 4, Appl
18	512	99.0	98	5	US-10-657-399-1 Sequence 1, Appl
19	512	99.0	98	5	US-10-858-384-12 Sequence 12, Appl
20	512	99.0	98	5	US-10-343-448-5 Sequence 5, Appl
21	512	99.0	98	5	US-10-367-057-17 Sequence 17, Appl
22	512	99.0	98	5	US-10-530-253-14 Sequence 14, Appl
23	512	99.0	98	6	US-11-077-939-5 Sequence 5, Appl
24	512	99.0	98	6	US-11-179-478-4 Sequence 4, Appl
25	512	99.0	121	4	US-10-267-311-12 Sequence 12, Appl
26	512	99.0	121	5	US-10-679-956-12 Sequence 12, Appl
27	512	99.0	198	4	US-10-267-311-35 Sequence 35, Appl

28	512	99.0	198	5	US-10-679-956-35 Sequence 35, Appl
29	512	99.0	220	4	US-10-000-903-1 Sequence 1, Appl
30	512	99.0	220	5	US-10-899-771-1 Sequence 1, Appl
31	512	99.0	239	4	US-10-000-903-12 Sequence 12, Appl
32	512	99.0	239	5	US-10-899-771-12 Sequence 12, Appl
33	512	99.0	248	5	US-10-530-253-7 Sequence 7, Appl
34	512	99.0	266	6	US-11-192-923A-2 Sequence 2, Appl
35	512	99.0	266	3	US-09-367-309A-1 Sequence 1, Appl
36	512	99.0	266	4	US-10-267-311-33 Sequence 33, Appl
37	512	99.0	266	5	US-10-679-956-33 Sequence 33, Appl
38	512	99.0	266	5	US-10-679-956-33 Sequence 33, Appl
39	512	99.0	334	5	US-10-679-956-25 Sequence 25, Appl
40	512	99.0	334	4	US-10-472-724-10 Sequence 10, Appl
41	512	99.0	371	4	US-10-000-903-6 Sequence 6, Appl
42	512	99.0	371	5	US-10-899-771-6 Sequence 6, Appl
43	512	99.0	380	4	US-10-000-903-14 Sequence 14, Appl
44	512	99.0	380	5	US-10-899-771-14 Sequence 14, Appl
45	512	99.0	421	4	US-10-296-770-7 Sequence 7, Appl
46	512	99.0	493	4	US-10-267-311-19 Sequence 19, Appl
47	512	99.0	493	5	US-10-679-956-19 Sequence 19, Appl
48	512	99.0	639	4	US-10-267-311-17 Sequence 17, Appl
49	512	99.0	639	5	US-10-679-956-17 Sequence 17, Appl
50	512	99.0	641	4	US-10-267-311-51 Sequence 51, Appl
51	512	99.0	641	5	US-10-679-956-51 Sequence 51, Appl
52	512	99.0	647	4	US-10-267-311-53 Sequence 53, Appl
53	512	99.0	647	5	US-10-679-956-53 Sequence 53, Appl
54	511	98.8	248	5	US-10-530-253-5 Sequence 5, Appl
55	510	98.6	248	5	US-10-530-253-3 Sequence 3, Appl
56	509	98.5	248	5	US-10-530-253-1 Sequence 1, Appl
57	507	98.1	98	4	US-10-201-764-19 Sequence 19, Appl
58	507	98.1	98	4	US-10-681-410-19 Sequence 19, Appl
59	507	98.1	98	5	US-10-484-063-26 Sequence 26, Appl
60	507	98.1	111	4	US-10-472-724-4 Sequence 4, Appl
61	504	97.5	98	4	US-10-392-113-29 Sequence 29, Appl
62	503	97.3	98	4	US-10-267-311-8 Sequence 8, Appl
63	503	97.3	98	5	US-10-679-956-8 Sequence 8, Appl
64	503	97.3	648	5	US-10-267-311-29 Sequence 29, Appl
65	503	97.3	648	5	US-10-679-956-29 Sequence 29, Appl
66	503	97.3	711	4	US-10-267-311-41 Sequence 41, Appl
67	503	97.3	711	5	US-10-679-956-41 Sequence 41, Appl
68	503	97.3	724	4	US-10-267-311-45 Sequence 45, Appl
69	503	97.3	724	5	US-10-679-956-45 Sequence 45, Appl
70	500	96.7	99	4	US-10-115-440-7 Sequence 7, Appl
71	500	96.7	289	4	US-10-115-440-5 Sequence 5, Appl
72	478	92.5	185	6	US-11-072-288-2 Sequence 2, Appl
73	381.5	73.8	99	5	US-10-530-253-30 Sequence 30, Appl
74	372	72.0	98	5	US-10-530-253-28 Sequence 28, Appl
75	295	57.1	97	5	US-10-530-253-29 Sequence 29, Appl
76	294	56.9	99	5	US-10-530-253-34 Sequence 34, Appl
77	289.5	56.0	98	5	US-10-530-253-36 Sequence 36, Appl
78	245	47.4	98	5	US-10-367-057-12 Sequence 12, Appl
79	215	41.6	117	5	US-10-751-845-126 Sequence 126, Appl
80	215	41.6	236	5	US-10-751-845-157 Sequence 157, Appl
81	215	41.6	237	5	US-10-751-845-158 Sequence 158, Appl
82	215	41.6	261	5	US-10-751-845-160 Sequence 160, Appl
83	213	41.2	106	5	US-10-530-253-32 Sequence 32, Appl
84	202.5	39.2	105	4	US-10-433-091-4 Sequence 4, Appl
85	202.5	39.2	105	5	US-10-530-253-27 Sequence 27, Appl
86	201.5	39.0	227	4	US-10-000-903-19 Sequence 19, Appl
87	201.5	39.0	227	5	US-10-899-771-19 Sequence 19, Appl
88	200.5	38.8	383	4	US-10-000-903-23 Sequence 23, Appl
89	200.5	38.8	383	5	US-10-899-771-23 Sequence 23, Appl
90	198.5	38.4	105	5	US-10-800-023-28 Sequence 28, Appl
91	196	37.9	35	6	US-11-041-993-101 Sequence 101, Appl
92	195.5	37.8	107	4	US-10-530-253-37 Sequence 37, Appl
93	195.5	37.8	118	4	US-10-472-724-8 Sequence 8, Appl
94	192.5	37.2	227	5	US-10-000-903-16 Sequence 16, Appl
95	192.5	37.2	227	5	US-10-899-771-16 Sequence 16, Appl
96	178.5	34.5	105	5	US-10-530-253-35 Sequence 35, Appl
97	178	34.4	101	5	US-10-530-253-33 Sequence 33, Appl
98	170	32.9	109	5	US-10-530-253-31 Sequence 31, Appl
99	164.5	31.8	110	5	US-10-530-253-38 Sequence 38, Appl
100	156	30.2	517	5	US-10-475-203A-14 Sequence 14, Appl

## ALIGNMENTS

## RESULT 1

US-10-530-253-11  
; Sequence 11, Application US/10530253  
; Publication No. US20060014926A1  
; GENERAL INFORMATION:  
; APPLICANT: Casasetti, Maria C.  
; APPLICANT: Smith, Larry  
; APPLICANT: Jeffrey K. Pullen  
; APPLICANT: Susan P. McElhinney  
; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS  
; FILE REFERENCE: 00630/100M137-US2  
; CURRENT APPLICATION NUMBER: US/10/530, 253  
; PRIOR FILING DATE: 2005-04-04  
; PRIOR APPLICATION NUMBER: PCT/US2003/031726  
; PRIOR FILING DATE: 2003-10-02  
; PRIOR APPLICATION NUMBER: US 60/415, 929  
; PRIOR FILING DATE: 2002-10-03  
; NUMBER OF SEQ ID NOS: 65  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 11  
; LENGTH: 248  
; TYPE: PRT  
; ORGANISM: Human papillomavirus type 16  
US-10-530-253-11

Query Match 99.4%; Score 514; DB 5; Length 248;  
Best Local Similarity 96.9%; Pred. No. 3,3e-53;

Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDPPTLHEYMDLQPEPTDLYXXQLNDSSEEDIDGPAGQAEPRRAHYNIVTFCK 60  
Db 1 MHGDPPTLHEYMDLQPEPTDLYGYQLNDSSEEDIDGPAGQAEPRRAHYNIVTFCK 60

Qy 61 CDSTLRLCVOSTHYDRTLEDLMLGTLGIYXPICQKP 98  
Db 61 CDSTLRLCVOSTHYDRTLEDLMLGTLGIYCPICQKP 98

## RESULT 2

US-10-000-903-8  
; Sequence 8, Application US/10000903  
; Publication No. US20020182221A1  
; GENERAL INFORMATION:  
; APPLICANT: Bruck, Claudine  
; APPLICANT: Cabezon Silva, Teresa  
; APPLICANT: Delisse, Anne-Marie Eva Bernande  
; APPLICANT: Gerard, Catherine Marie Ghislaine  
; APPLICANT: Lombardo-Benchelkh, Angela  
; TITLE OF INVENTION: Vaccine  
; FILE REFERENCE: B45107  
; CURRENT APPLICATION NUMBER: US/10/000, 903  
; PRIOR FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: PCT/EP98/05285  
; PRIOR FILING DATE: 1998-08-17  
; PRIOR APPLICATION NUMBER: GB 9717953.5  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 8  
; LENGTH: 220  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-10-000-903-8

Query Match 99.2%; Score 513; DB 4; Length 220;  
Best Local Similarity 96.9%; Pred. No. 3.8e-53;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDPPTLHEYMDLQPEPTDLYXXQLNDSSEEDIDGPAGQAEPRRAHYNIVTFCK 60  
Db 114 MHGDPPTLHEYMDLQPEPTDLYGYQLNDSSEEDIDGPAGQAEPRRAHYNIVTFCK 173

Qy 61 CDSTLRLCVOSTHYDRTLEDLMLGTLGIYXPICQKP 98  
Db 174 CDSTLRLCVOSTHYDRTLEDLMLGTLGIYCPICQKP 211

## RESULT 3

US-10-899-771-8  
; Sequence 8, Application US/10899771  
; Publication No. US20050031638A1  
; GENERAL INFORMATION:  
; APPLICANT: Dalemans, Wilfried L.J.  
; APPLICANT: Gerard, Catherine Marie Ghislaine  
; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins  
and Fusion Proteins Adjuvanted with a CpG Oligonucleotide  
; FILE REFERENCE: B45124  
; CURRENT APPLICATION NUMBER: US/10/899, 771  
; PRIOR FILING DATE: 2004-07-27  
; PRIOR APPLICATION NUMBER: US/09/581, 976  
; PRIOR FILING DATE: 2000-06-20  
; PRIOR APPLICATION NUMBER: PCT/EP98/08563  
; PRIOR FILING DATE: 1998-12-18  
; PRIOR APPLICATION NUMBER: GB 9727262.9  
; PRIOR FILING DATE: 1997-12-24  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 8  
; LENGTH: 220  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; OTHER INFORMATION: Chimaeic protein (protein D from Haemophilus  
; OTHER INFORMATION: Influenzae B and mutated E7 from Human papilloma  
; OTHER INFORMATION: virus type 16)  
US-10-899-771-8

Query Match 99.2%; Score 513; DB 5; Length 220;  
Best Local Similarity 96.9%; Pred. No. 3.8e-53;

Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDPPTLHEYMDLQPEPTDLYXXQLNDSSEEDIDGPAGQAEPRRAHYNIVTFCK 60  
Db 114 MHGDPPTLHEYMDLQPEPTDLYGYQLNDSSEEDIDGPAGQAEPRRAHYNIVTFCK 173

Qy 61 CDSTLRLCVOSTHYDRTLEDLMLGTLGIYXPICQKP 98  
Db 174 CDSTLRLCVOSTHYDRTLEDLMLGTLGIYCPICQKP 211

## RESULT 4

US-10-530-253-9  
; Sequence 9, Application US/10530253  
; Publication No. US20060014926A1  
; GENERAL INFORMATION:  
; APPLICANT: Casasetti, Maria C.  
; APPLICANT: Smith, Larry  
; APPLICANT: Jeffrey K. Pullen  
; APPLICANT: Susan P. McElhinney  
; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS  
; FILE REFERENCE: 00630/100M137-US2  
; CURRENT APPLICATION NUMBER: US/10/530, 253  
; PRIOR FILING DATE: 2005-04-04  
; PRIOR APPLICATION NUMBER: PCT/US2003/031726  
; PRIOR FILING DATE: 2003-10-02  
; PRIOR APPLICATION NUMBER: US 60/415, 929  
; PRIOR FILING DATE: 2002-10-03  
; NUMBER OF SEQ ID NOS: 65  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9  
; LENGTH: 248

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; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
; US-10-530-253-9
Query Match      99.2%; Score 513; DB 5; Length 248;
Best Local Similarity 96.9%; Pred. No. 4.4e-53;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEHYMLDLOPETTDLYXXQLNDSSEBEIDGPAGQAEPRAHYNIIVTFCK 60
Db 1 MHGDTPLHEHYMLDLOPETTDLYGYQLNDSSEBEIDGPAGQAEPRAHYNIIVTFCK 60

Qy 61 CDSTLRICVQSTHYDRTTLEDLMTGTYGIVCPICSOQR 98
Db 61 CDSTLRICVQSTHYDRTTLEDLMTGTYGIVCPICSOQR 98

RESULT 5
US-10-367-095-9
; Sequence 9, Application US/10367095
; Publication No. US20030228696A1
; GENERAL INFORMATION:
; APPLICANT: Robin A. Robinson
; TITLE OR INVENTION: No. US20030228696A1 Insect Cell Line
; FILE REFERENCE: 44149-1US1
; CURRENT APPLICATION NUMBER: US/10/367,095
; PRIOR FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 60/356,119
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,161
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,118
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,133
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,157
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,156
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,123
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,113
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,154
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,135
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 805
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HPV-16 L2/E7/E2 fusion protein
; US-10-367-095-9
Query Match      99.2%; Score 513; DB 4; Length 805;
Best Local Similarity 96.9%; Pred. No. 1.9e-53;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEHYMLDLOPETTDLYXXQLNDSSEBEIDGPAGQAEPRAHYNIIVTFCK 60
Db 471 MHGDTPLHEHYMLDLOPETTDLYGYQLNDSSEBEIDGPAGQAEPRAHYNIIVTFCK 530

Qy 61 CDSTLRICVQSTHYDRTTLEDLMTGTYGIVCPICSOQR 98
Db 531 CDSTLRICVQSTHYDRTTLEDLMTGTYGIVCPICSOQR 568

RESULT 6
US-10-368-046-9
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; Sequence 9, Application US/10368046
; Publication No. US20040063188A1
; GENERAL INFORMATION:
; APPLICANT: Robin A. Robinson
; TITLE OR INVENTION: Method for Isolation and Purification of
; TITLE OR INVENTION: Expressed Gene Products In Vitro
; FILE REFERENCE: 44149-3US1
; CURRENT APPLICATION NUMBER: US/10/368,046
; PRIOR FILING DATE: 2003-02-15
; PRIOR APPLICATION NUMBER: US 60/356,119
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,161
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,118
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,133
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,157
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,156
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,123
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,113
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,154
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,135
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 805
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HPV-16 L2/E7/E2 fusion protein
; US-10-368-046-9
Query Match      99.2%; Score 513; DB 4; Length 805;
Best Local Similarity 96.9%; Pred. No. 1.9e-53;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEHYMLDLOPETTDLYXXQLNDSSEBEIDGPAGQAEPRAHYNIIVTFCK 60
Db 471 MHGDTPLHEHYMLDLOPETTDLYGYQLNDSSEBEIDGPAGQAEPRAHYNIIVTFCK 530

Qy 61 CDSTLRICVQSTHYDRTTLEDLMTGTYGIVCPICSOQR 98
Db 531 CDSTLRICVQSTHYDRTTLEDLMTGTYGIVCPICSOQR 568

RESULT 7
US-10-367-367-9
; Sequence 9, Application US/10367367
; Publication No. US20040121465A1
; GENERAL INFORMATION:
; APPLICANT: Robin A. Robinson
; TITLE OR INVENTION: Optimization of Gene Sequences of
; TITLE OR INVENTION: Virus-like Particles for Expression in Insect Cells
; FILE REFERENCE: 44149-2US1
; CURRENT APPLICATION NUMBER: US/10/367,367
; PRIOR FILING DATE: 2003-02-15
; PRIOR APPLICATION NUMBER: US 60/356,119
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,161
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,118
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,133
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PRIOR APPLICATION NUMBER: US 60/356,157  
PRIOR FILING DATE: 2002-02-14  
PRIOR APPLICATION NUMBER: US 60/356,156  
PRIOR FILING DATE: 2002-02-14  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 9  
LENGTH: 805  
TYPE: PR  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: HPV-16 L2/E7/E2 fusion protein  
US-10-367-367-9

Query Match 99.2% Score 513; DB 4; Length 805;  
Best Local Similarity 96.9% Pred. No. 1.9e-52;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEYMLDLPETTDLYXXYXQNDSSSEDEIDGPAGQAEPPRAHYNIVTFCK 60  
Db 471 MHGDTPLHEYMLDLPETTDLYGEQLNDSSEDEIDGPAGQAEPPRAHYNIVTFCK 530  
Qy 61 CDSTRLCVOSTHVDIRTLDELMTGLGIYXPCISQKP 98  
Db 531 CDSTRLCVOSTHVDIRTLDELMTGLGIYXPCISQKP 568

RESULT 8  
US-10-918-337-9  
Sequence 9, Application US/10918337  
Publication No. US2005018191A1  
GENERAL INFORMATION:  
APPLICANT: NOVAVAX, INC., et al.  
TITLE OF INVENTION: Optimization of Gene Sequences of  
FILE REFERENCE: 19065/2132  
CURRENT APPLICATION NUMBER: US/10/918,337  
PRIOR FILING DATE: 2004-08-13  
PRIOR APPLICATION NUMBER: PCT/US03/04473  
PRIOR FILING DATE: 2003-02-14  
PRIOR APPLICATION NUMBER: US 60/356,119  
PRIOR FILING DATE: 2002-02-14  
PRIOR APPLICATION NUMBER: US 60/356,161  
PRIOR FILING DATE: 2002-02-14  
PRIOR APPLICATION NUMBER: US 60/356,118  
PRIOR FILING DATE: 2002-02-14  
PRIOR APPLICATION NUMBER: US 60/356,133  
PRIOR FILING DATE: 2002-02-14  
PRIOR APPLICATION NUMBER: US 60/356,157  
PRIOR FILING DATE: 2002-02-14  
PRIOR APPLICATION NUMBER: US 60/356,156  
PRIOR FILING DATE: 2002-02-14  
PRIOR APPLICATION NUMBER: US 60/356,123  
PRIOR FILING DATE: 2002-02-14  
PRIOR APPLICATION NUMBER: US 60/356,113  
PRIOR FILING DATE: 2002-02-14  
PRIOR APPLICATION NUMBER: US 60/356,154  
PRIOR FILING DATE: 2002-02-14  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 9  
LENGTH: 805  
TYPE: PR  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: HPV-16 L2/E7/E2 fusion protein  
US-10-918-337-9

Query Match 99.2% Score 513; DB 5; Length 805;  
Best Local Similarity 96.9% Pred. No. 1.9e-52;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEYMLDLPETTDLYXXYXQNDSSSEDEIDGPAGQAEPPRAHYNIVTFCK 60  
Db 471 MHGDTPLHEYMLDLPETTDLYGEQLNDSSEDEIDGPAGQAEPPRAHYNIVTFCK 530  
Qy 61 CDSTRLCVOSTHVDIRTLDELMTGLGIYXPCISQKP 98  
Db 531 CDSTRLCVOSTHVDIRTLDELMTGLGIYXPCISQKP 568

RESULT 9  
US-09-728-466-1  
Sequence 1, Application US/09728466  
Patent No. US20010029022A1  
GENERAL INFORMATION:  
APPLICANT: Fisher, Christopher  
TITLE OF INVENTION: Methods to Identify Anti-Viral Agents  
FILE REFERENCE: 28341/6216  
CURRENT APPLICATION NUMBER: US/09/728,466  
PRIOR FILING DATE: 2000-12-01  
PRIOR APPLICATION NUMBER: 09/382,616  
NUMBER OF SEQ ID NOS: 43  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1  
LENGTH: 98  
TYPE: PR  
ORGANISM: Papillomavirus gylv1lag1  
US-09-728-466-1

Query Match 99.0% Score 512; DB 3; Length 98;  
Best Local Similarity 96.9% Pred. No. 1.8e-53;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEYMLDLPETTDLYXXYXQNDSSSEDEIDGPAGQAEPPRAHYNIVTFCK 60  
Db 1 MHGDTPLHEYMLDLPETTDLYCYEQLNDSSEDEIDGPAGQAEPPRAHYNIVTFCK 60  
Qy 61 CDSTRLCVOSTHVDIRTLDELMTGLGIYXPCISQKP 98  
Db 61 CDSTRLCVOSTHVDIRTLDELMTGLGIYXPCISQKP 98

RESULT 10  
US-09-820-765-4  
Sequence 4, Application US/09820765  
Publication No. US20020039584A1  
GENERAL INFORMATION:  
APPLICANT: BURGER, Alexander  
TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE  
FORMULATIONS AND METHODS OF USE  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FOLEY & LARDNER  
STREET: 3000 K Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/820,765  
FILING DATE: 30-Mar-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/026,896  
FILING DATE: 20-FEB-1998  
ATTORNEY/AGENT INFORMATION:

NAME: Sandercock, Colin G.  
REGISTRATION NUMBER: 31,298  
REFERENCE/DOCKET NUMBER: 37067/102  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 98 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-09-820-765-4

Query Match 99.0%; Score 512; DB 3; Length 98;  
Best Local Similarity 96.9%; Pred. No. 1.8e-53;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDTPLHEHYMDLQPETTDLYXXQLNDSSEEDIDGPAGQAEPPDRAHYNIVTFCK 60  
DB 1 MHGDTPLHEHYMDLQPETTDLYCYEQLNDSSEEDIDGPAGQAEPPDRAHYNIVTFCK 60  
61 CDSTLRICVOSTHVDIRITLEDLMGTIGIVPCISQKP 98  
DB 61 CDSTLRICVOSTHVDIRITLEDLMGTIGIVPCISQKP 98

RESULT 11  
US-09-824-017-4  
Sequence 4, Application US/09824017  
Publication No. US20020197668A1  
GENERAL INFORMATION:  
APPLICANT: BURGER, Alexander  
HALBEK, Michael  
TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE  
FORMULATIONS AND METHODS OF USE  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FOLEY & LARDNER  
STREET: 3000 K Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/824,017  
FILING DATE: 03-Apr-2001  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/026,896  
FILING DATE: 1998-02-20  
ATTORNEY/AGENT INFORMATION:  
NAME: Sandercock, Colin G.  
REGISTRATION NUMBER: 31,298  
REFERENCE/DOCKET NUMBER: 37067/102  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 98 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-09-824-017-4

Query Match 99.0%; Score 512; DB 3; Length 98;  
Best Local Similarity 96.9%; Pred. No. 1.8e-53;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDTPLHEHYMDLQPETTDLYXXQLNDSSEEDIDGPAGQAEPPDRAHYNIVTFCK 60  
DB 1 MHGDTPLHEHYMDLQPETTDLYCYEQLNDSSEEDIDGPAGQAEPPDRAHYNIVTFCK 60  
61 CDSTLRICVOSTHVDIRITLEDLMGTIGIVPCISQKP 98  
DB 61 CDSTLRICVOSTHVDIRITLEDLMGTIGIVPCISQKP 98

RESULT 12  
US-09-986-118A-4  
Sequence 4, Application US/09986118A  
Publication No. US20030021806A1  
GENERAL INFORMATION:  
APPLICANT: BURGER, Alexander  
HALBEK, Michael

TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE  
FORMULATIONS AND METHODS OF USE

NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FOLEY & LARDNER  
STREET: 3000 K Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/986,118A  
FILING DATE: 07-No. US20030021806A1-2001  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/026,896  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Sandercock, Colin G.  
REGISTRATION NUMBER: 31,298  
REFERENCE/DOCKET NUMBER: 37067/102  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 98 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-09-986-118A-4

Query Match 99.0%; Score 512; DB 3; Length 98;  
Best Local Similarity 96.9%; Pred. No. 1.8e-53;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDTPLHEHYMDLQPETTDLYXXQLNDSSEEDIDGPAGQAEPPDRAHYNIVTFCK 60  
DB 1 MHGDTPLHEHYMDLQPETTDLYCYEQLNDSSEEDIDGPAGQAEPPDRAHYNIVTFCK 60  
61 CDSTLRICVOSTHVDIRITLEDLMGTIGIVPCISQKP 98  
DB 61 CDSTLRICVOSTHVDIRITLEDLMGTIGIVPCISQKP 98

RESULT 13  
US-10-177-390-8

Sequence 8, Application US/10177390  
Publication No. US20030143743A1  
GENERAL INFORMATION:  
APPLICANT: Schuler, Gerold  
TITLE OF INVENTION: Improved transfection of Eucaryotic Cells with linear  
FILE REFERENCE: 021505wo/JH/ml  
CURRENT APPLICATION NUMBER: US/10/177,390  
CURRENT FILING DATE: 2002-06-20  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO: 8  
LENGTH: 98  
TYPE: PRN  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: fragment of  
US-10-177-390-8

Query Match 99.0%; Score 512; DB 4; Length 98;  
Best Local Similarity 96.9%; Pred. No. 1.8e-53;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 MHGDPPTLHEYMLDLOPETTDLYXXYXQNDSSSEDEIDGPAGQAEPRDRAHYNIVTFCK 60  
Db 1 MHGDPPTLHEYMLDLOPETTDLYXXYXQNDSSSEDEIDGPAGQAEPRDRAHYNIVTFCK 60  
61 CDSTLRLCVOSTHVDIRTDLMDLMTGTLGIYXPCISQKP 98  
Db 61 CDSTLRLCVOSTHVDIRTDLMDLMTGTLGIYXPCISQKP 98

## RESULT 14

US-10-654-129-4  
Sequence 4, Application US/10654129  
Publication No. US2004008161A1  
GENERAL INFORMATION:  
APPLICANT: BURGER, Alexander

TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE  
FORMULATIONS AND METHODS OF USE  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FOLEY & LARDNER  
STREET: 3000 K Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20007-5109

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/654,129  
FILING DATE: 04-Sep-2003  
CLASSIFICATION: 424

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/824,017  
FILING DATE: 03-Apr-2001  
APPLICATION NUMBER: 09/026,896  
FILING DATE: 1998-02-20

## ATTORNEY/AGENT INFORMATION:

NAME: Sandercok, Colin G.  
REGISTRATION NUMBER: 31,298  
REFERENCE/DOCKET NUMBER: 37067/102  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:  
LENGTH: 98 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-10-654-129-4

Query Match 99.0%; Score 512; DB 4; Length 98;  
Best Local Similarity 96.9%; Pred. No. 1.8e-53;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 MHGDPPTLHEYMLDLOPETTDLYXXYXQNDSSSEDEIDGPAGQAEPRDRAHYNIVTFCK 60  
Db 1 MHGDPPTLHEYMLDLOPETTDLYXXYXQNDSSSEDEIDGPAGQAEPRDRAHYNIVTFCK 60  
61 CDSTLRLCVOSTHVDIRTDLMDLMTGTLGIYXPCISQKP 98  
Db 61 CDSTLRLCVOSTHVDIRTDLMDLMTGTLGIYXPCISQKP 98

## RESULT 15

US-10-772-988-3  
Sequence 3, Application US/10772988  
Publication No. US20040139485A1  
GENERAL INFORMATION:  
APPLICANT: Thorgelsson, Snorri S.  
APPLICANT: Moltach, Joseph T.

TITLE OF INVENTION: CDNA ENCODING A GENE BOG (BET OVER-EXPRESSED GENE) AND ITS PROTEIN  
FILE REFERENCE: 11613.29USW1  
CURRENT APPLICATION NUMBER: US/10/772,988  
CURRENT FILING DATE: 2004-02-05  
PRIOR APPLICATION NUMBER: US/09/637,746  
PRIOR FILING DATE: 2000-08-11  
PRIOR APPLICATION NUMBER: PCT/US99/04142  
PRIOR FILING DATE: 1999-02-25  
PRIOR APPLICATION NUMBER: US 60/079,567  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: US 60/075,922  
PRIOR FILING DATE: 1998-02-25  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO: 3  
LENGTH: 98  
TYPE: PRN  
ORGANISM: Human papillomavirus  
US-10-772-988-3

Query Match 99.0%; Score 512; DB 4; Length 98;  
Best Local Similarity 96.9%; Pred. No. 1.8e-53;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 MHGDPPTLHEYMLDLOPETTDLYXXYXQNDSSSEDEIDGPAGQAEPRDRAHYNIVTFCK 60  
Db 1 MHGDPPTLHEYMLDLOPETTDLYXXYXQNDSSSEDEIDGPAGQAEPRDRAHYNIVTFCK 60  
61 CDSTLRLCVOSTHVDIRTDLMDLMTGTLGIYXPCISQKP 98  
Db 61 CDSTLRLCVOSTHVDIRTDLMDLMTGTLGIYXPCISQKP 98

## RESULT 16

US-10-479-541-5  
Sequence 5, Application US/10479541  
Publication No. US20040151723A1  
GENERAL INFORMATION:  
APPLICANT: Kirin Beer Kabushiki Kaisha

TITLE OF INVENTION: Novel E7 antigen epitope from human papillomavirus and  
FILE REFERENCE: 137240PX  
CURRENT APPLICATION NUMBER: US/10/479,541

;; CURRENT FILING DATE: 2003-12-04  
;; PRIOR APPLICATION NUMBER: 173803/2001  
;; PRIOR FILING DATE: 2001-06-08  
;; NUMBER OF SEQ ID NOS: 5  
;; SOFTWARE: Patentin Ver. 2.1  
;; SEQ ID NO 5  
;; LENGTH: 98  
;; TYPE: PRT  
;; ORGANISM: Human papillomavirus type 16  
US-10-479-541-5

Query Match 99.0%; Score 512; DB 4; Length 98;  
Best Local Similarity 96.9%; Pred. No. 1.8e-53;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHMYMDLQPETTDLYXXQLNDSSEEDIDGPAGAEPPRAHYNIVTFCK 60  
Db 1 MHGDTPLHMYMDLQPETTDLYCYEQLNDSSEEDIDGPAGAEPPRAHYNIVTFCK 60  
Qy 61 CDSTLRVCVOSTHVDIRTLLEDLMGTIGIVPCISQKP 98  
Db 61 CDSTLRVCVOSTHVDIRTLLEDLMGTIGIVPCISQKP 98

RESULT 17  
US-10-042-526A-4  
; Sequence 4, Application US/10042526A  
; Publication No. US20050031636A1  
; GENERAL INFORMATION:  
; APPLICANT: GISMANN, et al.  
; TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE FORMULATIONS AND METHODS OF USE  
; FILE REFERENCE: 27013/38150  
; CURRENT APPLICATION NUMBER: US/10/042,526A  
; CURRENT FILING DATE: 2002-04-29  
; PRIOR APPLICATION NUMBER: US 09/632,286  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: US 08/944,368  
; PRIOR FILING DATE: 1997-10-06  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: Patentin version 3.3  
; SEQ ID NO 4  
; LENGTH: 98  
; TYPE: PRT  
; ORGANISM: Human Papilloma Virus  
US-10-042-526A-4

Query Match 99.0%; Score 512; DB 5; Length 98;  
Best Local Similarity 96.9%; Pred. No. 1.8e-53;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHMYMDLQPETTDLYXXQLNDSSEEDIDGPAGAEPPRAHYNIVTFCK 60  
Db 1 MHGDTPLHMYMDLQPETTDLYCYEQLNDSSEEDIDGPAGAEPPRAHYNIVTFCK 60  
Qy 61 CDSTLRVCVOSTHVDIRTLLEDLMGTIGIVPCISQKP 98  
Db 61 CDSTLRVCVOSTHVDIRTLLEDLMGTIGIVPCISQKP 98

RESULT 18  
US-10-657-399-1  
; Sequence 1, Application US/10657399  
; Publication No. US2005003038A1  
; GENERAL INFORMATION:  
; APPLICANT: Fisher, Christopher  
; APPLICANT: He, Manxia  
; TITLE OF INVENTION: Methods to Identify Anti-Viral Agents  
; FILE REFERENCE: 28341/6216  
; CURRENT APPLICATION NUMBER: US/10/657,399  
; CURRENT FILING DATE: 2003-09-08  
; PRIOR APPLICATION NUMBER: US/09/728,466  
; PRIOR FILING DATE: 2000-12-01  
; PRIOR APPLICATION NUMBER: 09/382,616

;; PRIOR FILING DATE: 1999-08-25  
;; NUMBER OF SEQ ID NOS: 43  
;; SOFTWARE: Patentin Ver. 2.0  
;; SEQ ID NO 1  
;; LENGTH: 98  
;; TYPE: PRT  
;; ORGANISM: Papillomavirus sylviaagi  
US-10-657-399-1

Query Match 99.0%; Score 512; DB 5; Length 98;  
Best Local Similarity 96.9%; Pred. No. 1.8e-53;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHMYMDLQPETTDLYXXQLNDSSEEDIDGPAGAEPPRAHYNIVTFCK 60  
Db 1 MHGDTPLHMYMDLQPETTDLYCYEQLNDSSEEDIDGPAGAEPPRAHYNIVTFCK 60  
Qy 61 CDSTLRVCVOSTHVDIRTLLEDLMGTIGIVPCISQKP 98  
Db 61 CDSTLRVCVOSTHVDIRTLLEDLMGTIGIVPCISQKP 98

RESULT 19  
US-10-858-384-12  
; Sequence 12, Application US/10858384  
; Publication No. US2005003025A1  
; GENERAL INFORMATION:  
; APPLICANT: CHOPIN, JEANNINE  
; APPLICANT: BOURGAULT VILLADA, ISABELLE  
; APPLICANT: GUILLET, JEAN-GERARD  
; APPLICANT: CONNAN, FRANCINE  
; APPLICANT: FERRIES, ESTELLE  
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 PROTEIN  
; TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE  
; FILE REFERENCE: 0508-1037-1  
; CURRENT APPLICATION NUMBER: US/10/858,384  
; CURRENT FILING DATE: 2004-06-02  
; PRIOR APPLICATION NUMBER: FR 9907012  
; PRIOR FILING DATE: 1999-06-03  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: Patentin Ver. 3.2  
; SEQ ID NO 12  
; LENGTH: 98  
; TYPE: PRT  
; ORGANISM: Human Papillomavirus  
US-10-858-384-12

Query Match 99.0%; Score 512; DB 5; Length 98;  
Best Local Similarity 96.9%; Pred. No. 1.8e-53;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHMYMDLQPETTDLYXXQLNDSSEEDIDGPAGAEPPRAHYNIVTFCK 60  
Db 1 MHGDTPLHMYMDLQPETTDLYCYEQLNDSSEEDIDGPAGAEPPRAHYNIVTFCK 60  
Qy 61 CDSTLRVCVOSTHVDIRTLLEDLMGTIGIVPCISQKP 98  
Db 61 CDSTLRVCVOSTHVDIRTLLEDLMGTIGIVPCISQKP 98

RESULT 20  
US-10-343-448-5  
; Sequence 5, Application US/10343448  
; Publication No. US20050054820A1  
; GENERAL INFORMATION:  
; APPLICANT: WU, Tzy-Chouu  
; APPLICANT: HUNG, Chien-Fu  
; TITLE OF INVENTION: MOLECULAR VACCINE LINKING AN ENDOPLASMIC RETICULUM CHAPERONE  
; FILE REFERENCE: 2240-186463  
; CURRENT APPLICATION NUMBER: US/10/343,448  
; CURRENT FILING DATE: 2003-01-31

; PRIOR APPLICATION NUMBER: PCT/US01/24134  
; PRIOR FILING DATE: 2001-08-02  
; PRIOR APPLICATION NUMBER: US 60/222,902  
; PRIOR FILING DATE: 2000-08-03  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5  
; LENGTH: 98  
; TYPE: PRT  
; ORGANISM: Human papillomavirus  
US-10-343-448-5

Query Match 99.0%; Score 512; DB 5; Length 98;  
Best Local Similarity 96.9%; Pred. No. 1.8e-53;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPTLHEWMLDLOPETTDLYXXQLNDSSEDEIDGPAGQAEPRAHYNIYTFCK 60  
Db 1 MHGDTPTLHEWMLDLOPETTDLYXXQLNDSSEDEIDGPAGQAEPRAHYNIYTFCK 60

Qy 61 CDSTLRLCVOSTHVDIRTELDLMGTIGIVPCISQKP 98  
Db 61 CDSTLRLCVOSTHVDIRTELDLMGTIGIVPCISQKP 98

RESULT 21  
US-10-367-057-17

; Sequence 17, Application US/10367057  
; Publication No. US20050100554A1  
; GENERAL INFORMATION:  
; APPLICANT: Cuttill, Scott;  
; APPLICANT: Jackson, Amanda;  
; APPLICANT: Lewin, David A.;  
; APPLICANT: Ooi, Chean Eng  
; TITLE OF INVENTION: Complexes and Methods of Using Same  
; FILE REFERENCE: 21402-559  
; CURRENT APPLICATION NUMBER: US/10/367,057  
; CURRENT FILING DATE: 2003-02-14  
; PRIOR APPLICATION NUMBER: 60/256,911  
; PRIOR FILING DATE: 2002-02-14  
; NUMBER OF SEQ ID NOS: 198  
; SOFTWARE: CuroseqList version 0.1  
; SEQ ID NO 17  
; LENGTH: 98  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-367-057-17

Query Match 99.0%; Score 512; DB 5; Length 98;  
Best Local Similarity 96.9%; Pred. No. 1.8e-53;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPTLHEWMLDLOPETTDLYXXQLNDSSEDEIDGPAGQAEPRAHYNIYTFCK 60  
Db 1 MHGDTPTLHEWMLDLOPETTDLYXXQLNDSSEDEIDGPAGQAEPRAHYNIYTFCK 60

Qy 61 CDSTLRLCVOSTHVDIRTELDLMGTIGIVPCISQKP 98  
Db 61 CDSTLRLCVOSTHVDIRTELDLMGTIGIVPCISQKP 98

RESULT 22  
US-10-530-253-14

; Sequence 14, Application US/10530253  
; Publication No. US20060014926A1  
; GENERAL INFORMATION:  
; APPLICANT: Casasetti, Maria C.  
; APPLICANT: Smith, Larry  
; APPLICANT: Jeffrey K. Pullen  
; APPLICANT: Susan P. McElhinney  
; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS  
; FILE REFERENCE: 00630/100M137-US2  
; CURRENT APPLICATION NUMBER: US/10/530, 253

; CURRENT FILING DATE: 2005-04-04  
; PRIOR APPLICATION NUMBER: PCT/US2003/031726  
; PRIOR FILING DATE: 2003-10-02  
; PRIOR APPLICATION NUMBER: US 60/415,929  
; PRIOR FILING DATE: 2002-10-03  
; NUMBER OF SEQ ID NOS: 65  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 14  
; LENGTH: 98  
; TYPE: PRT  
; ORGANISM: Human papillomavirus type 16  
US-10-530-253-14

Query Match 99.0%; Score 512; DB 5; Length 98;  
Best Local Similarity 96.9%; Pred. No. 1.8e-53;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPTLHEWMLDLOPETTDLYXXQLNDSSEDEIDGPAGQAEPRAHYNIYTFCK 60  
Db 1 MHGDTPTLHEWMLDLOPETTDLYXXQLNDSSEDEIDGPAGQAEPRAHYNIYTFCK 60

Qy 61 CDSTLRLCVOSTHVDIRTELDLMGTIGIVPCISQKP 98  
Db 61 CDSTLRLCVOSTHVDIRTELDLMGTIGIVPCISQKP 98

RESULT 23  
US-11-077-939-5

; Sequence 5, Application US/11077939  
; Publication No. US20050196865A1  
; GENERAL INFORMATION:  
; APPLICANT: Frazer, Ian Hector  
; TITLE OF INVENTION: Gene Expression System Based on Codon Translation Efficiency  
; FILE REFERENCE: 10338-1101  
; CURRENT APPLICATION NUMBER: US/11/077,939  
; CURRENT FILING DATE: 2005-03-11  
; PRIOR APPLICATION NUMBER: PCT/AU2003/001200  
; PRIOR FILING DATE: 2003-09-12  
; PRIOR APPLICATION NUMBER: US 60/410410  
; PRIOR FILING DATE: 2002-09-13  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 5  
; LENGTH: 98  
; TYPE: PRT  
; ORGANISM: Human papillomavirus type 16  
US-11-077-939-5

Query Match 99.0%; Score 512; DB 6; Length 98;  
Best Local Similarity 96.9%; Pred. No. 1.8e-53;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPTLHEWMLDLOPETTDLYXXQLNDSSEDEIDGPAGQAEPRAHYNIYTFCK 60  
Db 1 MHGDTPTLHEWMLDLOPETTDLYXXQLNDSSEDEIDGPAGQAEPRAHYNIYTFCK 60

Qy 61 CDSTLRLCVOSTHVDIRTELDLMGTIGIVPCISQKP 98  
Db 61 CDSTLRLCVOSTHVDIRTELDLMGTIGIVPCISQKP 98

RESULT 24  
US-11-179-478-4

; Sequence 4, Application US/11179478  
; Publication No. US20050249745A1  
; GENERAL INFORMATION:  
; APPLICANT: BURGER, Alexander  
; APPLICANT: HALBEK, Michael  
; TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE  
; TITLE OF INVENTION: FORMULATIONS AND METHODS OF USE  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: FOLEY & LARDNER

STREET: 3000 K Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/11/179,478  
FILING DATE: 13-JULY-2005  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/10/654,129  
FILING DATE: 04-Sep-2003  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Sandercock, Colin G.  
REGISTRATION NUMBER: 31,298  
REFERENCE/DOCKET NUMBER: 37067/102  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 98 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-11-179-478-4

Query Match 99.0%; Score 512; DB 6; Length 98;  
Best Local Similarity 96.9%; Pred. No. 1.8e-53;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHRYMDLQPETTDLYXXQLNDSSEEDIDDPAGQAEPRRAHYNIVTFCK 60  
Db 1 MHGDTPLHRYMDLQPETTDLYCYEQLNDSSEEDIDDPAGQAEPRRAHYNIVTFCK 60  
Qy 61 CDSTLRLCVOSTHYDRTLEDLMGTGIVXPICSQKP 98  
Db 61 CDSTLRLCVOSTHYDRTLEDLMGTGIVCPICSQKP 98

RESULT 25  
US-10-267-311-12  
Sequence 12, Application US/10267311  
Publication No. US20030050469A1  
GENERAL INFORMATION:  
APPLICANT: Siegel, Marvin  
APPLICANT: Chu, N. Randall  
APPLICANT: Mizzen, Lee A.  
TITLE OF INVENTION: INDUCTION OF A THI-LIKE RESPONSE IN VITRO  
FILE REFERENCE: 12071/002001  
CURRENT APPLICATION NUMBER: US/10/267,311  
CURRENT FILING DATE: 2002-10-09  
PRIOR APPLICATION NUMBER: US/09/613,303  
PRIOR FILING DATE: 2000-07-10  
PRIOR APPLICATION NUMBER: US 60/143,757  
PRIOR FILING DATE: 1999-07-08  
NUMBER OF SEQ ID NOS: 55  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 12  
LENGTH: 121  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: fusion sequence  
US-10-267-311-12

Query Match 99.0%; Score 512; DB 4; Length 121;

Best Local Similarity 96.9%; Pred. No. 2.4e-53;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHRYMDLQPETTDLYXXQLNDSSEEDIDDPAGQAEPRRAHYNIVTFCK 60  
Db 24 MHGDTPLHRYMDLQPETTDLYCYEQLNDSSEEDIDDPAGQAEPRRAHYNIVTFCK 83  
Qy 61 CDSTLRLCVOSTHYDRTLEDLMGTGIVXPICSQKP 98  
Db 84 CDSTLRLCVOSTHYDRTLEDLMGTGIVCPICSQKP 121

RESULT 26  
US-10-679-956-12  
Sequence 12, Application US/10679956  
Publication No. US20050089841A1  
GENERAL INFORMATION:  
APPLICANT: Siegel, Marvin  
APPLICANT: Chu, N. Randall  
APPLICANT: Mizzen, Lee A.  
TITLE OF INVENTION: INDUCTION OF A THI-LIKE RESPONSE IN VITRO  
FILE REFERENCE: 12071/002001  
CURRENT APPLICATION NUMBER: US/10/679,956  
CURRENT FILING DATE: 2003-10-06  
PRIOR APPLICATION NUMBER: US/09/613,303  
PRIOR FILING DATE: 2000-07-10  
PRIOR APPLICATION NUMBER: US 60/143,757  
PRIOR FILING DATE: 1999-07-08  
NUMBER OF SEQ ID NOS: 55  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 12  
LENGTH: 121  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: fusion sequence  
US-10-679-956-12

Query Match 99.0%; Score 512; DB 5; Length 121;  
Best Local Similarity 96.9%; Pred. No. 2.4e-53;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHRYMDLQPETTDLYXXQLNDSSEEDIDDPAGQAEPRRAHYNIVTFCK 60  
Db 24 MHGDTPLHRYMDLQPETTDLYCYEQLNDSSEEDIDDPAGQAEPRRAHYNIVTFCK 83  
Qy 61 CDSTLRLCVOSTHYDRTLEDLMGTGIVXPICSQKP 98  
Db 84 CDSTLRLCVOSTHYDRTLEDLMGTGIVCPICSQKP 121

RESULT 27  
US-10-267-311-35  
Sequence 35, Application US/10267311  
Publication No. US20030050469A1  
GENERAL INFORMATION:  
APPLICANT: Siegel, Marvin  
APPLICANT: Chu, N. Randall  
APPLICANT: Mizzen, Lee A.  
TITLE OF INVENTION: INDUCTION OF A THI-LIKE RESPONSE IN VITRO  
FILE REFERENCE: 12071/002001  
CURRENT APPLICATION NUMBER: US/10/267,311  
CURRENT FILING DATE: 2002-10-09  
PRIOR APPLICATION NUMBER: US/09/613,303  
PRIOR FILING DATE: 2000-07-10  
PRIOR APPLICATION NUMBER: US 60/143,757  
PRIOR FILING DATE: 1999-07-08  
NUMBER OF SEQ ID NOS: 55  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 35  
LENGTH: 198  
TYPE: PRT  
ORGANISM: Artificial Sequence

```
/ FEATURE:
/ OTHER INFORMATION: fusion sequence
US-10-267-311-35

Query Match          99.0%; Score 512; DB 4; Length 198;
Best Local Similarity 96.9%; Pred. No. 4,4e-53;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDPPTLHEYMLDLPETTTDLYXXQLNDSSEEDIDGPAGQAEPPRAHYNIVTFCK 60
Db 101 MHGDPPTLHEYMLDLPETTTDLYCYEQLNDSSEEDIDGPAGQAEPPRAHYNIVTFCK 160

Qy 61 CDSTLRLCVOSTHVDIRLTEDLMGTGIVXPICSOQP 98
Db 161 CDSTLRLCVOSTHVDIRLTEDLMGTGIVCPICSOQP 198

RESULT 28
US-10-679-956-35
/ Sequence 35, Application US/10679956
/ Publication No. US20050089841A1
/ GENERAL INFORMATION:
/ APPLICANT: Siegel, Marvin
/ APPLICANT: Chu, N. Randall
/ APPLICANT: Mizeen, Lee A.
/ TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
/ FILE REFERENCE: 12071/002001
/ CURRENT APPLICATION NUMBER: US/10/679,956
/ CURRENT FILING DATE: 2003-10-06
/ PRIOR APPLICATION NUMBER: US/09/613,303
/ PRIOR FILING DATE: 2000-07-10
/ PRIOR APPLICATION NUMBER: US 60/143,757
/ PRIOR FILING DATE: 1999-07-08
/ NUMBER OF SEQ ID NOS: 55
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 35
/ LENGTH: 198
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: fusion sequence
US-10-679-956-35

Query Match          99.0%; Score 512; DB 5; Length 198;
Best Local Similarity 96.9%; Pred. No. 4,4e-53;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDPPTLHEYMLDLPETTTDLYXXQLNDSSEEDIDGPAGQAEPPRAHYNIVTFCK 60
Db 101 MHGDPPTLHEYMLDLPETTTDLYCYEQLNDSSEEDIDGPAGQAEPPRAHYNIVTFCK 160

Qy 61 CDSTLRLCVOSTHVDIRLTEDLMGTGIVXPICSOQP 98
Db 161 CDSTLRLCVOSTHVDIRLTEDLMGTGIVCPICSOQP 198

RESULT 29
US-10-000-903-1
/ Sequence 1, Application US/10000903
/ Publication No. US20020182221A1
/ GENERAL INFORMATION:
/ APPLICANT: Bruck, Claudine
/ APPLICANT: Cabezon Silva, Teresa
/ APPLICANT: Delisse, Anne-Marie Eva Fernande
/ APPLICANT: Gerard, Catherine Marie Ghislaine
/ APPLICANT: Lombardo-Bencheikh, Angela
/ TITLE OF INVENTION: Vaccine
/ FILE REFERENCE: B45107
/ CURRENT APPLICATION NUMBER: US/10/000,903
/ CURRENT FILING DATE: 2001-10-01
/ PRIOR APPLICATION NUMBER: PCT/EP98/05285
/ PRIOR FILING DATE: 1998-08-17
/ PRIOR APPLICATION NUMBER: GB 9717953.5
```

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/ PRIOR FILING DATE: 1997-08-22
/ NUMBER OF SEQ ID NOS: 23
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 1
/ LENGTH: 220
/ TYPE: PRT
/ ORGANISM: Homo sapien
US-10-000-903-1

Query Match          99.0%; Score 512; DB 4; Length 220;
Best Local Similarity 96.9%; Pred. No. 5e-53;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDPPTLHEYMLDLPETTTDLYXXQLNDSSEEDIDGPAGQAEPPRAHYNIVTFCK 60
Db 114 MHGDPPTLHEYMLDLPETTTDLYCYEQLNDSSEEDIDGPAGQAEPPRAHYNIVTFCK 173

Qy 61 CDSTLRLCVOSTHVDIRLTEDLMGTGIVXPICSOQP 98
Db 174 CDSTLRLCVOSTHVDIRLTEDLMGTGIVCPICSOQP 211

RESULT 30
US-10-899-771-1
/ Sequence 1, Application US/10899771
/ Publication No. US20050031638A1
/ GENERAL INFORMATION:
/ APPLICANT: Dalemans, Wilfried L.J.
/ APPLICANT: Gerard, Catherine Marie Ghislaine
/ TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
/ TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
/ FILE REFERENCE: B45124
/ CURRENT APPLICATION NUMBER: US/10/899,771
/ CURRENT FILING DATE: 2004-07-27
/ PRIOR APPLICATION NUMBER: US/09/581,976
/ PRIOR FILING DATE: 2000-06-20
/ PRIOR APPLICATION NUMBER: PCT/EP98/08563
/ PRIOR FILING DATE: 1998-12-18
/ PRIOR APPLICATION NUMBER: GB 9727262.9
/ PRIOR FILING DATE: 1997-12-24
/ NUMBER OF SEQ ID NOS: 28
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 1
/ LENGTH: 220
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Chimaeic protein (protein D from Haemophilus
/ OTHER INFORMATION: influenzae B and E7 from Human papilloma virus type
/ OTHER INFORMATION: 16)
US-10-899-771-1

Query Match          99.0%; Score 512; DB 5; Length 220;
Best Local Similarity 96.9%; Pred. No. 5e-53;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDPPTLHEYMLDLPETTTDLYXXQLNDSSEEDIDGPAGQAEPPRAHYNIVTFCK 60
Db 114 MHGDPPTLHEYMLDLPETTTDLYCYEQLNDSSEEDIDGPAGQAEPPRAHYNIVTFCK 173

Qy 61 CDSTLRLCVOSTHVDIRLTEDLMGTGIVXPICSOQP 98
Db 174 CDSTLRLCVOSTHVDIRLTEDLMGTGIVCPICSOQP 211

RESULT 31
US-10-000-903-12
/ Sequence 12, Application US/10000903
/ Publication No. US20020182221A1
/ GENERAL INFORMATION:
/ APPLICANT: Bruck, Claudine
/ APPLICANT: Cabezon Silva, Teresa
/ APPLICANT: Delisse, Anne-Marie Eva Fernande
```

APPLICANT: Gerard, Catherine Marie Ghislaine  
APPLICANT: Lombardo-Bencheikh, Angela  
TITLE OF INVENTION: Vaccine  
FILE REFERENCE: B45107  
CURRENT APPLICATION NUMBER: US/10/000,903  
CURRENT FILING DATE: 2001-10-01  
PRIOR APPLICATION NUMBER: PCT/EP98/05585  
PRIOR FILING DATE: 1998-08-17  
PRIOR APPLICATION NUMBER: GB 9717953.5  
PRIOR FILING DATE: 1997-08-22  
NUMBER OF SEQ ID NOS: 23  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 12  
LENGTH: 239  
TYPE: PRT  
ORGANISM: Homo sapien  
US-10-000-903-12

Query Match 99.0%; Score 512; DB 4; Length 239;  
Best Local Similarity 96.9%; Pred. No. 5.5e-53;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHRYMDLQPEETDLYXXYXQNDSEEDIDGPAGQAEPPRAHYNIVTFCK 60  
Db 133 MHGDTPLHRYMDLQPEETDLYCYEQNDSEEDIDGPAGQAEPPRAHYNIVTFCK 192  
Qy 61 CDSTLRICVQSTHVDIRTLBDMGLGIYXPCSQKP 98  
Db 193 CDSTLRICVQSTHVDIRTLBDMGLGIYCPICSQKP 230

RESULT 32  
US-10-899-771-12  
Sequence 12, Application US/10899771  
Publication No. US20050031638A1  
GENERAL INFORMATION:  
APPLICANT: Dalemans, Wilfried L.J.  
APPLICANT: Gerard, Catherine Marie Ghislaine  
TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins  
and Fusion Proteins Adjuncted with a CpG Oligonucleotide  
FILE REFERENCE: B45124  
CURRENT APPLICATION NUMBER: US/10/899,771  
CURRENT FILING DATE: 2004-07-27  
PRIOR APPLICATION NUMBER: US/09/581,976  
PRIOR FILING DATE: 2000-06-20  
PRIOR APPLICATION NUMBER: PCT/EP98/08563  
PRIOR FILING DATE: 1998-12-18  
PRIOR APPLICATION NUMBER: GB 9727262.9  
PRIOR FILING DATE: 1997-12-24  
NUMBER OF SEQ ID NOS: 28  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 12  
LENGTH: 239  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Chimaeic protein (C)yta from Streptococcus  
OTHER INFORMATION: pneumoniae and E7 from Human papilloma virus type  
OTHER INFORMATION: 16)  
US-10-899-771-12

Query Match 99.0%; Score 512; DB 5; Length 239;  
Best Local Similarity 96.9%; Pred. No. 5.5e-53;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHRYMDLQPEETDLYXXYXQNDSEEDIDGPAGQAEPPRAHYNIVTFCK 60  
Db 133 MHGDTPLHRYMDLQPEETDLYCYEQNDSEEDIDGPAGQAEPPRAHYNIVTFCK 192  
Qy 61 CDSTLRICVQSTHVDIRTLBDMGLGIYXPCSQKP 98  
Db 193 CDSTLRICVQSTHVDIRTLBDMGLGIYCPICSQKP 230

RESULT 33  
US-10-530-253-7  
Sequence 7, Application US/10530253  
Publication No. US20060014926A1  
GENERAL INFORMATION:  
APPLICANT: Cassecci, Maria C.  
APPLICANT: Smith, Larry  
APPLICANT: Jeffrey K. Pullen  
APPLICANT: Susan P. McElhinney  
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS  
FILE REFERENCE: 00630/100M137-US2  
CURRENT APPLICATION NUMBER: US/10/530,253  
CURRENT FILING DATE: 2005-04-04  
PRIOR APPLICATION NUMBER: PCT/US2003/031726  
PRIOR FILING DATE: 2003-10-02  
PRIOR APPLICATION NUMBER: US 60/415,929  
PRIOR FILING DATE: 2002-10-03  
NUMBER OF SEQ ID NOS: 65  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 7  
LENGTH: 248  
TYPE: PRT  
ORGANISM: Human papillomavirus type 16  
US-10-530-253-7

Query Match 99.0%; Score 512; DB 5; Length 248;  
Best Local Similarity 96.9%; Pred. No. 5.8e-53;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHRYMDLQPEETDLYXXYXQNDSEEDIDGPAGQAEPPRAHYNIVTFCK 60  
Db 1 MHGDTPLHRYMDLQPEETDLYCYEQNDSEEDIDGPAGQAEPPRAHYNIVTFCK 60  
Qy 61 CDSTLRICVQSTHVDIRTLBDMGLGIYXPCSQKP 98  
Db 61 CDSTLRICVQSTHVDIRTLBDMGLGIYCPICSQKP 98

RESULT 34  
US-11-192-923A-2  
Sequence 2, Application US/11192923A  
Publication No. US20060018928A1  
GENERAL INFORMATION:  
APPLICANT: PANG, XIAOWU  
TITLE OF INVENTION: VIRUS-LIKE PARTICLE CONTAINING A DENGUE VIRUS  
FILE REFERENCE: 116620-003  
CURRENT APPLICATION NUMBER: US/11/192,923A  
CURRENT FILING DATE: 2005-07-29  
PRIOR APPLICATION NUMBER: CN 03115272.4  
PRIOR FILING DATE: 2003-01-30  
PRIOR APPLICATION NUMBER: CN 03115273.2  
PRIOR FILING DATE: 2003-01-30  
NUMBER OF SEQ ID NOS: 45  
SOFTWARE: PatentIn Ver. 3.3  
SEQ ID NO 2  
LENGTH: 256  
TYPE: PRT  
ORGANISM: Human papillomavirus  
US-11-192-923A-2

Query Match 99.0%; Score 512; DB 6; Length 256;  
Best Local Similarity 96.9%; Pred. No. 6e-53;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHRYMDLQPEETDLYXXYXQNDSEEDIDGPAGQAEPPRAHYNIVTFCK 60  
Db 1 MHGDTPLHRYMDLQPEETDLYCYEQNDSEEDIDGPAGQAEPPRAHYNIVTFCK 60  
Qy 61 CDSTLRICVQSTHVDIRTLBDMGLGIYXPCSQKP 98  
Db 61 CDSTLRICVQSTHVDIRTLBDMGLGIYCPICSQKP 98

RESULT 35  
US-09-367-309A-1  
; Sequence 1, Application US/09367309A  
; Publication No. US20020081329A1  
; GENERAL INFORMATION:  
; APPLICANT: MACFARLAN, RODERICK I.  
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES  
; FILE REFERENCE: 017227/0149  
; CURRENT APPLICATION NUMBER: US/09/367,309A  
; PRIOR FILING DATE: 1999-08-11  
; PRIOR APPLICATION NUMBER: PCT/AU98/00080  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: AU PO 5178  
; PRIOR FILING DATE: 1997-02-19  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 266  
; TYPE: PRT  
; ORGANISM: Human papillomavirus type 16  
US-09-367-309A-1

Query Match 99.0%; Score 512; DB 3; Length 266;  
Best Local Similarity 96.9%; Pred. No. 6.3e-53;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 MHGDPFLHEYMLDLOPETTDLYXXQLNDSSEDEIDGPAQAEPDRAHYNIVTFCK 60  
DB 161 MHGDPFLHEYMLDLOPETTDLYCYEQLNDSSEDEIDGPAQAEPDRAHYNIVTFCK 220  
OY 61 CDSTLRFCVOSTHVDIRTELDLMGTGIVXPCISQKP 98  
DB 221 CDSTLRFCVOSTHVDIRTELDLMGTGIVXPCISQKP 258

RESULT 36  
US-10-267-311-33  
; Sequence 33, Application US/10267311  
; Publication No. US20030050469A1  
; GENERAL INFORMATION:  
; APPLICANT: Siegel, Marvin  
; APPLICANT: Chu, N. Randall  
; APPLICANT: Mizen, Lee A.  
; TITLE OF INVENTION: INDUCTION OF A THI-LIKE RESPONSE IN VITRO  
; FILE REFERENCE: 12071/002001  
; CURRENT APPLICATION NUMBER: US/10/267,311  
; CURRENT FILING DATE: 2002-10-09  
; PRIOR APPLICATION NUMBER: US/09/613,303  
; PRIOR FILING DATE: 2000-07-10  
; PRIOR APPLICATION NUMBER: US 60/143,757  
; PRIOR FILING DATE: 1999-07-08  
; NUMBER OF SEQ ID NOS: 55  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 33  
; LENGTH: 295  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: fusion sequence  
US-10-267-311-33

Query Match 99.0%; Score 512; DB 4; Length 295;  
Best Local Similarity 96.9%; Pred. No. 7.2e-53;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 MHGDPFLHEYMLDLOPETTDLYXXQLNDSSEDEIDGPAQAEPDRAHYNIVTFCK 60  
DB 198 MHGDPFLHEYMLDLOPETTDLYCYEQLNDSSEDEIDGPAQAEPDRAHYNIVTFCK 257  
OY 61 CDSTLRFCVOSTHVDIRTELDLMGTGIVXPCISQKP 98

DB 258 CDSTLRFCVOSTHVDIRTELDLMGTGIVXPCISQKP 295

RESULT 37  
US-10-679-956-33  
; Sequence 33, Application US/10679956  
; Publication No. US20050089841A1  
; GENERAL INFORMATION:  
; APPLICANT: Siegel, Marvin  
; APPLICANT: Chu, N. Randall  
; APPLICANT: Mizen, Lee A.  
; TITLE OF INVENTION: INDUCTION OF A THI-LIKE RESPONSE IN VITRO  
; FILE REFERENCE: 12071/002001  
; CURRENT APPLICATION NUMBER: US/10/679,956  
; CURRENT FILING DATE: 2003-10-06  
; PRIOR APPLICATION NUMBER: US/09/613,303  
; PRIOR FILING DATE: 2000-07-10  
; PRIOR APPLICATION NUMBER: US 60/143,757  
; PRIOR FILING DATE: 1999-07-08  
; NUMBER OF SEQ ID NOS: 55  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 33  
; LENGTH: 295  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: fusion sequence  
US-10-679-956-33

Query Match 99.0%; Score 512; DB 5; Length 295;  
Best Local Similarity 96.9%; Pred. No. 7.2e-53;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 MHGDPFLHEYMLDLOPETTDLYXXQLNDSSEDEIDGPAQAEPDRAHYNIVTFCK 60  
DB 198 MHGDPFLHEYMLDLOPETTDLYCYEQLNDSSEDEIDGPAQAEPDRAHYNIVTFCK 257  
OY 61 CDSTLRFCVOSTHVDIRTELDLMGTGIVXPCISQKP 98  
DB 258 CDSTLRFCVOSTHVDIRTELDLMGTGIVXPCISQKP 295

RESULT 38  
US-10-267-311-25  
; Sequence 25, Application US/10267311  
; Publication No. US20030050469A1  
; GENERAL INFORMATION:  
; APPLICANT: Siegel, Marvin  
; APPLICANT: Chu, N. Randall  
; APPLICANT: Mizen, Lee A.  
; TITLE OF INVENTION: INDUCTION OF A THI-LIKE RESPONSE IN VITRO  
; FILE REFERENCE: 12071/002001  
; CURRENT APPLICATION NUMBER: US/10/267,311  
; CURRENT FILING DATE: 2002-10-09  
; PRIOR APPLICATION NUMBER: US/09/613,303  
; PRIOR FILING DATE: 2000-07-10  
; PRIOR APPLICATION NUMBER: US 60/143,757  
; PRIOR FILING DATE: 1999-07-08  
; NUMBER OF SEQ ID NOS: 55  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 25  
; LENGTH: 324  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: fusion sequence  
US-10-267-311-25

Query Match 99.0%; Score 512; DB 4; Length 324;  
Best Local Similarity 96.9%; Pred. No. 8.1e-53;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;



```
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimeric protein (protein D from Haemophilus
; OTHER INFORMATION: Influenza B and B6E7 fusion from Human Papilloma
; OTHER INFORMATION: virus type 16)
US-10-899-771-6

Query Match          99.0%; Score 512; DB 5; Length 371;
Best Local Similarity 96.9%; Pred. No. 9.5e-53;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MGGPTPLHEMYMDLQPEETDLYXXYXQLNDSSEDEIDGPAGQAEPPRAHYNIVTFCK 60
Db 265 MGGPTPLHEMYMDLQPEETDLYCYEQLNDSSEDEIDGPAGQAEPPRAHYNIVTFCK 324

Qy 61 CDSTLRFCVOSTHVDIRLTEDLMLGTGIVXPICSOXP 98
Db 325 CDSTLRFCVOSTHVDIRLTEDLMLGTGIVCPICSOXP 362

RESULT 43
US-10-000-903-14
; Sequence 14, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000.903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-14

Query Match          99.0%; Score 512; DB 4; Length 390;
Best Local Similarity 96.9%; Pred. No. 1e-52;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MGGPTPLHEMYMDLQPEETDLYXXYXQLNDSSEDEIDGPAGQAEPPRAHYNIVTFCK 60
Db 284 MGGPTPLHEMYMDLQPEETDLYCYEQLNDSSEDEIDGPAGQAEPPRAHYNIVTFCK 343

Qy 61 CDSTLRFCVOSTHVDIRLTEDLMLGTGIVXPICSOXP 98
Db 344 CDSTLRFCVOSTHVDIRLTEDLMLGTGIVCPICSOXP 381

RESULT 44
US-10-899-771-14
; Sequence 14, Application US/10899771
; Publication No. US20050031638A1
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.
; APPLICANT: Gerard, Catherine Marie Ghislaine
; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
; TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a Cpg Oligonucleotide
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/10/899.771
; CURRENT FILING DATE: 2004-07-27
```

```
; PRIOR APPLICATION NUMBER: US/09/581.976
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP96/08563
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: GB 9727262.9
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimeric protein (Clyta from Streptococcus
; OTHER INFORMATION: pneumoniae and E5E7 fusion from Human papilloma
; OTHER INFORMATION: virus type 16)
US-10-899-771-14

Query Match          99.0%; Score 512; DB 5; Length 390;
Best Local Similarity 96.9%; Pred. No. 1e-52;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MGGPTPLHEMYMDLQPEETDLYXXYXQLNDSSEDEIDGPAGQAEPPRAHYNIVTFCK 60
Db 284 MGGPTPLHEMYMDLQPEETDLYCYEQLNDSSEDEIDGPAGQAEPPRAHYNIVTFCK 343

Qy 61 CDSTLRFCVOSTHVDIRLTEDLMLGTGIVXPICSOXP 98
Db 344 CDSTLRFCVOSTHVDIRLTEDLMLGTGIVCPICSOXP 381

RESULT 45
US-10-296-770-7
; Sequence 7, Application US/10296770
; Publication No. US20030104570A1
; GENERAL INFORMATION:
; APPLICANT: Cabezon Silva, Teresa Elisa Virginia
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; TITLE OF INVENTION: Triple Fusion Proteins Comprising
; TITLE OF INVENTION: Ubiquitin Fused Between Thiorodoxin and a polypeptide of
; TITLE OF INVENTION: Interest
; FILE REFERENCE: B45221
; CURRENT APPLICATION NUMBER: US/10/296.770
; CURRENT FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: PCT/EP01/06952
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: GB 0015619.0
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: GB 0026484.6
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 421
; TYPE: PRT
; ORGANISM: Chimeric (B. coli - human)
US-10-296-770-7

Query Match          99.0%; Score 512; DB 4; Length 421;
Best Local Similarity 96.9%; Pred. No. 1.1e-52;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MGGPTPLHEMYMDLQPEETDLYXXYXQLNDSSEDEIDGPAGQAEPPRAHYNIVTFCK 60
Db 315 MGGPTPLHEMYMDLQPEETDLYCYEQLNDSSEDEIDGPAGQAEPPRAHYNIVTFCK 374

Qy 61 CDSTLRFCVOSTHVDIRLTEDLMLGTGIVXPICSOXP 98
Db 375 CDSTLRFCVOSTHVDIRLTEDLMLGTGIVCPICSOXP 412

RESULT 46
US-10-267-311-19
```

```
; Sequence 19, Application US/10267311
; Publication No. US20030050469A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 493
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
US-10-267-311-19
```

```
Query Match          99.0%; Score 512; DB 4; Length 493;
Best Local Similarity 96.9%; Pred. No. 1.4e-52;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy 1 MHGDTPLHEYMLDLOPETTDLYXXQLNDSSEDEIDGPAQAEPDRAHYNIVTFCK 60
```

```
Db 396 MHGDTPLHEYMLDLOPETTDLYCYEQUNDSEDEIDGPAQAEPDRAHYNIVTFCK 455
```

```
Qy 61 CDSTLRLCVOSTHYDRTLEDLMLGTLGIYCPICSKP 98
```

```
Db 456 CDSTLRLCVOSTHYDRTLEDLMLGTLGIYCPICSKP 493
```

```
RESULT 47
US-10-679-956-19
```

```
; Sequence 19, Application US/10679956
; Publication No. US20050089841A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/679,956
; CURRENT FILING DATE: 2003-10-06
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 493
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
US-10-679-956-19
```

```
Query Match          99.0%; Score 512; DB 5; Length 493;
Best Local Similarity 96.9%; Pred. No. 1.4e-52;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy 1 MHGDTPLHEYMLDLOPETTDLYXXQLNDSSEDEIDGPAQAEPDRAHYNIVTFCK 60
```

```
Db 396 MHGDTPLHEYMLDLOPETTDLYCYEQUNDSEDEIDGPAQAEPDRAHYNIVTFCK 455
```

```
Qy 61 CDSTLRLCVOSTHYDRTLEDLMLGTLGIYCPICSKP 98
```

```
Db 456 CDSTLRLCVOSTHYDRTLEDLMLGTLGIYCPICSKP 493
```

```
RESULT 48
US-10-267-311-17
```

```
; Sequence 17, Application US/10267311
; Publication No. US20030050469A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 639
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
US-10-267-311-17
```

```
Query Match          99.0%; Score 512; DB 4; Length 639;
Best Local Similarity 96.9%; Pred. No. 1.9e-52;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy 1 MHGDTPLHEYMLDLOPETTDLYXXQLNDSSEDEIDGPAQAEPDRAHYNIVTFCK 60
```

```
Db 542 MHGDTPLHEYMLDLOPETTDLYCYEQUNDSEDEIDGPAQAEPDRAHYNIVTFCK 601
```

```
Qy 61 CDSTLRLCVOSTHYDRTLEDLMLGTLGIYCPICSKP 98
```

```
Db 602 CDSTLRLCVOSTHYDRTLEDLMLGTLGIYCPICSKP 639
```

```
RESULT 49
US-10-679-956-17
```

```
; Sequence 17, Application US/10679956
; Publication No. US20050089841A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/679,956
; CURRENT FILING DATE: 2003-10-06
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 639
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
US-10-679-956-17
```

```
Query Match          99.0%; Score 512; DB 5; Length 639;
Best Local Similarity 96.9%; Pred. No. 1.9e-52;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy 1 MHGDTPLHEYMLDLOPETTDLYXXQLNDSSEDEIDGPAQAEPDRAHYNIVTFCK 60
```

Db 542 MHGDTPLHEMYMLDQPEPTDLYCYEQNDSSSEDEIDGPAGQAEPPRAHYNIVTFCK 601  
Qy 61 CDSTRLCVOGTHVDIRTLBDMGTGIVXPICQKP 98  
Db 602 CDSTRLCVOGTHVDIRTLBDMGTGIVCPICQKP 639

## RESULT 50

US-10-267-311-51  
; Sequence 51, Application US/10267311  
; Publication No. US20030050469A1  
; GENERAL INFORMATION:  
; APPLICANT: Siegel, Marvin  
; APPLICANT: Chu, N. Randall  
; APPLICANT: Mizzen, Lee A.  
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO  
; FILE REFERENCE: 12071/002001  
; CURRENT APPLICATION NUMBER: US/10/267,311  
; CURRENT FILING DATE: 2002-10-09  
; PRIOR APPLICATION NUMBER: US/09/613,303  
; PRIOR FILING DATE: 2000-07-10  
; PRIOR APPLICATION NUMBER: US 60/143,757  
; PRIOR FILING DATE: 1999-07-08  
; NUMBER OF SEQ ID NOS: 55  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 51  
; LENGTH: 641  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: fusion sequence  
US-10-267-311-51

Query Match 99.0%; Score 512; DB 4; Length 641;  
Best Local Similarity 96.9%; Pred. No. 1.9e-52;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEMYMLDQPEPTDLYCYEQNDSSSEDEIDGPAGQAEPPRAHYNIVTFCK 60  
Db 544 MHGDTPLHEMYMLDQPEPTDLYCYEQNDSSSEDEIDGPAGQAEPPRAHYNIVTFCK 603  
Qy 61 CDSTRLCVOGTHVDIRTLBDMGTGIVXPICQKP 98  
Db 604 CDSTRLCVOGTHVDIRTLBDMGTGIVCPICQKP 641

## RESULT 51

US-10-679-956-51  
; Sequence 51, Application US/10679956  
; Publication No. US20050089841A1  
; GENERAL INFORMATION:  
; APPLICANT: Siegel, Marvin  
; APPLICANT: Chu, N. Randall  
; APPLICANT: Mizzen, Lee A.  
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO  
; FILE REFERENCE: 12071/002001  
; CURRENT APPLICATION NUMBER: US/10/679,956  
; CURRENT FILING DATE: 2003-10-06  
; PRIOR APPLICATION NUMBER: US/09/613,303  
; PRIOR FILING DATE: 2000-07-10  
; PRIOR APPLICATION NUMBER: US 60/143,757  
; PRIOR FILING DATE: 1999-07-08  
; NUMBER OF SEQ ID NOS: 55  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 51  
; LENGTH: 641  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: fusion sequence  
US-10-679-956-51

Query Match 99.0%; Score 512; DB 5; Length 641;  
Best Local Similarity 96.9%; Pred. No. 1.9e-52;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEMYMLDQPEPTDLYCYEQNDSSSEDEIDGPAGQAEPPRAHYNIVTFCK 60  
Db 544 MHGDTPLHEMYMLDQPEPTDLYCYEQNDSSSEDEIDGPAGQAEPPRAHYNIVTFCK 603  
Qy 61 CDSTRLCVOGTHVDIRTLBDMGTGIVXPICQKP 98  
Db 604 CDSTRLCVOGTHVDIRTLBDMGTGIVCPICQKP 641

## RESULT 52

US-10-267-311-53  
; Sequence 53, Application US/10267311  
; Publication No. US20030050469A1  
; GENERAL INFORMATION:  
; APPLICANT: Siegel, Marvin  
; APPLICANT: Chu, N. Randall  
; APPLICANT: Mizzen, Lee A.  
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO  
; FILE REFERENCE: 12071/002001  
; CURRENT APPLICATION NUMBER: US/10/267,311  
; CURRENT FILING DATE: 2002-10-09  
; PRIOR APPLICATION NUMBER: US/09/613,303  
; PRIOR FILING DATE: 2000-07-10  
; PRIOR APPLICATION NUMBER: US 60/143,757  
; PRIOR FILING DATE: 1999-07-08  
; NUMBER OF SEQ ID NOS: 55  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 53  
; LENGTH: 647  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: fusion sequence  
US-10-267-311-53

Query Match 99.0%; Score 512; DB 4; Length 647;  
Best Local Similarity 96.9%; Pred. No. 1.9e-52;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEMYMLDQPEPTDLYCYEQNDSSSEDEIDGPAGQAEPPRAHYNIVTFCK 60  
Db 550 MHGDTPLHEMYMLDQPEPTDLYCYEQNDSSSEDEIDGPAGQAEPPRAHYNIVTFCK 609  
Qy 61 CDSTRLCVOGTHVDIRTLBDMGTGIVXPICQKP 98  
Db 610 CDSTRLCVOGTHVDIRTLBDMGTGIVCPICQKP 647

## RESULT 53

US-10-679-956-53  
; Sequence 53, Application US/10679956  
; Publication No. US20050089841A1  
; GENERAL INFORMATION:  
; APPLICANT: Siegel, Marvin  
; APPLICANT: Chu, N. Randall  
; APPLICANT: Mizzen, Lee A.  
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO  
; FILE REFERENCE: 12071/002001  
; CURRENT APPLICATION NUMBER: US/10/679,956  
; CURRENT FILING DATE: 2003-10-06  
; PRIOR APPLICATION NUMBER: US/09/613,303  
; PRIOR FILING DATE: 2000-07-10  
; PRIOR APPLICATION NUMBER: US 60/143,757  
; PRIOR FILING DATE: 1999-07-08  
; NUMBER OF SEQ ID NOS: 55  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 53  
; LENGTH: 647  
; TYPE: PRT

ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: fusion sequence  
US-10-679-956-53

Query Match 99.0%; Score 512; DB 5; Length 647;  
Best Local Similarity 96.9%; Pred. No. 1.9e-52;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEHYMDLQPEETDLYXXQLNDSSEDEIDGPAGAEPRRAHNIIVTFCK 60  
Db 550 MHGDTPLHEHYMDLQPEETDLYCYEQLNDSSEDEIDGPAGAEPRRAHNIIVTFCK 609  
Qy 61 CDSTLRICVOSTHVDIRLTEDLMGTIGIYXPCISQKP 98  
Db 610 CDSTLRICVOSTHVDIRLTEDLMGTIGIYXPCISQKP 647

RESULT 54  
US-10-530-253-5  
Sequence 5, Application US/10530253  
Publication No. US20060014926A1  
GENERAL INFORMATION:  
APPLICANT: Casaretti, Maria C.  
APPLICANT: Smith, Larry  
APPLICANT: Jeffrey K. Pullen  
APPLICANT: Susan P. McElhinney  
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS  
FILE REFERENCE: 00630/100M137-US2  
CURRENT APPLICATION NUMBER: US/10/530,253  
CURRENT FILING DATE: 2005-04-04  
PRIOR APPLICATION NUMBER: PCT/US2003/031726  
PRIOR FILING DATE: 2003-10-02  
PRIOR APPLICATION NUMBER: US 60/415,929  
PRIOR FILING DATE: 2002-10-03  
NUMBER OF SEQ ID NOS: 65  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 5  
LENGTH: 248  
TYPE: PRT  
ORGANISM: Human papillomavirus type 16  
US-10-530-253-5

Query Match 98.8%; Score 511; DB 5; Length 248;  
Best Local Similarity 95.9%; Pred. No. 7.6e-53;  
Matches 94; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEHYMDLQPEETDLYXXQLNDSSEDEIDGPAGAEPRRAHNIIVTFCK 60  
Db 151 LHGDTPLHEHYMDLQPEETDLYCYEQLNDSSEDEIDGPAGAEPRRAHNIIVTFCK 210  
Qy 61 CDSTLRICVOSTHVDIRLTEDLMGTIGIYXPCISQKP 98  
Db 211 CDSTLRICVOSTHVDIRLTEDLMGTIGIYXPCISQKP 248

RESULT 55  
US-10-530-253-3  
Sequence 3, Application US/10530253  
Publication No. US20060014926A1  
GENERAL INFORMATION:  
APPLICANT: Casaretti, Maria C.  
APPLICANT: Smith, Larry  
APPLICANT: Jeffrey K. Pullen  
APPLICANT: Susan P. McElhinney  
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS  
FILE REFERENCE: 00630/100M137-US2  
CURRENT APPLICATION NUMBER: US/10/530,253  
CURRENT FILING DATE: 2005-04-04  
PRIOR APPLICATION NUMBER: PCT/US2003/031726  
PRIOR FILING DATE: 2003-10-02  
PRIOR APPLICATION NUMBER: US 60/415,929  
PRIOR FILING DATE: 2002-10-03

NUMBER OF SEQ ID NOS: 65  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 3  
LENGTH: 248  
TYPE: PRT  
ORGANISM: Human papillomavirus type 16  
US-10-530-253-3

Query Match 98.6%; Score 510; DB 5; Length 248;  
Best Local Similarity 95.9%; Pred. No. 1e-52;  
Matches 94; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEHYMDLQPEETDLYXXQLNDSSEDEIDGPAGAEPRRAHNIIVTFCK 60  
Db 151 LHGDTPLHEHYMDLQPEETDLYCYEQLNDSSEDEIDGPAGAEPRRAHNIIVTFCK 210  
Qy 61 CDSTLRICVOSTHVDIRLTEDLMGTIGIYXPCISQKP 98  
Db 211 CDSTLRICVOSTHVDIRLTEDLMGTIGIYXPCISQKP 248

RESULT 56  
US-10-530-253-1  
Sequence 1, Application US/10530253  
Publication No. US20060014926A1  
GENERAL INFORMATION:  
APPLICANT: Casaretti, Maria C.  
APPLICANT: Smith, Larry  
APPLICANT: Jeffrey K. Pullen  
APPLICANT: Susan P. McElhinney  
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS  
FILE REFERENCE: 00630/100M137-US2  
CURRENT APPLICATION NUMBER: US/10/530,253  
CURRENT FILING DATE: 2005-04-04  
PRIOR APPLICATION NUMBER: PCT/US2003/031726  
PRIOR FILING DATE: 2003-10-02  
PRIOR APPLICATION NUMBER: US 60/415,929  
PRIOR FILING DATE: 2002-10-03  
NUMBER OF SEQ ID NOS: 65  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1  
LENGTH: 248  
TYPE: PRT  
ORGANISM: Human papillomavirus type 16  
US-10-530-253-1

Query Match 98.5%; Score 509; DB 5; Length 248;  
Best Local Similarity 95.9%; Pred. No. 1.3e-52;  
Matches 94; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEHYMDLQPEETDLYXXQLNDSSEDEIDGPAGAEPRRAHNIIVTFCK 60  
Db 151 LHGDTPLHEHYMDLQPEETDLYCYEQLNDSSEDEIDGPAGAEPRRAHNIIVTFCK 210  
Qy 61 CDSTLRICVOSTHVDIRLTEDLMGTIGIYXPCISQKP 98  
Db 211 CDSTLRICVOSTHVDIRLTEDLMGTIGIYXPCISQKP 248

RESULT 57  
US-10-201-764-19  
Sequence 19, Application US/10201764  
Publication No. US20030166140A1  
GENERAL INFORMATION:  
APPLICANT: CHEN, SI-YI AND ZHAOYANG, YOU  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANTIGENS WHICH ELICIT AN  
TITLE OF INVENTION: IMMUNE RESPONSE  
FILE REFERENCE: TEA  
CURRENT APPLICATION NUMBER: US/10/201,764  
CURRENT FILING DATE: 2002-07-22  
PRIOR APPLICATION NUMBER: US/09/566,420  
PRIOR FILING DATE: 2000-05-05  
PRIOR APPLICATION NUMBER: 60/132,752

;; PRIOR FILING DATE: 1999-05-06  
;; PRIOR APPLICATION NUMBER: 60/132,750  
;; PRIOR FILING DATE: 1999-05-06  
;; NUMBER OF SEQ ID NOS: 19  
;; SOFTWARE: Patentin Ver. 2.0  
;; SEQ ID NO 19  
;; LENGTH: 98  
;; TYPE: PRT  
;; ORGANISM: Human papillomavirus type E7  
US-10-201-764-19

Query Match 98.1%; Score 507; DB 4; Length 98;  
Best Local Similarity 95.9%; Pred. No. 7.4e-53;  
Matches 94; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 1 MHGDPPTLHEWMLDQPEPTTDLXXYXQUNDSESEDEIDGPAGQAEPPRAHNYITVFCCK 60  
Db 1 MHGDPPTLHEWMLDQPEPTTDLXXYXQUNDSESEDEIDGPAGQAEPPRAHNYITVFCCK 60  
Oy 61 CDSTLRCLCVOSTHVDIRLTEDLTMGTGIVXPICSOXP 98  
Db 61 CDSTLRCLCVOSTHVDIRLTEDLTMGTGIVXPICSOXP 98

RESULT 58  
US-10-681-410-19  
;; Sequence 19, Application US/10681410  
;; Publication No. US20040096426A1  
;; GENERAL INFORMATION:  
;; APPLICANT: CHEN, SI-YI AND ZHAOYANG, YOU  
;; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANTIGENS WHICH ELICIT AN  
;; FILE REFERENCE: TBA  
;; CURRENT APPLICATION NUMBER: US/10/681,410  
;; CURRENT FILING DATE: 2003-10-08  
;; PRIOR APPLICATION NUMBER: US/10/201,764  
;; PRIOR FILING DATE: 2002-07-22  
;; PRIOR APPLICATION NUMBER: US/09/566,420  
;; PRIOR FILING DATE: 2000-05-05  
;; PRIOR APPLICATION NUMBER: 60/132,752  
;; PRIOR FILING DATE: 1999-05-06  
;; PRIOR APPLICATION NUMBER: 60/132,750  
;; PRIOR FILING DATE: 1999-05-06  
;; NUMBER OF SEQ ID NOS: 19  
;; SOFTWARE: Patentin Ver. 2.0  
;; SEQ ID NO 19  
;; LENGTH: 98  
;; TYPE: PRT  
;; ORGANISM: Human papillomavirus type E7  
US-10-681-410-19

Query Match 98.1%; Score 507; DB 4; Length 98;  
Best Local Similarity 95.9%; Pred. No. 7.4e-53;  
Matches 94; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 1 MHGDPPTLHEWMLDQPEPTTDLXXYXQUNDSESEDEIDGPAGQAEPPRAHNYITVFCCK 60  
Db 1 MHGDPPTLHEWMLDQPEPTTDLXXYXQUNDSESEDEIDGPAGQAEPPRAHNYITVFCCK 60  
Oy 61 CDSTLRCLCVOSTHVDIRLTEDLTMGTGIVXPICSOXP 98  
Db 61 CDSTLRCLCVOSTHVDIRLTEDLTMGTGIVXPICSOXP 98

RESULT 59  
US-10-484-063-26  
;; Sequence 26, Application US/10484063  
;; Publication No. US20050048467A1  
;; GENERAL INFORMATION:  
;; APPLICANT: SASSTRY, K. JAGANNADHA  
;; APPLICANT: TORTOLERO-LUNA, GUILTERMO  
;; APPLICANT: FOLLEN, MICHAEL  
;; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED

;; TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN  
;; FILE REFERENCE: UTSC:560US  
;; CURRENT APPLICATION NUMBER: US/10/484,063  
;; CURRENT FILING DATE: 2004-01-16  
;; PRIOR APPLICATION NUMBER: PCT/US02/23198  
;; PRIOR FILING DATE: 2002-07-19  
;; PRIOR APPLICATION NUMBER: 60/306,809  
;; PRIOR FILING DATE: 2001-07-20  
;; NUMBER OF SEQ ID NOS: 27  
;; SOFTWARE: Patentin Ver. 2.1  
;; SEQ ID NO 26  
;; LENGTH: 98  
;; TYPE: PRT  
;; ORGANISM: Human papillomavirus type 16  
US-10-484-063-26

Query Match 98.1%; Score 507; DB 5; Length 98;  
Best Local Similarity 95.9%; Pred. No. 7.4e-53;  
Matches 94; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 1 MHGDPPTLHEWMLDQPEPTTDLXXYXQUNDSESEDEIDGPAGQAEPPRAHNYITVFCCK 60  
Db 1 MHGDPPTLHEWMLDQPEPTTDLXXYXQUNDSESEDEIDGPAGQAEPPRAHNYITVFCCK 60  
Oy 61 CDSTLRCLCVOSTHVDIRLTEDLTMGTGIVXPICSOXP 98  
Db 61 CDSTLRCLCVOSTHVDIRLTEDLTMGTGIVXPICSOXP 98

RESULT 60  
US-10-472-724-4  
;; Sequence 4, Application US/10472724  
;; Publication No. US20040171806A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Cid-Arregui, Angel  
;; APPLICANT: Zur Hausen, Harald  
;; TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination  
;; FILE REFERENCE: 4121-154  
;; CURRENT APPLICATION NUMBER: US/10/472,724  
;; CURRENT FILING DATE: 2003-09-17  
;; PRIOR APPLICATION NUMBER: PCT/EP02/03271  
;; PRIOR FILING DATE: 2002-03-22  
;; PRIOR APPLICATION NUMBER: EP 01107271.7  
;; PRIOR FILING DATE: 2001-03-23  
;; NUMBER OF SEQ ID NOS: 27  
;; SOFTWARE: Patentin version 3.2  
;; SEQ ID NO 4  
;; LENGTH: 111  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Synthetic Construct  
US-10-472-724-4

Query Match 98.1%; Score 507; DB 4; Length 111;  
Best Local Similarity 96.9%; Pred. No. 8.6e-53;  
Matches 94; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 HGDPTLHEWMLDQPEPTTDLXXYXQUNDSESEDEIDGPAGQAEPPRAHNYITVFCCK 61  
Db 7 HGDPTLHEWMLDQPEPTTDLXXYXQUNDSESEDEIDGPAGQAEPPRAHNYITVFCCK 66  
Oy 62 DSTLRCLCVOSTHVDIRLTEDLTMGTGIVXPICSOXP 98  
Db 67 DSTLRCLCVOSTHVDIRLTEDLTMGTGIVXPICSOXP 103

RESULT 61  
US-10-392-113-29  
;; Sequence 29, Application US/10392113  
;; Publication No. US20030224993A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Land, Hartmut

```
APPLICANT: Deleu, Laurent
TITLE OF INVENTION: COMPOSITIONS THAT INHIBIT PROLIFERATION
FILE REFERENCE: 21108.000503
CURRENT APPLICATION NUMBER: US/10/392,113
PRIOR FILING DATE: 2003-03-17
PRIOR APPLICATION NUMBER: 60/365,078
PRIOR FILING DATE: 2002-03-15
PRIOR APPLICATION NUMBER: PCT/US01/32127
PRIOR FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 60/239,705
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 29
LENGTH: 98
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:/Note =
US-10-392-113-29
```

```
Query Match          97.5%; Score 504; DB 4; Length 98;
Best Local Similarity 95.9%; Pred. No. 1.7e-52;
Matches 94; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy 1 MHGDTPLHEMYMDLOPETTDLYXXQNDSSSEEDIDGPAGAEPRAHYNIIVTFCK 60
Db 1 MHGDTPLHEMYMDLOPETTDLYCYEQNDSSSEEDIDGPAGAEPRAHYNIIVTFCK 60
```

```
Qy 61 CDSTLRLCVOSTHYDITLEDLMGTGIVXPCISQKP 98
Db 61 CDSTLRLCVOSTHYDITLEDLMGTGIVCPCISQKP 98
```

```
RESULT 62
US-10-267-311-8
Sequence 8, Application US/10267311
Publication No. US20030050469A1
GENERAL INFORMATION:
APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
FILE REFERENCE: 12071/002001
CURRENT APPLICATION NUMBER: US/10/267,311
CURRENT FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: US/09/613,303
PRIOR FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 55
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 98
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: fusion sequence
US-10-267-311-8
```

```
Query Match          97.3%; Score 503; DB 4; Length 98;
Best Local Similarity 95.9%; Pred. No. 2.2e-52;
Matches 94; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy 1 MHGDTPLHEMYMDLOPETTDLYXXQNDSSSEEDIDGPAGAEPRAHYNIIVTFCK 60
Db 1 MHGDTPLHEMYMDLOPETTDLYCYEQNDSSSEEDIDGPAGAEPRAHYNIIVTFCK 60
Qy 61 CDSTLRLCVOSTHYDITLEDLMGTGIVXPCISQKP 98
Db 61 CDSTLRLCVOSTHYDITLEDLMGTGIVCPCISQKP 98
```

```
RESULT 63
US-10-679-956-8
Sequence 8, Application US/10679956
Publication No. US20050089841A1
GENERAL INFORMATION:
APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
FILE REFERENCE: 12071/002001
CURRENT APPLICATION NUMBER: US/10/679,956
CURRENT FILING DATE: 2003-10-06
PRIOR APPLICATION NUMBER: US/09/613,303
PRIOR FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 55
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 98
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: fusion sequence
US-10-679-956-8
```

```
Query Match          97.3%; Score 503; DB 5; Length 98;
Best Local Similarity 95.9%; Pred. No. 2.2e-52;
Matches 94; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy 1 MHGDTPLHEMYMDLOPETTDLYXXQNDSSSEEDIDGPAGAEPRAHYNIIVTFCK 60
Db 1 MHGDTPLHEMYMDLOPETTDLYCYEQNDSSSEEDIDGPAGAEPRAHYNIIVTFCK 60
```

```
Qy 61 CDSTLRLCVOSTHYDITLEDLMGTGIVXPCISQKP 98
Db 61 CDSTLRLCVOSTHYDITLEDLMGTGIVCPCISQKP 98
```

```
RESULT 64
US-10-267-311-29
Sequence 29, Application US/10267311
Publication No. US20030050469A1
GENERAL INFORMATION:
APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
FILE REFERENCE: 12071/002001
CURRENT APPLICATION NUMBER: US/10/267,311
CURRENT FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: US/09/613,303
PRIOR FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 55
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 29
LENGTH: 648
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: fusion sequence
US-10-267-311-29
```

```
Query Match          97.3%; Score 503; DB 4; Length 648;
Best Local Similarity 95.9%; Pred. No. 2.3e-51;
Matches 94; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy 1 MHGDTPLHEMYMDLOPETTDLYXXQNDSSSEEDIDGPAGAEPRAHYNIIVTFCK 60
Db 1 MHGDTPLHEMYMDLOPETTDLYCYEQNDSSSEEDIDGPAGAEPRAHYNIIVTFCK 60
```

Dh 1 MDGPTPLHEHYMLDLPETTDLYCYEQLNDSSEDEIDGPAGQAEPPRAHYNIVTFCK 60  
Qy 61 CDSTLRVCVOSTHVDIRTLIEDLMGTGIVXPICSOQP 98  
Dh 61 CDSTLRVCVOSTHVDIRTLIEDLMGTGIVXPICSOQP 98

RESULT 65  
US-10-679-956-29  
; Sequence 29, Application US/10679956  
; Publication No. US20050089841A1  
; GENERAL INFORMATION:  
; APPLICANT: Siegel, Marvin  
; APPLICANT: Chu, N. Randall  
; APPLICANT: Mizzen, Lee A.  
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO  
; FILE REFERENCE: 12071/002001  
; CURRENT APPLICATION NUMBER: US/10/679,956  
; CURRENT FILING DATE: 2003-10-06  
; PRIOR APPLICATION NUMBER: US/09/613,303  
; PRIOR FILING DATE: 2000-07-10  
; PRIOR APPLICATION NUMBER: US 60/143,757  
; PRIOR FILING DATE: 1999-07-08  
; NUMBER OF SEQ ID NOS: 55  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 29  
; LENGTH: 648  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: fusion sequence  
US-10-679-956-29

Query Match 97.3%; Score 503; DB 5; Length 648;  
Best Local Similarity 95.9%; Pred. No. 2.3e-51;  
Matches 94; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEHYMLDLPETTDLYXXYQLNDSSEDEIDGPAGQAEPPRAHYNIVTFCK 60  
Dh 1 MDGPTPLHEHYMLDLPETTDLYCYEQLNDSSEDEIDGPAGQAEPPRAHYNIVTFCK 60  
Qy 61 CDSTLRVCVOSTHVDIRTLIEDLMGTGIVXPICSOQP 98  
Dh 61 CDSTLRVCVOSTHVDIRTLIEDLMGTGIVXPICSOQP 98

RESULT 66  
US-10-267-311-41  
; Sequence 41, Application US/10267311  
; Publication No. US20030050469A1  
; GENERAL INFORMATION:  
; APPLICANT: Siegel, Marvin  
; APPLICANT: Chu, N. Randall  
; APPLICANT: Mizzen, Lee A.  
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO  
; FILE REFERENCE: 12071/002001  
; CURRENT APPLICATION NUMBER: US/10/267,311  
; CURRENT FILING DATE: 2002-10-09  
; PRIOR APPLICATION NUMBER: US/09/613,303  
; PRIOR FILING DATE: 2000-07-10  
; PRIOR APPLICATION NUMBER: US 60/143,757  
; PRIOR FILING DATE: 1999-07-08  
; NUMBER OF SEQ ID NOS: 55  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 41  
; LENGTH: 711  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: fusion sequence  
US-10-267-311-41

Query Match 97.3%; Score 503; DB 4; Length 711;

Best Local Similarity 95.9%; Pred. No. 2.3e-51;  
Matches 94; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEHYMLDLPETTDLYXXYQLNDSSEDEIDGPAGQAEPPRAHYNIVTFCK 60  
Dh 1 MDGPTPLHEHYMLDLPETTDLYCYEQLNDSSEDEIDGPAGQAEPPRAHYNIVTFCK 60  
Qy 61 CDSTLRVCVOSTHVDIRTLIEDLMGTGIVXPICSOQP 98  
Dh 61 CDSTLRVCVOSTHVDIRTLIEDLMGTGIVXPICSOQP 98

RESULT 67  
US-10-679-956-41  
; Sequence 41, Application US/10679956  
; Publication No. US20050089841A1  
; GENERAL INFORMATION:  
; APPLICANT: Siegel, Marvin  
; APPLICANT: Chu, N. Randall  
; APPLICANT: Mizzen, Lee A.  
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO  
; FILE REFERENCE: 12071/002001  
; CURRENT APPLICATION NUMBER: US/10/679,956  
; CURRENT FILING DATE: 2003-10-06  
; PRIOR APPLICATION NUMBER: US/09/613,303  
; PRIOR FILING DATE: 2000-07-10  
; PRIOR APPLICATION NUMBER: US 60/143,757  
; PRIOR FILING DATE: 1999-07-08  
; NUMBER OF SEQ ID NOS: 55  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 41  
; LENGTH: 711  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: fusion sequence  
US-10-679-956-41

Query Match 97.3%; Score 503; DB 5; Length 711;  
Best Local Similarity 95.9%; Pred. No. 2.3e-51;  
Matches 94; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEHYMLDLPETTDLYXXYQLNDSSEDEIDGPAGQAEPPRAHYNIVTFCK 60  
Dh 1 MDGPTPLHEHYMLDLPETTDLYCYEQLNDSSEDEIDGPAGQAEPPRAHYNIVTFCK 60  
Qy 61 CDSTLRVCVOSTHVDIRTLIEDLMGTGIVXPICSOQP 98  
Dh 61 CDSTLRVCVOSTHVDIRTLIEDLMGTGIVXPICSOQP 98

RESULT 68  
US-10-267-311-45  
; Sequence 45, Application US/10267311  
; Publication No. US20030050469A1  
; GENERAL INFORMATION:  
; APPLICANT: Siegel, Marvin  
; APPLICANT: Chu, N. Randall  
; APPLICANT: Mizzen, Lee A.  
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO  
; FILE REFERENCE: 12071/002001  
; CURRENT APPLICATION NUMBER: US/10/267,311  
; CURRENT FILING DATE: 2002-10-09  
; PRIOR APPLICATION NUMBER: US/09/613,303  
; PRIOR FILING DATE: 2000-07-10  
; PRIOR APPLICATION NUMBER: US 60/143,757  
; PRIOR FILING DATE: 1999-07-08  
; NUMBER OF SEQ ID NOS: 55  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 45  
; LENGTH: 724  
; TYPE: PRT  
; ORGANISM: Artificial Sequence

```

; FEATURE:
; OTHER INFORMATION: fusion sequence
US-10-267-311-45

```

Query Match 97.3%; Score 503; DB 4; Length 724;  
Best Local Similarity 95.9%;  
Pred. No. 2.6e-51;  
Matches 94; Conservative 0; Indels 0; Gaps 0;

Qy 1 MHGDPPTLHXYMLDLPETTDLYXXQGLNDSSEEDRIDGPAGQAEPPRAHYNIVTFCK 60

Db 1 MDGDPPTLHXYMLDLPETTDLYCYEQGLNDSSEEDRIDGPAGQAEPPRAHYNIVTFCK 60

Dy 61 CDSTRICVQSHVDIRTLBEDLMGILGIVPICSKXP 98  
|||  
Db 61 CDSTRICVQSHVDIRTLBEDLMGILGIVPICSKXP 98

RESULT 69  
INC-10-678

US-10-679-956-45  
; Sequence 45, Application US/10679956  
; Publication No. US20050089841A1  
Journal INFORMATION

APPLICANT: Siegel, Marvin  
APPLICANT: Chu, N. Randall  
APPLICANT: Mizzen, Lee A.  
TITLE OR INVENTION: INDUCTION OF A TWO-LIVE RESPONSE IN VITRO

FILE REFERENCE: 120/1/002001  
CURRENT APPLICATION NUMBER: US/10/679, 956  
CURRENT FILING DATE: 2003-10-06  
PRIOR APPLICATION NUMBER: US/09/613 303

```

:
: PRIOR FILING DATE: 2000-07-10
:
: PRIOR APPLICATION NUMBER: US 60/143,757
:
: PRIOR FILING DATE: 1999-07-08
:
: NUMBER OF SEQ ID NOS: 55
:

```

```

;          ;      COL INAME: LUNCLDZ   LOT WINCLS   VELSLON 7.0
;          ; SEQ ID NO 45
;          ; LENGTH: 724
;          ; TYPE: PRT

```

```

; FEATURE: fusion sequence
; OTHER INFORMATION: fusion sequence
US-10-679-956-45

```

;; PRIOR FILING DATE: 2000-02-09  
;; PRIOR APPLICATION NUMBER: US 09/421,608  
; PRIOR FILING DATE: 1999-10-20

```
; SOFTWARE: Patentin version 3.1  
; SEO ID NO 7  
; LENGTH: 99  
; END
```

US-10-115-440-7  
ORGANISM: Human papillomavirus  
96.7% Score E00. No A. Length 99.  
Query Match

1 MCGDPTHEVMDILOBETTDI VVVVYOLNDSGRERDIT  
Best Local Similarity 96.9%; Pred. No. 5,2e-52;  
Matches 93; Conservative 0; Mismatches 3;

**D**b****

QY           61 CDSTLRICVQSTHVDIRTEDLL  
|||  
|||

RESULT 71  
UC-10-11E-AAA-E

```

; sequence 5, Application US/10115440
; Publication No. US20040086845A1
; GENERAL INFORMATION:
; APPLICANT: WII T210/CHOU

```

? APPLICANT: KUNO, CHIDEN-FU  
 ? TITLE OF INVENTION: SUPERIOR MOLECULAR VACCINE LINKING THE TRANSLOCATION DOMAIN OF A  
 ? TITLE OF INVENTION: BACTERIAL TOXIN TO AN ANTIGEN  
 ? FTR REFERENCE: 02240-178934

CURRENT FILING DATE: 2002-09-30  
 PRIOR APPLICATION NUMBER: US 60/281,003  
 PRIOR FILING DATE: 2001-04-04

;  
 ;  
 ; PRIOR FILING DATE: 2000-10-20  
 ;  
 ; PRIOR APPLICATION NUMBER: US 09/50  
 ;  
 ; PRIOR FILING DATE: 2000-02-09  
 ;

PRIOR FILING DATE: 1999-10-20  
 NUMBER OF SEQ ID NOS: 15  
 SOFTWARE: PatentIn version 3.1

```

;
; LENGTH: 289
;
; TYPE: PRT
;
; ORGANISM: Human papillomavirus

```

Query Match	96.7%;	Score 500;	DB 4;
Best Local Similarity	96.9%;	Pred. No. 1.9e-51;	

1 MHGDTPTLHEXVMDLPETTDLYXXVQINDSSEDEIDGPAGABPDRAHYNIYTFCK 60

```

0y      61 CDSTLRLCVOSTHVDIRTLIEDLLMGTVGIVXPICSQ 96
          |||||
0b      324 CDSMTPIGVOCTHNDPBTEDNIMCMTCTVCPTCSO 360
          |||||

```

RESULT 72  
HS-11-072-2A8-2

```

; APPLICANT: KIRBY, Marie-Paul
;
; GENERAL INFORMATION:
; Publication No. US20050159386A1
;
; sequence & Application US/110/2200

```

APPLICANT: BIZOUARNE, Nadine

```
; TITLE OF INVENTION: ANTITUMORAL COMPOSITION BASED ON IMMUNOGENIC
; TITLE OF INVENTION: POLYPEPTIDE WITH MODIFIED CELL LOCATION
; FILE REFERENCE: 01753-122
; CURRENT APPLICATION NUMBER: US/11/072,288
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US/09/462,993
; PRIOR FILING DATE: 2000-04-17
; PRIOR APPLICATION NUMBER: PCT/FR98/01576
; PRIOR FILING DATE: 1998-07-17
; PRIOR APPLICATION NUMBER: FR 97/09152
; PRIOR FILING DATE: 1997-07-18
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patentin Ver. 2.2
; SEQ ID NO 2
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Derived from human papillomavirus, strain
; OTHER INFORMATION: HPV-16, E7 fusion signals of the rabies
; OTHER INFORMATION: glycoprotein, clone E7*TKR.
US-11-072-288-2
```

```
Query Match 92.5%; Score 478; DB 6; Length 185;
Best Local Similarity 92.9%; Pred. No. 5e-49;
Matches 91; Conservative 0; Mismatches 1; Indels 6; Gaps 1;
```

```
Oy 1 MHGDPFLHEYMLDLOPETTDLYXXQLNDSSEDEIDPAGQAEPRAHYIVTFCC 60
Db 26 MHGDPFLHEYMLDLOPETT-----QLNDSSEDEIDPAGQAEPRAHYIVTFCK 79
Oy 61 CDSTLRKCVOSTHVDIRLTEDLLMGTLGIYXPCSQK 98
Db 80 CDSTLRKCVOSTHVDIRLTEDLLMGTLGIYCPICSQK 117
```

```
RESULT 73
US-10-530-253-30
; Sequence 30, Application US/10530253
; Publication No. US20060014926A1
; GENERAL INFORMATION:
; APPLICANT: Casaretti, Maria C.
; APPLICANT: Smith, Larry
; APPLICANT: Jeffrey K. Pullen
; APPLICANT: Susan P. McElhinney
; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
; FILE REFERENCE: 00630/100M137-US2
; CURRENT APPLICATION NUMBER: US/10/530,253
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US2003/031726
; PRIOR FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/415,929
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 30
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Human papillomavirus type 35
US-10-530-253-30
```

```
Query Match 73.8%; Score 381.5; DB 5; Length 99;
Best Local Similarity 73.5%; Pred. No. 9.4e-38;
Matches 72; Conservative 11; Mismatches 14; Indels 1; Gaps 1;
```

```
Oy 1 MHGDPFLHEYMLDLOPETTDLYXXQLNDS-EEDEIDPAGQAEPRAHYIVTFCC 59
Db 1 MHGDPFLHEYMLDLOPETTDLYXXQLNDS-EEDEIDPAGQAEPRAHYIVTFCC 60
Oy 60 KCDSTLRKCVOSTHVDIRLTEDLLMGTLGIYXPCSQK 97
Db 61 KCDSTLRKCVOSTHVDIRLTEDLLMGTLGIYCPICSQK 98
```

```
RESULT 74
US-10-530-253-28
; Sequence 28, Application US/10530253
; Publication No. US20060014926A1
; GENERAL INFORMATION:
; APPLICANT: Casaretti, Maria C.
; APPLICANT: Smith, Larry
; APPLICANT: Jeffrey K. Pullen
; APPLICANT: Susan P. McElhinney
; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
; FILE REFERENCE: 00630/100M137-US2
; CURRENT APPLICATION NUMBER: US/10/530,253
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US2003/031726
; PRIOR FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/415,929
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 28
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Human papillomavirus type 31
US-10-530-253-28
```

```
Query Match 72.0%; Score 372; DB 5; Length 98;
Best Local Similarity 71.1%; Pred. No. 1.3e-36;
Matches 69; Conservative 12; Mismatches 16; Indels 0; Gaps 0;
```

```
Oy 1 MHGDPFLHEYMLDLOPETTDLYXXQLNDSSEDEIDPAGQAEPRAHYIVTFCC 60
Db 1 MHGDPFLHEYMLDLOPETTDLYXXQLNDSSEDEIDPAGQAEPRAHYIVTFCC 60
Oy 61 CDSTLRKCVOSTHVDIRLTEDLLMGTLGIYXPCSQK 97
Db 61 CDSTLRKCVOSTHVDIRLTEDLLMGTLGIYCPICSQK 97
```

```
RESULT 75
US-10-530-253-29
; Sequence 29, Application US/10530253
; Publication No. US20060014926A1
; GENERAL INFORMATION:
; APPLICANT: Casaretti, Maria C.
; APPLICANT: Smith, Larry
; APPLICANT: Jeffrey K. Pullen
; APPLICANT: Susan P. McElhinney
; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
; FILE REFERENCE: 00630/100M137-US2
; CURRENT APPLICATION NUMBER: US/10/530,253
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US2003/031726
; PRIOR FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/415,929
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 29
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Human papillomavirus type 33
US-10-530-253-29
```

```
Query Match 57.1%; Score 295; DB 5; Length 97;
Best Local Similarity 57.7%; Pred. No. 2.3e-27;
Matches 56; Conservative 16; Mismatches 25; Indels 0; Gaps 0;
```

```
Oy 1 MHGDPFLHEYMLDLOPETTDLYXXQLNDSSEDEIDPAGQAEPRAHYIVTFCC 60
Db 1 MHGDPFLHEYMLDLOPETTDLYXXQLNDSSEDEIDPAGQAEPRAHYIVTFCC 60
Oy 61 CDSTLRKCVOSTHVDIRLTEDLLMGTLGIYXPCSQK 97
Db 61 CDSTLRKCVOSTHVDIRLTEDLLMGTLGIYCPICSQK 97
```



Matches 48; Conservative 0; Mismatches 2; Indels 42; Gaps 2;  
Qy 7 TLHEYMDLQPETTDLYXXYQLNDSSEDEIDGPAGQAEPRAHYNIYTFCCCKDSTLR 66  
Db 68 TLHEYMDLQPETTDLYSY-----QAEPRAHYNIYTF----- 100  
Qy 67 LCVQSTHVDIRTLLEDLMGTIGIVPICSQKP 98  
Db 101 -----LTMGTIGIVCPICSQKP 117  
RESULT 80  
US-10-751-845-157  
; Sequence 157, Application US/10751845  
; Publication No. US20050100928A1  
; GENERAL INFORMATION:  
; APPLICANT: Hedley, Mary Lynne  
; APPLICANT: Urban, Robert G.  
; APPLICANT: Chiciz, Roman M.  
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES  
; FILE REFERENCE: 08191-013001  
; CURRENT APPLICATION NUMBER: US/10/751,845  
; CURRENT FILING DATE: 2004-01-05  
; PRIOR APPLICATION NUMBER: US/09/664,225  
; PRIOR FILING DATE: 2000-08-18  
; PRIOR APPLICATION NUMBER: US 60/169,846  
; PRIOR FILING DATE: 1999-12-09  
; PRIOR APPLICATION NUMBER: US 60/154,665  
; PRIOR FILING DATE: 1999-09-16  
; NUMBER OF SEQ ID NOS: 163  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 157  
; LENGTH: 236  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Artificial fusion sequence  
US-10-751-845-157  
Query Match 41.6%; Score 215; DB 5; Length 236;  
Best Local Similarity 52.2%; Pred. No. 3e-17;  
Matches 48; Conservative 0; Mismatches 2; Indels 42; Gaps 2;  
Qy 7 TLHEYMDLQPETTDLYXXYQLNDSSEDEIDGPAGQAEPRAHYNIYTFCCCKDSTLR 66  
Db 68 TLHEYMDLQPETTDLYSY-----QAEPRAHYNIYTF----- 100  
Qy 67 LCVQSTHVDIRTLLEDLMGTIGIVPICSQKP 98  
Db 101 -----LTMGTIGIVCPICSQKP 117  
RESULT 81  
US-10-751-845-158  
; Sequence 158, Application US/10751845  
; Publication No. US20050100928A1  
; GENERAL INFORMATION:  
; APPLICANT: Hedley, Mary Lynne  
; APPLICANT: Urban, Robert G.  
; APPLICANT: Chiciz, Roman M.  
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES  
; FILE REFERENCE: 08191-013001  
; CURRENT APPLICATION NUMBER: US/10/751,845  
; CURRENT FILING DATE: 2004-01-05  
; PRIOR APPLICATION NUMBER: US/09/664,225  
; PRIOR FILING DATE: 2000-08-18  
; PRIOR APPLICATION NUMBER: US 60/169,846  
; PRIOR FILING DATE: 1999-12-09  
; PRIOR APPLICATION NUMBER: US 60/154,665  
; PRIOR FILING DATE: 1999-09-16  
; NUMBER OF SEQ ID NOS: 163  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 158

; LENGTH: 237  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Artificial fusion sequence  
US-10-751-845-158  
Query Match 41.6%; Score 215; DB 5; Length 237;  
Best Local Similarity 52.2%; Pred. No. 3e-17;  
Matches 48; Conservative 0; Mismatches 2; Indels 42; Gaps 2;  
Qy 7 TLHEYMDLQPETTDLYXXYQLNDSSEDEIDGPAGQAEPRAHYNIYTFCCCKDSTLR 66  
Db 69 TLHEYMDLQPETTDLYSY-----QAEPRAHYNIYTF----- 101  
Qy 67 LCVQSTHVDIRTLLEDLMGTIGIVPICSQKP 98  
Db 102 -----LTMGTIGIVCPICSQKP 118  
RESULT 82  
US-10-751-845-160  
; Sequence 160, Application US/10751845  
; Publication No. US20050100928A1  
; GENERAL INFORMATION:  
; APPLICANT: Hedley, Mary Lynne  
; APPLICANT: Urban, Robert G.  
; APPLICANT: Chiciz, Roman M.  
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES  
; FILE REFERENCE: 08191-013001  
; CURRENT APPLICATION NUMBER: US/10/751,845  
; CURRENT FILING DATE: 2004-01-05  
; PRIOR APPLICATION NUMBER: US/09/664,225  
; PRIOR FILING DATE: 2000-08-18  
; PRIOR APPLICATION NUMBER: US 60/169,846  
; PRIOR FILING DATE: 1999-12-09  
; PRIOR APPLICATION NUMBER: US 60/154,665  
; PRIOR FILING DATE: 1999-09-16  
; NUMBER OF SEQ ID NOS: 163  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 160  
; LENGTH: 261  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Artificial fusion sequence  
US-10-751-845-160  
Query Match 41.6%; Score 215; DB 5; Length 261;  
Best Local Similarity 52.2%; Pred. No. 3.3e-17;  
Matches 48; Conservative 0; Mismatches 2; Indels 42; Gaps 2;  
Qy 7 TLHEYMDLQPETTDLYXXYQLNDSSEDEIDGPAGQAEPRAHYNIYTFCCCKDSTLR 66  
Db 93 TLHEYMDLQPETTDLYSY-----QAEPRAHYNIYTF----- 125  
Qy 67 LCVQSTHVDIRTLLEDLMGTIGIVPICSQKP 98  
Db 126 -----LTMGTIGIVCPICSQKP 142  
RESULT 83  
US-10-530-253-32  
; Sequence 32, Application US/10530253  
; Publication No. US20060014926A1  
; GENERAL INFORMATION:  
; APPLICANT: Casasetti, Maria C.  
; APPLICANT: Smith, Larry  
; APPLICANT: Jeffrey K. Pullen  
; APPLICANT: Susan P. McElhinney  
; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS  
; FILE REFERENCE: 00630/100M17-US2  
; CURRENT APPLICATION NUMBER: US/10/530,253

```

; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US2003/031726
; PRIOR FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/415,929
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Human papillomavirus type 45
US-10-530-253-32

Query Match          41.2%; Score 213; DB 5; Length 106;
Best Local Similarity 43.8%; Pred. No. 1.9e-17;
Matches 46; Conservative 15; Mismatches 32; Indels 12; Gaps 3;

QY 1 MHGDTPLHEHYMLDLOPET---TDLYXXYQXQNDSSSEEDIDG-----PAGQAEPPRAH 50
DB 1 MHGPKATLQDVIHLLEPQNEIPVDLCHQQLSDSEENDEIDGVNHQHLPARRAEPOR-- 59
51 HNYIVTFCKCDSTLRKCVQSTHVDIRTLBDMGLGIVXPICS 95
60 -HKILCVCKCKDGRIRIELTVESSADLRAFLQQLFLNTLSFVCPWCASQ 103

RESULT 84
US-10-433-091-4
; Sequence 4, Application US/10433091
; Publication No. US20040101533A1
; GENERAL INFORMATION:
; APPLICANT: MULLER, RAINER
; APPLICANT: NIELAND, JOHN
; APPLICANT: GABELSBERGER, JOSEF
; APPLICANT: HERBST, RUTH
; TITLE OF INVENTION: MEDICAMENT FOR PREVENTING OR TREATING TUMORS CAUSED BY
; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS TYPE 18
; FILE REFERENCE: 037067/0115
; CURRENT APPLICATION NUMBER: US/10/433,091
; CURRENT FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: PCT/EP01/14038
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: DE 100 59 630.4
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Human papillomavirus type 18
US-10-433-091-4

Query Match          39.2%; Score 202.5; DB 4; Length 105;
Best Local Similarity 39.6%; Pred. No. 3.5e-16;
Matches 42; Conservative 21; Mismatches 32; Indels 11; Gaps 3;

QY 1 MHGDTPLHEHYMLDLOPET---TDLYXXYQXQNDSSSEEDIDG-----PAGQAEPPRAH 51
DB 1 MHGPKATLQDVIHLLEPQNEIPVDLCHQQLSDSEENDEIDGVNHQHLPARRAEPOR-- 58
52 YNIVTFCKCDSTLRKCVQSTHVDIRTLBDMGLGIVXPICSQK 97
59 HTMLCMCKCKCEARIKLVNESSADLRAFLQQLFLNTLSFVCPWCASQ 104

RESULT 85
US-10-530-253-27
; Sequence 27, Application US/10530253
; Publication No. US20060014926A1
; GENERAL INFORMATION:
; APPLICANT: Casasetti, Maria C.
; APPLICANT: Smith, Larry
; APPLICANT: Jeffrey K. Pullen
```

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; APPLICANT: Susan P. McElhinney
; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
; FILE REFERENCE: 00630/100M137-US2
; CURRENT APPLICATION NUMBER: US/10/530,253
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US2003/031726
; PRIOR FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/415,929
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Human papillomavirus type 18
US-10-530-253-27

Query Match          39.2%; Score 202.5; DB 5; Length 105;
Best Local Similarity 39.6%; Pred. No. 3.5e-16;
Matches 42; Conservative 21; Mismatches 32; Indels 11; Gaps 3;

QY 1 MHGDTPLHEHYMLDLOPET---TDLYXXYQXQNDSSSEEDIDG-----PAGQAEPPRAH 51
DB 1 MHGPKATLQDVIHLLEPQNEIPVDLCHQQLSDSEENDEIDGVNHQHLPARRAEPOR-- 58
52 YNIVTFCKCDSTLRKCVQSTHVDIRTLBDMGLGIVXPICSQK 97
59 HTMLCMCKCKCEARIKLVNESSADLRAFLQQLFLNTLSFVCPWCASQ 104

RESULT 86
US-10-000-903-19
; Sequence 19, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Benchelkn, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-19

Query Match          39.0%; Score 201.5; DB 4; Length 227;
Best Local Similarity 39.6%; Pred. No. 1.2e-15;
Matches 42; Conservative 20; Mismatches 33; Indels 11; Gaps 3;

QY 1 MHGDTPLHEHYMLDLOPET---TDLYXXYQXQNDSSSEEDIDG-----PAGQAEPPRAH 51
DB 114 MHGPKATLQDVIHLLEPQNEIPVDLCHQQLSDSEENDEIDGVNHQHLPARRAEPOR-- 171
52 YNIVTFCKCDSTLRKCVQSTHVDIRTLBDMGLGIVXPICSQK 97
172 HTMLCMCKCKCEARIKLVNESSADLRAFLQQLFLNTLSFVCPWCASQ 217

RESULT 87
US-10-899-771-19
; Sequence 19, Application US/10899771
; Publication No. US20050031638A1
```

```
GENERAL INFORMATION:
APPLICANT: Dalemans, Wilfried L.J.
TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
FILE REFERENCE: B45124
CURRENT FILING DATE: 2004-07-27
PRIOR APPLICATION NUMBER: US/10/899,771
PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: PCT/EP98/08563
PRIOR FILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: GB 9727262.9
PRIOR FILING DATE: 1997-12-24
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 19
LENGTH: 227
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Chimeric protein (protein D from Haemophilus
OTHER INFORMATION: Influenzae B and mutated E7 from Human papilloma
OTHER INFORMATION: virus type 18)
US-10-899-771-19
```

```
Query Match          39.0%; Score 201.5; DB 5; Length 227;
Best Local Similarity 39.6%; Pred. No. 1.2e-15;
Matches 42; Conservative 20; Mismatches 33; Indels 11; Gaps 3;
```

```
Qy 1 MHGDPPLHEMYMLDLOPET---TDLYXXYXQINDSSEEDIDG-----PAGQAEPPRAH 51
Db 114 MHGKATLQDVLHLEPQNEIPVDLGHQQLSDSEENDEIDGVNHQHLFARRAEPR-- 171
```

```
Qy 52 YNIVTFCCKDSTRLCVQSTHVDIRLTEDLMGTGIVXPISOK 97
Db 172 HTMLCMCKCEARIELVVESSADDLRAFOQLFNTLSFVCPWCASQ 217
```

```
RESULT 88
US-10-000-903-23
Sequence 23, Application US/10000903
Publication No. US20020182221A1
GENERAL INFORMATION:
APPLICANT: Bruck, Claudine
APPLICANT: Delisse, Anne-Marie Eva Bernarde
APPLICANT: Gerard, Catherine Marie Ghislaine
APPLICANT: Lombardo-Bencheikh, Angela
TITLE OF INVENTION: Vaccine
FILE REFERENCE: B45107
CURRENT APPLICATION NUMBER: US/10/000,903
CURRENT FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: GB 9717953.5
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 23
LENGTH: 383
TYPE: PRT
ORGANISM: Homo sapien
US-10-000-903-23
```

```
Query Match          38.8%; Score 200.5; DB 4; Length 383;
Best Local Similarity 39.6%; Pred. No. 3e-15;
Matches 42; Conservative 20; Mismatches 33; Indels 11; Gaps 3;
```

```
Qy 1 MHGDPPLHEMYMLDLOPET---TDLYXXYXQINDSSEEDIDG-----PAGQAEPPRAH 51
Db 270 MHGKATLQDVLHLEPQNEIPVDLGHQQLSDSEENDEIDGVNHQHLFARRAEPR-- 327
```

```
Qy 52 YNIVTFCCKDSTRLCVQSTHVDIRLTEDLMGTGIVXPISOK 97
Db 328 HTMLCMCKCEARIELVVESSADDLRAFOQLFNTLSFVCPWCASQ 373
```

```
RESULT 89
US-10-899-771-23
Sequence 23, Application US/10899771
Publication No. US20050031638A1
GENERAL INFORMATION:
APPLICANT: Dalemans, Wilfried L.J.
APPLICANT: Gerard, Catherine Marie Ghislaine
TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
FILE REFERENCE: B45124
CURRENT APPLICATION NUMBER: US/10/899,771
CURRENT FILING DATE: 2004-07-27
PRIOR APPLICATION NUMBER: US/09/581,976
PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: PCT/EP98/08563
PRIOR FILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: GB 9727262.9
PRIOR FILING DATE: 1997-12-24
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 23
LENGTH: 383
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Chimeric protein (protein D from Haemophilus
OTHER INFORMATION: Influenzae B and B6E7 fusion from Human papilloma
OTHER INFORMATION: virus type 18)
US-10-899-771-23
```

```
Query Match          38.8%; Score 200.5; DB 5; Length 383;
Best Local Similarity 39.6%; Pred. No. 3e-15;
Matches 42; Conservative 20; Mismatches 33; Indels 11; Gaps 3;
```

```
Qy 1 MHGDPPLHEMYMLDLOPET---TDLYXXYXQINDSSEEDIDG-----PAGQAEPPRAH 51
Db 270 MHGKATLQDVLHLEPQNEIPVDLGHQQLSDSEENDEIDGVNHQHLFARRAEPR-- 327
```

```
Qy 52 YNIVTFCCKDSTRLCVQSTHVDIRLTEDLMGTGIVXPISOK 97
Db 328 HTMLCMCKCEARIELVVESSADDLRAFOQLFNTLSFVCPWCASQ 373
```

```
RESULT 90
US-10-800-023-28
Sequence 28, Application US/10800023
Publication No. US20040258688A1
GENERAL INFORMATION:
APPLICANT: Steinman, Ralph
APPLICANT: Nussenzweig, Michel
APPLICANT: Hawiger, Daniel
APPLICANT: Bonifaz, Laura
TITLE OF INVENTION: Enhanced Antigen Delivery and Modulation
TITLE OF INVENTION: of the Immune Response Therefrom
FILE REFERENCE: 600-1-081CONCIP1
CURRENT APPLICATION NUMBER: US/10/800,023
CURRENT FILING DATE: 2004-03-14
PRIOR APPLICATION NUMBER: 09/925,284
PRIOR FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 09/586,704
PRIOR FILING DATE: 2000-06-05
PRIOR APPLICATION NUMBER: PCT/US96/01383
PRIOR FILING DATE: 1996-01-31
PRIOR APPLICATION NUMBER: 08/381,528
PRIOR FILING DATE: 1995-01-31
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 28
```

```

; LENGTH: 105      ..
; TYPE: prt
; ORGANISM: human papilloma virus E7 protein
US-10-800-023-28

```

Query Match	38.4%	Score 198.5;	DB 5;	Length 105;
Best Local Similarity	39.6%	Pred. No. 1,1e-15;		
Matches 42;	Conservative 20;	Mismatches 33;	Indels 11;	Gaps 3,

```

QY      1 MHGDTPTLHEVNLADLPET--TDLYXXHQNDSEEDSDIG-----PAGQAEPPRAH 51
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      1 MHGPRATLDIYLAHPQNEIPVDLLCHEQLSDSEENDEIDGVNHQHLPARAEPPQR-- 58

```

```

Oy      52 YNIITPCCCKDSTLRLCVQSHVDIRTEEDLMGLIIVXPICSQK 97
          : :: ||| :: : | : | : | : | : | : | : | :
Db      59 HTMLCMCKCEARIELVVESSADDLRAFGQLFLKTLISFVCPWCASQ 104

```

RESULT 91  
US-11-041-893-101

```

? APPLICANT: Mahataas, Gregory G.
? TITLE OF INVENTION: COMPOSITIONS COMPRISING IMMUNE RESPONSE
? TITLE OF INVENTION: ALTERING AGENTS AND METHODS OF USE
? FILE REFERENCE: 100123.401
? CURRENT APPLICATION NUMBER: US/11/041,893
? CURRENT FILING DATE: 2005-01-24
? PRIOR APPLICATION NUMBER: US 60/616,855
? PRIOR FILING DATE: 2004-10-06
? PRIOR APPLICATION NUMBER: US 60/538,713
? PRIOR FILING DATE: 2004-01-23
? NUMBER OF SEQ ID NOS: 295
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 101
? LENGTH: 35
? TYPE: PRF
? ORGANISM: Human Papillomavirus E7
? US-11-041-893-101

```

Query Match	37.9%	Score 196;	DB 6;	Length 35;
Best Local Similarity	100.0%	Pred. No. 5.5e-16;		
Matches	35;	Conservative	0;	Mismatches 0;
			Indels	0;
			Gaps	0;

Qy	Db
43	1
GOAEBDRAHYNIVTECKCKDSTLRACYOSTHVDIR	GOAEBDRAHYNIVTECKCKDSTLRACYOSTHVDIR
77	35

```

1 RESULT 92
2 US-10-530-253-37
3
4 Sequence 37, Application US/10530253
5 Publication No. US20060014926A1
6
7 GENERAL INFORMATION:
8
9 APPLICANT: Cassetti, Maria C.
10 APPLICANT: Smith, Larry
11 APPLICANT: Jeffrey K. Pullen
12 APPLICANT: Susan P. McBibney
13
14 TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
15
16 FILE REFERENCE: 00630/100M137-US2
17
18 CURRENT APPLICATION NUMBER: US/10/530,253
19
20 CURRENT FILING DATE: 2005-04-04
21
22 PRIOR APPLICATION NUMBER: PCT/US2003/031726
23
24 PRIOR FILING DATE: 2003-10-02
25
26 PRIOR APPLICATION NUMBER: US 60/415,929
27
28 PRIOR FILING DATE: 2002-10-03
29
30 NUMBER OF SEQ ID NOS: 65
31
32 SOFTWARE: PatentIn version 3.1.1
33
34 SEQ ID NO 37
35
36 LENGTH: 107
37
38 TYPE: PRT
39
40 ORGANISM: Human papillomavirus type 59

```

US-10-530-253-37

Query Match	37.8%;	Score 195.5;	DB 5;	Length 107;
Best Local Similarity	43.4%;	Pred. No. 2.5e-15;		
Matches	46;	Conservative	17;	Mismatches 30;
				Indels 13;
				Gaps 4

```
QY 1 MHGDTPTLHEXYMLDLP--ETTDLYXXQL--NDSSEBEDEIGP-----AGQAPDR 45
    ||| ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1 MHGRATLCQIVLDLEPQNYEVDVCEQQLPSDSENEKDEPDGVNHPLLARRAEPQR 60
```

```
QY      50 AHNYIVTFCCKDSTLRCLVQSTHVDIRLTLEDLMGLGI VPICS   95  
        :||| |||::|:||::|:||| |||::|:||:  
Db      61 --HNIVCVCCKCNNGQLGVETVSQDGRLAQGLENDTLTFVCPLCA 100
```

RESULT 93  
US-10-472-724-8  
; Sequence 8, Application US/10472724

```

? APPLICANT: Cid-Arregui, Angel
? APPLICANT: Zur Hausen, Harald
? TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination
? FILE REFERENCE: 4121-154
? CURRENT APPLICATION NUMBER: US/10/472,724
? CURRENT FILING DATE: 2003-09-17
? PRIOR APPLICATION NUMBER: PCT/EP02/03271
? PRIOR FILING DATE: 2002-03-22
? PRIOR APPLICATION NUMBER: EP 01107271.7
? PRIOR FILING DATE: 2001-03-23
? NUMBER OF SEQ ID NOS: 27
? SOFTWARE: PatentIn version 3.2
? SEQ ID NO 8
? LENGTH: 118
? TYPE: PRT
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Synthetic Construct
? US-10-472-724-8

```

Query Match	37.8%;	Score 195.5;	DB 4;	Length 118;
Best Local Similarity	39.0%;	Pred. No. 2.8e-15;		
Matches 41; Conservative	20;	Mismatches 33;	Indels 11;	Gaps 3

```

QY      2 HGDTPTLHEWMLDQET---TDLYXXQXQNDSSSEEDIDG-----PAGQAEPPDRAHY 5
      ||| : : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
DB      7 HGRKATLQDLYLHLRPNQEPVLLCHEQLSDSEENDELDGVNHOHLPARAEPPOR--H 6

```

Oy 53 NIVTFCKCKDSTIRLCVOSTHVDIRTLEDLGMGTGLVXPICSOÄ 97  
:: ||| :: : | :: : | :: : | :: : | :: :  
Db 65 TMLCMCKCKEARIELVVESSADDIRAFOOLFINTTSEFCPCWCASO 109

RESULT 94  
 US-10-000-903-16  
 Sequence 16, Application US/10000903  
 Publication No. US20020182221A1  
 GENERAL INFORMATION:  
 APPLICANT: Bruck, Claudine  
 APPLICANT: Cabezon Silva, Teresa  
 APPLICANT: Delisse, Anne-Marie Eva Fernande  
 APPLICANT: Gerard, Catherine Marie Christiane  
 APPLICANT: Lombardo-Benckelkh, Angela  
 TITLE OF INVENTION: Vaccine  
 FILE REFERENCE: B45107  
 CURRENT APPLICATION NUMBER: US/10/000,903  
 CURRENT FILING DATE: 2001-10-01  
 PRIOR APPLICATION NUMBER: PCT/EP99/05285  
 PRIOR FILING DATE: 1998-08-17  
 PRIOR APPLICATION NUMBER: GB 97117953.5  
 PRIOR FILING DATE: 1997-08-22  
 NUMBER OF SEQ ID NOS: 23  
 SOFTWARE: FASTSEQ for Windows Version 3.0

```

; SEQ ID NO 16
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-16

```

Query Match	37.2%;	Score 192.5;	DB 4;	Length 227;
Best Local Similarity	38.7%;	Pred. No. 1.4e-14;		
Matches	41;	Conservative	20;	Mismatches 34;
			Indels	11;
			Gaps	3;

```
Oy      1 MHGDPPTLHEVMDLOPET---TDLYXXYXQLANDSSEEDDEIDG-----PAGQAEPPDKAH 51
        ||| | : : : : | : ||| | ||| | | : ||| |
Db     114 MHGPXATLDIVLHLEPQNELPVDDLCHEQLSDEEENDEIDEVNHQHLPARRAEPQR-- 177
```

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OY      52 YNIVFPCKCDSTRLCQSTHVDIRTEDLMLGTLGIVXPICSOX 97
      : :: ||| :: : | :: : | :: : | :: : | :: :
DB      172 HTMLCMCKCEARIELVVESSADDLRAFOQLPLNTLSFVCPWCASQ 217

```

RESULT 95  
US-10-899-771-16  
; Sequence 16, Application US/108997711

: GENERAL INFORMATION: Wilfrid L.J.  
 : APPLICANT: Dalemans, Gerard  
 : APPLICANT: Catherine Marie Ghislaine  
 : TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins  
 : TITLE OF INVENTION: and Fusion Proteins Adjuncted with a CpG Oligonucleotide  
 : FILE REFERENCE: B45124  
 : CURRENT APPLICATION NUMBER: US/10/899,771

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?      LENGTH: 227
?      TYPE: PRT
?      ORGANISM: Artificial Sequence
?      FEATURE:
?      OTHER INFORMATION: Chimeraic protein (protein D from Haemophilus
?      OTHER INFORMATION: influenzae B and E7 from Human papilloma virus
?      OTHER INFORMATION: 18)
?      OS-10-899-771-16

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Query Match	37.2%	Score 192.5;	DB 5;	length 227;
Best Local Similarity	38.7%	Pred. No. 1.4e-14;		
Matches 41; Conservative	20;	Mismatches 34;	Indels 11;	Gaps 3;

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OY      1 MHGDTPTLHEYMLOLPET---TDLYXXQLNDSSEEDBEIDG-----PAGQAEPPDAH 51
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DB      114 MHGPKATLQDVLHLEPQNEIPVDLLCHEQLSSSEENDEIDENVNQHLPARRAEPR-- 17
        |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
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**Oy**     **52** YNIVPECKCDSTRLCVQSHVDIRTEDLLMGLGIYXPICSOX 97  
      :: ||| :: : | : : : | | : :  
**Db**     **172** HTMLCMCKCEARIELVVESSADDLRAFOQLPLNTLSFVCPCWCAO 217

RESULT 96  
US-10-530-253-35  
; Sequence 35, Application US/10530253

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: GENERAL INFORMATION:
: APPLICANT: Cassecci, Maria C.
: APPLICANT: Smith, Larry
: APPLICANT: Jeffrey K. Pullen
: APPLICANT: Susan P. McElhiney
: TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
: FILE REFERENCE: 00630/100M137-US2

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1 CURRENT APPLICATION NUMBER: US/10/530,253
2
3 CURRENT FILING DATE: 2005-04-04
4
5 PRIOR APPLICATION NUMBER: PCT/US2003/031722
6
7 PRIOR FILING DATE: 2003-10-02
8
9 PRIOR APPLICATION NUMBER: US 60/445,929
10
11 PRIOR FILING DATE: 2002-10-03
12
13 NUMBER OF SEQ ID NOS: 65
14
15 SOFTWARE: Patentin version 3.1
16
17 SEQ ID NO 35
18
19 LENGTH: 105
20
21 TYPE: PRT
22
23 ORGANISM: Human papillomavirus type 56
24
25 US-10-530-253-35

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Query Match	34.5%;	Score 178.5;	DB 5;	Length 105;
Best Local Similarity	-40.8%;	Pred. No. 2.7e-13;		
Matches 42;	Conservative 17;	Mismatches 35;	Indels 9;	Gaps 3

QY 1 MHGDLPTLHEFWLDLPET-TLYXXYXQNDSSSEDELDGPPAGAEPRDRAH-----Y 52

Db 1 MHGKVPRLQDVVLPTQTEIDLQCNEL-DSSDEDEDEVDNHLQERPQQAQAKHTCY 55

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QY      53 NIVTFCCCKDSTLRLCVQSTHVDIRLTLEDLLMGTLGIVPIC 95
          |  ||:|  ::|  :|||  |::|  ||||  |  :  ||:
Db      60 LIHVPCCECKFVQLDIQSTKEDLRVQQLMGTALVTVCPLCA 102

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RESULT 97  
US-10-530-253-33

Sequence, J3, APPLICATION: US/710530253  
Publication No. US200600014926A1  
GENERAL INFORMATION:  
APPLICANT: Casasetti, Maria C.  
APPLICANT: Smith, Larry  
APPLICANT: Jeffrey K. Pullen  
APPLICANT: Susan P. McElhinney  
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS

```

CURRENT APPLICATION NUMBER:US/10/530,253
CURRENT FILING DATE: 2005-04-04
PRIORITY APPLICATION NUMBER: PCT/US2003/031722
PRIORITY FILING DATE: 2003-10-02
PRIORITY APPLICATION NUMBER: US 60/415,929
PRIORITY FILING DATE: 2002-10-03
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PatentIn version 3.1
SEQ ID NO 33
LENGTH: 101
TYPE: PR1
ORGANISM: Human papillomavirus type 51
US-10-530-253-33

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Query Match	34.4%	Score 178;	DB 5;	Length 101;
Best Local Similarity	41.0%	Pred. No. 2.9e-13;		
Matches	41;	Conservative	16;	Mismatches 37;
			Indels	6;
			Gaps	3

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Oy      1 MHGDTPTLHEMYLQLQPET-IDLYXXYYQLNDSSSEEDIEDGACAGAEPPDRAH-----XNIV 55
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Db      1 MRGNVPQLKDVVHLTPQTEILDQCYELF-DSSEEDEDVDNMRDQLPERRAGQATCYRIE 55

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Oy 56 TPCKCKDSTLRLCVQSTHVDIRTELDLMGTLGIVPICS 95  
||:||::|::|::|::|::|:  
Db 60 APCCRCSVVQLAVESSGDTLRVVQMLMGEISLVCPCA 99

RESULT 98  
US-10-530-253-31  
; Sequence 31, Application US/10530253

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; GENERAL INFORMATION:
; APPLICANT: Cassetti, Maria C.
; APPLICANT: Smith, Larry
; APPLICANT: Jeffrey K. Pullen

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; APPLICANT: Susan P. McElhiney
; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
; FILE REFERENCE: 00630/100M137-US2
; CURRENT APPLICATION NUMBER: US/10/530,253
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US2003/031726
; PRIOR FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/415,929
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Human papillomavirus type 39
; US-10-530-253-31

Query Match          32.9%; Score 170; DB 5; Length 109;
Best Local Similarity 39.1%; Pred. No. 3e-12;
Matches 43; Conservative 16; Mismatches 31; Indels 20; Gaps 4;

QY 1 MHGDTPLHRYMLDLP-----ETDLYXXYQLNDSSEEDIDGP-----AGQA 45
DB 1 MRGKPTLQELIVDLCPYNEIQVDIVCHQLGSES---EDEIDEPDAVNHQQLARRD 57

QY 46 EPPRAHNYITFCCKDSTLRCLVQSTHVDIRLTEDLIMGTGIYXPICS 95
DB 58 EPQR--HTIQSCCKNNITLQVLEASRDPLRQLQFLMDSLGFVCPWCA 105

RESULT 99
US-10-530-253-38
; Sequence 38; Application US/10530253
; Publication No. US20060014926A1
; GENERAL INFORMATION:
; APPLICANT: Casaretti, Maria C.
; APPLICANT: Jeffrey K. Pullen
; APPLICANT: Susan P. McElhiney
; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
; FILE REFERENCE: 00630/100M137-US2
; CURRENT APPLICATION NUMBER: US/10/530,253
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US2003/031726
; PRIOR FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/415,929
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Human papillomavirus type 68
; US-10-530-253-38

Query Match          31.8%; Score 164.5; DB 5; Length 110;
Best Local Similarity 34.0%; Pred. No. 1.4e-11;
Matches 36; Conservative 20; Mismatches 39; Indels 11; Gaps 2;

QY 1 MHGDTPLHRYMLDLP-----ETDLYXXYQLNDSSEEDIDGPAGQAE-----PDR 49
DB 1 MRGKPTLQELIVDLCPYNEIQVDIVCHQLGSDSDIDEPDAVNHQQLARRDEQ 60

QY 50 AHYNIYVFCCKDSTLRCLVQSTHVDIRLTEDLIMGTGIYXPICS 95
DB 61 QBRRIQGLCKCKNNKALQVLEASRDNLRTLQQLFMDSLNFCPCWCA 106

RESULT 100
US-10-475-203A-14
; Sequence 14; Application US/10475203A
; Publication No. US20040241177A1
; GENERAL INFORMATION:
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; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND USES THEREFOR
; FILE REFERENCE: E1679-00002
; CURRENT APPLICATION NUMBER: US/10/475,203A
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: PCT/AU02/00486
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: AU PP4468/01
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 517
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide encoded by SEQ ID NO: 13
; US-10-475-203A-14

Query Match          30.2%; Score 156; DB 5; Length 517;
Best Local Similarity 40.9%; Pred. No. 9.7e-10;
Matches 36; Conservative 13; Mismatches 33; Indels 6; Gaps 3;

QY 16 QPETDLY---XXYQLNDSSEEDIDG--PAGQ--AEPDRAHNYITFCCKDSTLRCLV 69
DB 429 EKEKPPYKULSTWEVNLKEKFSSELDQYPLGKPKFLQSHGHFOIYVCCCGCSNRLVV 488

QY 70 QSTHVDIRLTEDLIMGTGIYXPICSQK 97
DB 489 QCTETDIRVQQLLGTINIVCICAPK 516
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Job time : 103.936 secs

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GenCore version 5.1.8  
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OM protein - protein search, using sw model

Run on: May 27, 2006, 05:33:42 ; Search time 6.69076 Seconds

(Without alignments)  
163.129 Million cell updates/sec

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Searched: 56051 seqs, 11137335 residues

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	511	98.8	98	US-10-511-814-11	Sequence 11, Appli
3	478	92.5	92	US-10-512-190-2	Sequence 2, Appli
4	62.5	12.1	148	US-11-293-697-2678	Sequence 2678, Ap
5	60.5	11.7	1287	US-10-505-928-341	Sequence 341, App
6	60	11.6	466	US-11-293-697-4473	Sequence 4473, Ap
7	58.5	11.3	462	US-10-953-349-39521	Sequence 39521, A
8	58.5	11.3	616	US-10-953-349-39520	Sequence 39520, A
9	58.5	11.3	646	US-10-953-349-39519	Sequence 39519, A
10	57.5	11.1	233	US-10-953-349-27426	Sequence 27426, A
11	57.5	11.1	296	US-10-953-349-27425	Sequence 27425, A
12	57.5	11.1	353	US-10-953-349-27424	Sequence 27424, A
13	57.5	11.1	446	US-10-953-349-39537	Sequence 39537, A
14	57.5	11.1	464	US-10-953-349-39536	Sequence 39536, A
15	57.5	11.1	499	US-10-953-349-3781	Sequence 3781, Ap
16	57.5	11.1	552	US-10-953-349-3780	Sequence 3780, Ap
17	57.5	11.1	618	US-10-953-349-39535	Sequence 39535, A
18	57	11.0	300	US-11-242-111-23	Sequence 23, Appli
19	57	11.0	314	US-09-981-845-1	Sequence 1, Appli
20	55.5	10.7	286	US-10-953-349-23406	Sequence 23406, A
21	55.5	10.7	293	US-10-953-349-23405	Sequence 23405, A
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23	55.5	10.7	544	US-10-953-349-5451	Sequence 5451, Ap
24	55.5	10.7	574	US-10-953-349-5450	Sequence 5450, Ap
25	55.5	10.7	876	US-10-468-193-32	Sequence 32, Appli

26	54.5	10.5	58	US-10-525-126-177	Sequence 177, App
27	54.5	10.5	88	US-10-525-126-215	Sequence 215, App
28	54.5	10.5	88	US-10-525-126-174	Sequence 174, App
29	54.5	10.5	88	US-10-525-126-175	Sequence 175, App
30	54.5	10.5	88	US-10-525-126-212	Sequence 212, App
31	54.5	10.5	88	US-10-525-126-213	Sequence 213, App
32	54.5	10.5	88	US-10-525-126-284	Sequence 284, App
33	54.5	10.5	88	US-10-525-126-299	Sequence 299, App
34	54.5	10.5	88	US-10-525-126-300	Sequence 300, App
35	54.5	10.5	255	US-10-953-349-20549	Sequence 20549, A
36	54.5	10.5	259	US-10-953-349-20548	Sequence 20548, A
37	54.5	10.5	489	US-11-293-697-2988	Sequence 2988, Ap
38	54	10.4	278	US-10-953-349-1526	Sequence 1526, Ap
39	54	10.4	323	US-10-518-114-1	Sequence 1, Appli
40	54	10.4	630	US-10-953-349-35808	Sequence 35808, A
41	54	10.4	676	US-10-953-349-35807	Sequence 35807, A
42	53.5	10.3	533	US-10-953-349-31198	Sequence 31198, A
43	53.5	10.3	639	US-10-953-349-23351	Sequence 23351, A
44	53.5	10.3	656	US-10-953-349-23350	Sequence 23350, A
45	53.5	10.3	664	US-10-953-349-23349	Sequence 23349, A
46	53	10.3	253	US-10-953-349-34172	Sequence 34172, A
47	53	10.3	283	US-10-953-349-34171	Sequence 34171, A
48	53	10.3	286	US-10-953-349-34170	Sequence 34170, A
49	53	10.3	377	US-10-953-349-12021	Sequence 12021, A
50	53	10.3	423	US-11-293-697-3292	Sequence 3292, Ap
51	53	10.3	749	US-10-505-928-443	Sequence 443, App
52	52.5	10.2	109	US-10-953-349-15959	Sequence 15959, A
53	52.5	10.2	275	US-11-293-697-3886	Sequence 3886, Ap
54	52.5	10.2	288	US-10-953-349-11222	Sequence 11222, A
55	52.5	10.2	1912	US-10-511-937-2561	Sequence 2561, Ap
56	52	10.1	90	US-10-525-126-296	Sequence 296, App
57	52	10.1	97	US-10-953-349-15960	Sequence 15960, A
58	52	10.1	324	US-10-953-349-21799	Sequence 21799, A
59	52	10.1	348	US-10-953-349-21798	Sequence 21798, A
60	52	10.1	352	US-10-953-349-21797	Sequence 21797, A
61	52	10.1	357	US-10-953-349-31968	Sequence 31968, A
62	52	10.1	405	US-10-953-349-31967	Sequence 31967, A
63	52	10.1	475	US-10-953-349-31966	Sequence 31966, A
64	52	10.1	507	US-10-514-462-4	Sequence 4, Appli
65	52	10.1	634	US-11-293-697-3174	Sequence 3174, Ap
66	52	10.1	1067	US-10-514-462-2	Sequence 2, Appli
67	51.5	10.0	61	US-10-525-126-302	Sequence 302, App
68	51.5	10.0	145	US-10-953-349-6871	Sequence 6871, Ap
69	51.5	10.0	158	US-10-953-349-6870	Sequence 6870, Ap
70	51.5	10.0	159	US-11-297-160-7	Sequence 7, Appli
71	51.5	10.0	315	US-10-953-349-24841	Sequence 24841, A
72	51.5	10.0	335	US-10-953-349-24840	Sequence 24840, A
73	51.5	10.0	500	US-11-121-154-195	Sequence 195, App
74	51	9.9	155	US-10-953-349-22956	Sequence 22956, A
75	51	9.9	171	US-10-953-349-22955	Sequence 22955, A
76	51	9.9	549	US-10-953-349-16871	Sequence 16871, A
77	51	9.9	557	US-10-953-349-16870	Sequence 16870, A
78	51	9.9	585	US-10-953-349-16869	Sequence 16869, A
79	51	9.9	744	US-11-293-697-4398	Sequence 4398, App
80	50.5	9.8	176	US-10-953-349-13813	Sequence 13813, A
81	50.5	9.8	218	US-10-953-349-23159	Sequence 23159, A
82	50.5	9.8	225	US-10-953-349-36029	Sequence 36029, A
83	50.5	9.8	333	US-10-953-349-23158	Sequence 23158, A
84	50.5	9.8	359	US-10-953-349-36028	Sequence 36028, A
85	50.5	9.8	382	US-10-953-349-23157	Sequence 23157, A
86	50	9.7	57	US-10-953-349-9399	Sequence 9399, App
87	50	9.7	81	US-10-953-349-9398	Sequence 9398, App
88	50	9.7	205	US-10-953-349-27383	Sequence 27383, App
89	50	9.7	211	US-10-953-349-38511	Sequence 38511, A
90	50	9.7	231	US-10-953-349-27382	Sequence 27382, App
91	50	9.7	272	US-10-511-937-2618	Sequence 2618, App
92	50	9.7	293	US-10-953-349-12546	Sequence 12546, App
93	50	9.7	343	US-10-953-349-38510	Sequence 38510, A
94	50	9.7	448	US-10-953-349-8835	Sequence 8835, App
95	50	9.7	476	US-10-953-349-8834	Sequence 8834, App
96	50	9.7	516	US-10-953-349-8833	Sequence 8833, App
97	50	9.7	527	US-10-953-349-13398	Sequence 13398, A
98	50	9.7	548	US-10-953-349-13397	Sequence 13397, A

99 50 9.7 634 6 US-10-953-349-13396 Sequence 13396, A  
100 50 9.7 878 7 US-11-293-697-3814 Sequence 3814, Ap

## ALIGNMENTS

RESULT 1  
US-10-511-814-8

; Sequence 8, Application US/10511814  
; Publication No. US20060088472A1  
; GENERAL INFORMATION:  
; APPLICANT: McCance, Dennis  
; APPLICANT: Westbrock, III, Thomas F.  
; TITLE OF INVENTION: E7 REGULATION OF P21 (CIP1) THROUGH AKT  
; FILE REFERENCE: 21108.0016U2  
; CURRENT APPLICATION NUMBER: US/10/511.814  
; PRIOR FILING DATE: 2004-10-19  
; PRIOR APPLICATION NUMBER: PCT/US03/12667  
; PRIOR FILING DATE: 2003-04-21  
; PRIOR APPLICATION NUMBER: 60/374,245  
; PRIOR FILING DATE: 2002-04-19  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:/Note =  
US-10-511-814-8

Query Match 99.0%; Score 512; DB 6; Length 98;  
Best Local Similarity 96.9%; Pred. No. 2.3e-50;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEMYMLDLOPETTDLYXXYXQUNDSEEDDEIDGPAGQAEPPRAHYNIVTFCK 60  
Db 1 MHGDTPLHEMYMLDLOPETTDLYCYEQUNDSEEDDEIDGPAGQAEPPRAHYNIVTFCK 60

Qy 61 CDSTLRVCVOSTHYDITRTLEDLMTGLGIVXPCISQKP 98  
Db 61 CDSTLRVCVOSTHYDITRTLEDLMTGLGIVCPCISQKP 98

RESULT 2  
US-10-511-814-11

; Sequence 11, Application US/10511814  
; Publication No. US20060088472A1  
; GENERAL INFORMATION:  
; APPLICANT: McCance, Dennis  
; APPLICANT: Westbrock, III, Thomas F.  
; TITLE OF INVENTION: E7 REGULATION OF P21 (CIP1) THROUGH AKT  
; FILE REFERENCE: 21108.0016U2  
; CURRENT APPLICATION NUMBER: US/10/511.814  
; PRIOR FILING DATE: 2004-10-19  
; PRIOR APPLICATION NUMBER: PCT/US03/12667  
; PRIOR FILING DATE: 2003-04-21  
; PRIOR APPLICATION NUMBER: 60/374,245  
; PRIOR FILING DATE: 2002-04-19  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:/Note =  
US-10-511-814-11

Query Match 98.8%; Score 511; DB 6; Length 98;

Best Local Similarity 95.9%; Pred. No. 3e-50;  
Matches 94; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEMYMLDLOPETTDLYXXYXQUNDSEEDDEIDGPAGQAEPPRAHYNIVTFCK 60  
Db 1 MHGDTPLHEMYMLDLOPETTDLYCYEQUNDSEEDDEIDGPAGQAEPPRAHYNIVTFCK 60

Qy 61 CDSTLRVCVOSTHYDITRTLEDLMTGLGIVXPCISQKP 98  
Db 61 CDSTLRVCVOSTHYDITRTLEDLMTGLGIVCPCISQKP 98

RESULT 3  
US-10-512-190-2

; Sequence 2, Application US/10512190  
; Publication No. US20060099219A1  
; GENERAL INFORMATION:  
; APPLICANT: Halliez, Sophie  
; APPLICANT: Burny, Arsene  
; APPLICANT: Jacquet, Alain  
; APPLICANT: Bolten, Alex  
; TITLE OF INVENTION: MUTATED HPV-16 E7 POLYPEPTIDE, PHARMACEUTICAL COMPOSITION  
; FILE REFERENCE: 9997.50USWO  
; CURRENT APPLICATION NUMBER: US/10/512.190  
; PRIOR FILING DATE: 2004-10-22  
; PRIOR APPLICATION NUMBER: PCT/BE03/000073  
; PRIOR FILING DATE: 2003-04-24  
; PRIOR APPLICATION NUMBER: US 60/410,461  
; PRIOR FILING DATE: 2002-09-13  
; PRIOR APPLICATION NUMBER: FR 0205173  
; PRIOR FILING DATE: 2002-04-24  
; PRIOR APPLICATION NUMBER: FR 0304170  
; PRIOR FILING DATE: 2003-04-03  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn Version 3.3  
; SEQ ID NO 2  
; LENGTH: 92  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Mutated (recombinant) HPV-16 E7  
US-10-512-190-2

Query Match 92.5%; Score 478; DB 6; Length 92;  
Best Local Similarity 92.9%; Pred. No. 1.3e-46;  
Matches 91; Conservative 0; Mismatches 1; Indels 6; Gaps 1;

Qy 1 MHGDTPLHEMYMLDLOPETTDLYXXYXQUNDSEEDDEIDGPAGQAEPPRAHYNIVTFCK 60  
Db 1 MHGDTPLHEMYMLDLOPETT-----QUNDSEEDDEIDGPAGQAEPPRAHYNIVTFCK 54

Qy 61 CDSTLRVCVOSTHYDITRTLEDLMTGLGIVXPCISQKP 98  
Db 55 CDSTLRVCVOSTHYDITRTLEDLMTGLGIVCPCISQKP 92

RESULT 4  
US-11-293-697-2678

; Sequence 2678, Application US/11293697  
; Publication No. US20060105376A1  
; GENERAL INFORMATION:  
; APPLICANT: Helix Research Institute  
; TITLE OF INVENTION: Novel full length cDNA  
; FILE REFERENCE: H1-A0106  
; CURRENT APPLICATION NUMBER: US/11/293.697  
; PRIOR FILING DATE: 2005-12-05  
; PRIOR APPLICATION NUMBER: US/10/108,260  
; PRIOR FILING DATE: 2002-03-28  
; NUMBER OF SEQ ID NOS: 5458  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2678  
; LENGTH: 148

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-2678
Query Match
Best Local Similarity 12.1%; Score 62.5; DB 7; Length 148;
Matches 19; Conservative 5; Mismatches 21; Indels 17; Gaps 2;

QY 31 SSEEDEIDGPAQAE-----DRAHYNIYTFCKCKDSTLRLCVOSTHVDIR 77
Db 50 SSGPEDSDGRAGPEPTGSSGCTGWSCLSPVHFHMGMECP-----ILCRSPHLHLR 105
QY 78 TL 79
Db 106 GL 107

RESULT 5
US-10-505-928-341
; Sequence 341, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; PRIOR FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 341
; LENGTH: 1287
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-341
Query Match
Best Local Similarity 11.7%; Score 60.5; DB 6; Length 1287;
Matches 19; Conservative 11; Mismatches 23; Indels 27; Gaps 3;

QY 23 YXXXLNDSESEDEIDGPA-----GOAPDRAHNIYTFCKCKD 62
Db 1126 YGLQSDNSEDEEPPNDKSEYLLNQLNSIPQLGQKSPSKNDHILN-CSI 1184
QY 63 STLRLCVOSTHVDIRLTLEDL 82
Db 1185 SV-----GTNADTPVLRNI 1198

RESULT 6
US-11-293-697-4473
; Sequence 4473, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4473
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-4473
Query Match
Best Local Similarity 11.6%; Score 60; DB 7; Length 468;
Matches 23; Conservative 17; Mismatches 30; Indels 52; Gaps 7;
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QY 16 QPETDLYXXQLNDSE-----EDEIDGPAQ-----QAE----- 47
Db 35 EPQDLDLVMPRLNLSAEAPQSLHPSRGVWNELPQSGQFSQYGRSRTFSQPHPT 94
QY 48 -----DRAHYNIYTFCKCKDSTLRLCVOSTHVDIRLTLEDL-----MGTGLIVXP 92
Db 95 SSGELPYVNSSAGNSCT--CNCOSTLQAIIG-----ELKTRKMLQIQAVGQNRQPP 148
QY 93 ---ICGQK 97
Db 149 ISLICQR 156

RESULT 7
US-10-953-349-39521
; Sequence 39521, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 39521
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-39521
Query Match
Best Local Similarity 11.3%; Score 58.5; DB 6; Length 462;
Matches 24; Conservative 15; Mismatches 30; Indels 35; Gaps 5;

QY 6 PTHRYMLDQPETDLYXXQLNDSE-----ED-----RIDGPAGQAEPPRAHNI 54
Db 351 PAVHMASVVDIKGRAYDV-----LRNSSRPLLDVYRNPGPLQFEGGADSKP----- 398
QY 55 VTFCKCKDSTLRLCVOSTHV--DIRTLEDLLMGTGLIVXPICQ 96
Db 399 -----ISLCVEDQDMGRIKLQETLEKYSIVKGCQ 432

RESULT 8
US-10-953-349-39520
; Sequence 39520, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 39520
; LENGTH: 616
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-39520
Query Match
Best Local Similarity 11.3%; Score 58.5; DB 6; Length 616;
Matches 24; Conservative 15; Mismatches 30; Indels 35; Gaps 5;

QY 6 PTHRYMLDQPETDLYXXQLNDSE-----ED-----RIDGPAGQAEPPRAHNI 54
Db 505 PAVHMASVVDIKGRAYDV-----LRNSSRPLLDVYRNPGPLQFEGGADSKP----- 552
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Oy 55 VTFCCKDSTLRKLCVOSTHV--DIRTLEDLMGTGIVXPICSQ 96  
Db 553 -----ISLCEVDODYGRKIKLQEVYLEKXSIKPCSCSQ 586

RESULT 9  
US-10-953-349-39519  
; Sequence 39519, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nikolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 39519  
; LENGTH: 646  
; TYPE: PRT  
; ORGANISM: Zea mays subsp. mays  
US-10-953-349-39519

Query Match 11.1%, Score 58.5; DB 6; Length 646;  
Best Local Similarity 23.1%; Pred. No. 33;  
Matches 24; Conservative 15; Mismatches 30; Indels 35; Gaps 5;  
Oy 6 PTLHEWMLDLOPETTDLYXXYQNDSEED--ED-----EIDGPAQAEPDRAHNYI 54  
Db 535 PAVHMASVDLKGAKAYDV-----LRONSSRFLEEDVYRNPGPLQEGEGADSKP----- 582  
Oy 55 VTFCCKDSTLRKLCVOSTHV--DIRTLEDLMGTGIVXPICSQ 96  
Db 583 -----ISLCEVDODYGRKIKLQEVYLEKXSIKPCSCSQ 616

RESULT 10  
US-10-953-349-27426  
; Sequence 27426, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nikolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 27426  
; LENGTH: 233  
; TYPE: PRT  
; ORGANISM: Triticum aestivum  
US-10-953-349-27426

Query Match 11.1%, Score 57.5; DB 6; Length 233;  
Best Local Similarity 27.6%; Pred. No. 14;  
Matches 16; Conservative 11; Mismatches 24; Indels 7; Gaps 2;  
Oy 8 LHEWMLDLOPETTDLYXXYQNDSEEDIDGPAQAEPDRAHNYIVTFCCKDST 64  
Db 85 IQEYVLGEYDPDATDAYHDNHTSESADBDHYKD-----TSKRHYHVHYTNGTVCDLT 136

RESULT 11  
US-10-953-349-27425  
; Sequence 27425, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nikolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 27425  
; LENGTH: 296  
; TYPE: PRT  
; ORGANISM: Triticum aestivum  
US-10-953-349-27425

; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 27425  
; LENGTH: 296  
; TYPE: PRT  
; ORGANISM: Triticum aestivum  
US-10-953-349-27425

Query Match 11.1%, Score 57.5; DB 6; Length 296;  
Best Local Similarity 27.6%; Pred. No. 18;  
Matches 16; Conservative 11; Mismatches 24; Indels 7; Gaps 2;  
Oy 8 LHEWMLDLOPETTDLYXXYQNDSEEDIDGPAQAEPDRAHNYIVTFCCKDST 64  
Db 148 IQEYVLGEYDPDATDAYHDNHTSESADBDHYKD-----TSKRHYHVHYTNGTVCDLT 199

RESULT 12  
US-10-953-349-27424  
; Sequence 27424, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nikolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 27424  
; LENGTH: 353  
; TYPE: PRT  
; ORGANISM: Triticum aestivum  
US-10-953-349-27424

Query Match 11.1%, Score 57.5; DB 6; Length 353;  
Best Local Similarity 27.6%; Pred. No. 22;  
Matches 16; Conservative 11; Mismatches 24; Indels 7; Gaps 2;  
Oy 8 LHEWMLDLOPETTDLYXXYQNDSEEDIDGPAQAEPDRAHNYIVTFCCKDST 64  
Db 205 IQEYVLGEYDPDATDAYHDNHTSESADBDHYKD-----TSKRHYHVHYTNGTVCDLT 256

RESULT 13  
US-10-953-349-39537  
; Sequence 39537, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nikolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 39537  
; LENGTH: 446  
; TYPE: PRT  
; ORGANISM: Zea mays subsp. mays  
US-10-953-349-39537

Query Match 11.1%, Score 57.5; DB 6; Length 446;  
Best Local Similarity 23.8%; Pred. No. 29;  
Matches 24; Conservative 15; Mismatches 33; Indels 29; Gaps 4;  
Oy 6 PTLHEWMLDLOPETTDLYXXYQNDSEED--EDGPAQAEPDRAHNYIVTFCCKDST 57  
Db 6 PTLHEWMLDLOPETTDLYXXYQNDSEED--EDGPAQAEPDRAHNYIVTFCCKDST 57

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Db      333 PAVHMASVDLKGKAYDV--LRONSSSFLEDDVYRNPGPLQFEGPGADSKP----- 380
Qy      58 CCKCDSTLRLCVQSTHV--DIRTLEDLMLGTLGIYXPICSQ 96
Db      381 -----ISLCVEDDQDYMGRIKLQGEYLEKVKRIIVRGCSQ 414

RESULT 14
US-10-953-349-39536
; Sequence 39536, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 39536
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-39536

Query Match      11.1%; Score 57.5; DB 6; Length 464;
Best Local Similarity 23.8%; Pred. No. 30;
Matches 24; Conservative 15; Mismatches 33; Indels 29; Gaps 4;

Qy      6 PTHHEWMLDQPTTDLVYXXQUNDSEED-----EIDPGAGAEPRRAHYNIYTF 57
Db      351 PAVHMASVDLKGKAYDV--LRONSSSFLEDDVYRNPGPLQFEGPGADSKP----- 388
Qy      58 CCKCDSTLRLCVQSTHV--DIRTLEDLMLGTLGIYXPICSQ 96
Db      399 -----ISLCVEDDQDYMGRIKLQGEYLEKVKRIIVRGCSQ 432

RESULT 15
US-10-953-349-3781
; Sequence 3781, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3781
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-3781

Query Match      11.1%; Score 57.5; DB 6; Length 499;
Best Local Similarity 28.8%; Pred. No. 33;
Matches 15; Conservative 8; Mismatches 18; Indels 11; Gaps 3;

Qy      28 LNDSESEDEIDPGAGAEPRRAHYNIYTFCC-KCOST-----LRLCVQSTH 73
Db      13 LNDDEDDDDCDW-----EPVQAPMEFVKWCVNCTMSNPGDMVHCICGSH 59

RESULT 16
US-10-953-349-3780
; Sequence 3780, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.

Db      66 LNDDEDDDDCDW-----EPVQAPMEFVKWCVNCTMSNPGDMVHCICGSH 112
Qy      28 LNDSESEDEIDPGAGAEPRRAHYNIYTFCC-KCOST-----LRLCVQSTH 73
Db      66 LNDDEDDDDCDW-----EPVQAPMEFVKWCVNCTMSNPGDMVHCICGSH 112

RESULT 17
US-10-953-349-39535
; Sequence 39535, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 39535
; LENGTH: 618
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-39535

Query Match      11.1%; Score 57.5; DB 6; Length 618;
Best Local Similarity 23.8%; Pred. No. 41;
Matches 24; Conservative 15; Mismatches 33; Indels 29; Gaps 4;

Qy      6 PTHHEWMLDQPTTDLVYXXQUNDSEED-----EIDPGAGAEPRRAHYNIYTF 57
Db      505 PAVHMASVDLKGKAYDV--LRONSSSFLEDDVYRNPGPLQFEGPGADSKP----- 552
Qy      58 CCKCDSTLRLCVQSTHV--DIRTLEDLMLGTLGIYXPICSQ 96
Db      553 -----ISLCVEDDQDYMGRIKLQGEYLEKVKRIIVRGCSQ 586

RESULT 18
US-11-242-111-23
; Sequence 23, Application US/11242111
; Publication No. US2006008862A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Nancy M
; TITLE OF INVENTION: DRUG SCREENING AND MOLECULAR DIAGNOSTIC TEST FOR EARLY DETECTION
; FILE REFERENCE: NIEB-010010U1 MCF/MLB
; CURRENT APPLICATION NUMBER: US/11/242,111
; CURRENT FILING DATE: 2005-09-29
; PRIOR APPLICATION NUMBER: 60/614,746
; PRIOR FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: 60/651,344
; PRIOR FILING DATE: 2005-02-08
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23
; LENGTH: 300
```

TYPE: PRT  
ORGANISM: HUMAN  
US-11-242-111-23

Query Match 11.0%; Score 57; DB 7; Length 300;  
Best Local Similarity 24.4%; Pred. No. 21;  
Matches 11; Conservative 12; Mismatches 22; Indels 0; Gaps 0;

QY 9 HEWMLDQPETTDLYXXQLNDSEEDDEIDGPGQAEPPRAHYN 53  
DB 68 HDHWDMDDEDDBDHVDSQDSIDNSDDVDVDTDSHQSDSHHS 112

RESULT 19  
US-09-981-845-1  
Sequence 1, Application US/09981845  
Publication No. US2006010501A1  
GENERAL INFORMATION:  
APPLICANT: Ashkar, Samy  
APPLICANT: Children's Medical Center Corporation  
TITLE OF INVENTION: Osteoporosis-Coated Surfaces and Methods of Use  
FILE REFERENCE: CMC 779  
CURRENT APPLICATION NUMBER: US/09/981,845  
CURRENT FILING DATE: 2001-10-18  
PRIOR APPLICATION NUMBER: US 60/241,248  
PRIOR FILING DATE: 2000-10-18  
PRIOR APPLICATION NUMBER: US 60/327,273  
PRIOR FILING DATE: 2001-10-05  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1  
LENGTH: 314  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-981-845-1

Query Match 11.0%; Score 57; DB 1; Length 314;  
Best Local Similarity 24.4%; Pred. No. 22;  
Matches 11; Conservative 12; Mismatches 22; Indels 0; Gaps 0;

QY 9 HEWMLDQPETTDLYXXQLNDSEEDDEIDGPGQAEPPRAHYN 53  
DB 82 HDHWDMDDEDDBDHVDSQDSIDNSDDVDVDTDSHQSDSHHS 126

RESULT 20  
US-10-953-349-23406  
Sequence 23406, Application US/10953349  
Publication No. US20060107345A1  
GENERAL INFORMATION:  
APPLICANT: ALEXANDROV, Nickolai et al.  
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
FILE REFERENCE: 2750-1579PUS2  
CURRENT APPLICATION NUMBER: US/10/953,349  
CURRENT FILING DATE: 2004-09-30  
NUMBER OF SEQ ID NOS: 40252  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 23406  
LENGTH: 286  
TYPE: PRT  
ORGANISM: Glycine max  
US-10-953-349-23406

Query Match 10.7%; Score 55.5; DB 6; Length 286;  
Best Local Similarity 31.4%; Pred. No. 30;  
Matches 11; Conservative 7; Mismatches 14; Indels 3; Gaps 1;

QY 37 EIDPGAGAEPPRAHYNIV--TFCCCKDSTLRLC 68  
DB 188 KVDGPGGWSYGRVRSYVQGNDFCGACGCAATAGTC 222

RESULT 21  
US-10-953-349-23405  
Sequence 23405, Application US/10953349  
Publication No. US20060107345A1  
GENERAL INFORMATION:  
APPLICANT: ALEXANDROV, Nickolai et al.  
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
FILE REFERENCE: 2750-1579PUS2  
CURRENT APPLICATION NUMBER: US/10/953,349  
CURRENT FILING DATE: 2004-09-30  
NUMBER OF SEQ ID NOS: 40252  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 23405  
LENGTH: 293  
TYPE: PRT  
ORGANISM: Glycine max  
US-10-953-349-23405

Query Match 10.7%; Score 55.5; DB 6; Length 293;  
Best Local Similarity 31.4%; Pred. No. 30;  
Matches 11; Conservative 7; Mismatches 14; Indels 3; Gaps 1;

QY 37 EIDPGAGAEPPRAHYNIV--TFCCCKDSTLRLC 68  
DB 195 KVDGPGGWSYGRVRSYVQGNDFCGACGCAATAGTC 229

RESULT 22  
US-10-953-349-5452  
Sequence 5452, Application US/10953349  
Publication No. US20060107345A1  
GENERAL INFORMATION:  
APPLICANT: ALEXANDROV, Nickolai et al.  
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
FILE REFERENCE: 2750-1579PUS2  
CURRENT APPLICATION NUMBER: US/10/953,349  
CURRENT FILING DATE: 2004-09-30  
NUMBER OF SEQ ID NOS: 40252  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 5452  
LENGTH: 538  
TYPE: PRT  
ORGANISM: Arabidopsis thaliana  
US-10-953-349-5452

Query Match 10.7%; Score 55.5; DB 6; Length 538;  
Best Local Similarity 27.7%; Pred. No. 59;  
Matches 26; Conservative 11; Mismatches 32; Indels 25; Gaps 5;

QY 14 DLOPETTDLYXXQLNDSEEDDEIDGPGQAEPPRAHYNIVTFCCCK 61  
DB 149 DEEPE---HDARFLPTEEBLEBANGP---PDLPKTRLEIVRAKNAKAPRK- 198

QY 62 DSTLRLCVQSTHYDIRT---LEDLNLGTLGIYXP 92  
DB 199 DTRKACVBEQKADLGSYGVNSFLIGTLVEMFP 232

RESULT 23  
US-10-953-349-5451  
Sequence 5451, Application US/10953349  
Publication No. US20060107345A1  
GENERAL INFORMATION:  
APPLICANT: ALEXANDROV, Nickolai et al.  
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
FILE REFERENCE: 2750-1579PUS2  
CURRENT APPLICATION NUMBER: US/10/953,349  
CURRENT FILING DATE: 2004-09-30  
NUMBER OF SEQ ID NOS: 40252  
SOFTWARE: PatentIn version 3.3

SEQ ID NO 5451  
LENGTH: 544  
TYPE: PRT  
ORGANISM: Arabidopsis thaliana  
US-10-953-349-5451

Query Match 10.7%; Score 55.5; DB 6; Length 544;  
Best Local Similarity 27.7%; Pred. No. 60;

Matches 26; Conservative 11; Mismatches 32; Indels 25; Gaps 5;

QY 14 DLQPTTDLXXYYQLNDSSEEDIDGPAGQAEPD-----RAHNYIVTFCCKC 61  
DB 155 DEEPE-----HDARLPTREELEERARGP-----PDLPLKTRLEIYRALKNFRAPRK- 204

QY 62 DSTLRLCVQSTHVDIRT--LEDLLMGTGIVXP 92  
DB 205 DTRKACVEQLKADLGSYGYNSFLIGTLVEMFP 238

RESULT 24  
US-10-953-349-5450  
Sequence 5450, Application US/10953349  
Publication No. US20060107345A1

GENERAL INFORMATION:  
APPLICANT: ALEXANDROV, Nicholas et al.

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
FILE REFERENCE: 2750-1579PUS2  
CURRENT APPLICATION NUMBER: US/10/953,349

CURRENT FILING DATE: 2004-09-30  
NUMBER OF SEQ ID NOS: 40252

SOFTWARE: PatentIn version 3.3  
SEQ ID NO 5450  
LENGTH: 574

TYPE: PRT  
ORGANISM: Arabidopsis thaliana  
US-10-953-349-5450

Query Match 10.7%; Score 55.5; DB 6; Length 574;  
Best Local Similarity 27.7%; Pred. No. 63;

Matches 26; Conservative 11; Mismatches 32; Indels 25; Gaps 5;

QY 14 DLQPTTDLXXYYQLNDSSEEDIDGPAGQAEPD-----RAHNYIVTFCCKC 61  
DB 185 DEEPE-----HDARLPTREELEERARGP-----PDLPLKTRLEIYRALKNFRAPRK- 234

QY 62 DSTLRLCVQSTHVDIRT--LEDLLMGTGIVXP 92  
DB 235 DTRKACVEQLKADLGSYGYNSFLIGTLVEMFP 268

RESULT 25

US-10-468-193-32  
Sequence 32, Application US/10468193

Publication No. US20060100416A1

GENERAL INFORMATION:

APPLICANT: Palli, Subba R.

APPLICANT: Cress, Dean E.

APPLICANT: Fujimoto, Ted T.

TITLE OF INVENTION: Novel Substitution Mutant Receptor and Their Use in a Nuclear

FILE REFERENCE: A01247-US

CURRENT APPLICATION NUMBER: US/10/468,193

CURRENT FILING DATE: 2002-02-20

PRIOR APPLICATION NUMBER: US 60/313,925

PRIOR FILING DATE: 2001-08-21

PRIOR APPLICATION NUMBER: PCT/US02/05090

PRIOR FILING DATE: 2002-02-20

NUMBER OF SEQ ID NOS: 113

SOFTWARE: PatentIn version 3.2  
SEQ ID NO 32  
LENGTH: 878

TYPE: PRT  
ORGANISM: Drosophila melanogaster  
US-10-468-193-32

Query Match 10.7%; Score 55.5; DB 6; Length 878;  
Best Local Similarity 24.8%; Pred. No. 1e+02;

Matches 27; Conservative 14; Mismatches 35; Indels 33; Gaps 7;

QY 14 DLQPTTDLXXYYQLNDSSEEDIDGPAGQAEPD-----DPA--HYNYIVT----- 56  
DB 230 DLSP-SSSLNGY-SANESCDKSKKGPAPRVOEELCLVGDRAAGYHVALTCGCKGF 287

QY 57 -----FCCCKDSTLRLCVQSTHVDIRTLEDLLMGTGIVXPIC 94  
DB 288 FRRSVTKSAVYCKCFG--RACEMDMYRRKQCEKIKKCLAVGMREPC 333

RESULT 26

US-10-525-126-177  
Sequence 177, Application US/10525126

Publication No. US2006093596A1

GENERAL INFORMATION:

APPLICANT: NATIONAL RESEARCH COUNCIL OF CANADA

TITLE OF INVENTION: A GENOMIC APPROACH TO IDENTIFICATION OF NOVEL BROAD-SPECTRUM

FILE REFERENCE: 6899-6/PAR

CURRENT APPLICATION NUMBER: US/10/525,126

CURRENT FILING DATE: 2005-02-18

PRIOR APPLICATION NUMBER: PCT/CA03/01323

PRIOR FILING DATE: 2003-08-22

PRIOR APPLICATION NUMBER: 60/404,922

PRIOR FILING DATE: 2002-08-22

NUMBER OF SEQ ID NOS: 329

SOFTWARE: PatentIn Ver. 3.2

SEQ ID NO 177

LENGTH: 58

TYPE: PRT

ORGANISM: Unknown Organism

FEATURE:

OTHER INFORMATION: Description of Unknown Organism: Hepcidin peptide

US-10-525-126-177

Query Match 10.5%; Score 54.5; DB 6; Length 58;  
Best Local Similarity 22.4%; Pred. No. 6.7;

Matches 10; Conservative 9; Mismatches 11; Indels 15; Gaps 1;

QY 32 SESEDEIDGPAGQAEPD-----RAHNYIVTFCCKC 61  
DB 2 TEEVESIDSPVGEHQPGGTSNMLPMHFRKQSHSLCKWCNC 46

RESULT 27

US-10-525-126-215  
Sequence 215, Application US/10525126

Publication No. US2006093596A1

GENERAL INFORMATION:

APPLICANT: NATIONAL RESEARCH COUNCIL OF CANADA

TITLE OF INVENTION: A GENOMIC APPROACH TO IDENTIFICATION OF NOVEL BROAD-SPECTRUM

FILE REFERENCE: 6899-6/PAR

CURRENT APPLICATION NUMBER: US/10/525,126

CURRENT FILING DATE: 2005-02-18

PRIOR APPLICATION NUMBER: PCT/CA03/01323

PRIOR FILING DATE: 2003-08-22

PRIOR APPLICATION NUMBER: 60/404,922

PRIOR FILING DATE: 2002-08-22

NUMBER OF SEQ ID NOS: 329

SOFTWARE: PatentIn Ver. 3.2

SEQ ID NO 215

LENGTH: 58

TYPE: PRT

ORGANISM: Salmo salar

US-10-525-126-215

Query Match	10.5%	Score 54.5;	DB 6;	Length 58;
Best Local Similarity	22.2%;	Pred. No. 6.7;		
Matches	10;	Conservative	9;	Mismatches 11;
				Indels 15;
				Gaps 1;

```

Oy      32 SEEDEIDGPAGQAEPP-----RAHNYIVTECKC 61
      :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      2 TEEVESIDSPVGEHQPGGTSNMLPMHFRFKQSHLSLCRWCN 46

```

RESULT 28  
US-10-525-126-174

```

Sequence 174, Application US/10525126
Publication No. US20060093596A1
GENERAL INFORMATION:
APPLICANT: NATIONAL RESEARCH COUNCIL OF CANADA
TITLE OF INVENTION: A GENOMIC APPROACH TO IDENTIFICATION OF NOVEL BROAD-SPECTRUM
FILE REFERENCE: 6899-6/PAR
CURRENT APPLICATION NUMBER: US/10/525,126
PRIOR FILING DATE: 2005-02-18
PRIOR APPLICATION NUMBER: PCT/CA03/01323
PRIOR FILING DATE: 2003-08-22
PRIOR APPLICATION NUMBER: 60/404,922
PRIOR FILING DATE: 2002-08-22
NUMBER OF SEQ ID NOS: 329
SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 174
LENGTH: 88
TYPE: PRT
ORGANISM: Unknown Organism
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: Hepcidin peptide
US-10-525-126-174

```

Query Match	10.5%	Score 54.5;	DB 6;	length 88;
Best Local Similarity	22.2%;	Pred. No. 11;		
Matches 10;	Conservative 9;	Mismatches 11;	Indels 15;	Gaps 1;

```

QY      32 SEEDEIDGPAGQAEPP-----RAHYNIYTFCKKC 61
      31 :||:||||:|
DB      32 TEEVESIDSFVGHEHQDPCGTSMLPMHFRFKRQSHLSLCRWCCNC 76
      31 :||:||||:|

```

RESULT 29  
US-10-525-126-175

```

? Sequence 175 Application US/10525126
? Publication No. US20060093596A1
? GENERAL INFORMATION:
? APPLICANT: NATIONAL RESEARCH COUNCIL OF CANADA
? TITLE OF INVENTION: A GENOMIC APPROACH TO IDENTIFICATION OF NOVEL BROAD-SPECTRUM
? TITLE OF INVENTION: ANTIMICROBIAL PEPTIDES FROM BONY FISH
? FILE REFERENCE: 6899-6/PAR
? CURRENT APPLICATION NUMBER: US/10/525,126
? PRIOR FILING DATE: 2005-02-18
? PRIOR APPLICATION NUMBER: PCT/CA03/01323
? PRIOR FILING DATE: 2003-08-22
? PRIOR APPLICATION NUMBER: 60/404,922
? NUMBER OF SEQ ID NOS: 329
? SOFTWARE: Patentin Ver. 3.2
? SEQ ID NO 175
? LENGTH: 88
? TYPE: PRT
? ORGANISM: Unknown Organism
? FEATURE:
? OTHER INFORMATION: Description of Unknown Organism: Hepcidin peptide
? US-10-525-126-175

```

Query Match 1.0.54; Score 54.5; DB 6; Length 88;

Best Local Similarity 22.2%; Pred. No. 11;  
Matches 10; Conservative 9; Mismatches 11; Indels 15; Gaps 1.

```

QY      32 SEEDEIDGPAGQAEPP-----RAHYNIVTFCCCKC 61
      :||: ||| : : ||| : |||
Db      32 TEEVESIDSPVGEHQDQPGCTSMNLPMHFRFKRQSHLSLCRCWCNC 76

```

RESULT 30  
US-10-525-126-212

Sequence 212, Application US/10525126  
Publication No. US20060093596A1  
GENERAL INFORMATION:  
APPLICANT: NATIONAL RESEARCH COUNCIL OF CANADA  
TITLE OF INVENTION: A GENOMIC APPROACH TO IDENTIFICATION OF NOVEL BROAD-SPECTRUM  
TITLE OF INVENTION: ANTIMICROBIAL PEPTIDES FROM BONY FISH  
FILE REFERENCE: 6899-6/PAR  
CURRENT APPLICATION NUMBER: US/10/525,126  
CURRENT FILING DATE: 2005-02-18  
PRIOR APPLICATION NUMBER: PCT/CA03/01323  
PRIOR FILING DATE: 2003-08-22  
PRIOR APPLICATION NUMBER: 60/404,922  
PRIOR FILING DATE: 2002-08-22  
NUMBER OF SEQ. ID NOS: 329  
SOFTWARE: PatentIn Ver. 3.2  
SEQ ID NO 212  
LENGTH: 88  
TYPE: PRT  
ORGANISM: Hippoglossus hippoglossus  
US-10-525-126-212

Query Match	10.5%;	Score 54.5;	DB 6;	Length 88;
Best Local Similarity	22.2%;	Pred. No. 11;		
Matches	10;	Conservative	9;	Mismatches 11;
				Indels 15;
				Gaps 1;

```

Qy      32 SEEDEIDGPAGQABPD-----RAHYNIVTFCCKC 61
      :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      32 TEEVESIDSPVGEHQPGGTSNNLPMHFRFKRQSHLSLRWCNC 76

```

RESULT 31  
US-10-525-126-213

Sequence 213 Application US/10525126  
Publication No. US20060093596A1  
GENERAL INFORMATION:  
APPLICANT: NATIONAL RESEARCH COUNCIL OF CANADA  
TITLE OF INVENTION: A GENOMIC APPROACH TO IDENTIFICATION OF NOVEL BROAD-SPECTRUM  
ANTIMICROBIAL PEPTIDES FROM BONY FISH  
FILE REFERENCE: 6899-6/PAR  
CURRENT APPLICATION NUMBER: US/10/525,126  
CURRENT FILING DATE: 2005-02-18  
PRIOR APPLICATION NUMBER: PCT/CA03/01323  
PRIOR FILING DATE: 2003-08-22  
PRIOR APPLICATION NUMBER: 60/404,922  
PRIOR FILING DATE: 2002-08-22  
NUMBER OF SEQ ID NOS: 329  
SOFTWARE: PatentIn Ver. 3.2  
SEQ ID NO 213  
LENGTH: 88  
TYPE: PRT  
ORGANISM: Salmo salar  
IS-10-525-126-213

Query Match 10.5%; Score 54.5; DB 6; Length 88;  
Best Local Similarity 22.2%; Pred. No. 11;  
Matches 10; Conservative 9; Mismatches 11; Indels 15; Gaps 1;

```

QY 32 SEEDEIDGAGQAEPPD-----RAHYNIVTFCCCK 61
      ||: ||| : : ||: |||
DB 32 TEEVESIDS PVGEHQPGGTSMLPMHFRFKRQSHSLCRWCNC 76

```

## RESULT 32

```
US-10-525-126-284
; Sequence 284, Application US/10525126
; Publication No. US20060093596A1
; GENERAL INFORMATION:
; APPLICANT: NATIONAL RESEARCH COUNCIL OF CANADA
; TITLE OF INVENTION: A GENOMIC APPROACH TO IDENTIFICATION OF NOVEL BROAD-SPECTRUM
; TITLE OF INVENTION: ANTIMICROBIAL PEPTIDES FROM BONY FISH
; FILE REFERENCE: 6899-6/PAR
; CURRENT APPLICATION NUMBER: US/10/525,126
; CURRENT FILING DATE: 2005-02-18
; PRIOR APPLICATION NUMBER: PCT/CA03/01323
; PRIOR FILING DATE: 2003-08-22
; PRIOR APPLICATION NUMBER: 60/404,922
; PRIOR FILING DATE: 2002-08-22
; NUMBER OF SEQ ID NOS: 329
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 284
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Type1 Hepcidin
; OTHER INFORMATION: sequence
US-10-525-126-284

Query Match 10.5%; Score 54.5; DB 6; Length 88;
Best Local Similarity 22.2%; Pred. No. 11;
Matches 10; Conservative 9; Mismatches 11; Indels 15; Gaps 1;

QY 32 SEEDRIDGPAQAEPD-----RAHNYIVFCKC 61
DB 32 TEVESIDSPVGEHQPGGTSMNLPMHFRKROSHSLCRWCNC 76

RESULT 33
US-10-525-126-299
; Sequence 299, Application US/10525126
; Publication No. US20060093596A1
; GENERAL INFORMATION:
; APPLICANT: NATIONAL RESEARCH COUNCIL OF CANADA
; TITLE OF INVENTION: A GENOMIC APPROACH TO IDENTIFICATION OF NOVEL BROAD-SPECTRUM
; TITLE OF INVENTION: ANTIMICROBIAL PEPTIDES FROM BONY FISH
; FILE REFERENCE: 6899-6/PAR
; CURRENT APPLICATION NUMBER: US/10/525,126
; CURRENT FILING DATE: 2005-02-18
; PRIOR APPLICATION NUMBER: PCT/CA03/01323
; PRIOR FILING DATE: 2003-08-22
; PRIOR APPLICATION NUMBER: 60/404,922
; PRIOR FILING DATE: 2002-08-22
; NUMBER OF SEQ ID NOS: 329
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 299
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Hippoglossus hippoglossus
US-10-525-126-299

Query Match 10.5%; Score 54.5; DB 6; Length 88;
Best Local Similarity 22.2%; Pred. No. 11;
Matches 10; Conservative 9; Mismatches 11; Indels 15; Gaps 1;

QY 32 SEEDRIDGPAQAEPD-----RAHNYIVFCKC 61
DB 32 TEVESIDSPVGEHQPGGTSMNLPMHFRKROSHSLCRWCNC 76

RESULT 34
US-10-525-126-300
; Sequence 300, Application US/10525126
; Publication No. US20060093596A1
; GENERAL INFORMATION:
; APPLICANT: NATIONAL RESEARCH COUNCIL OF CANADA
; TITLE OF INVENTION: A GENOMIC APPROACH TO IDENTIFICATION OF NOVEL BROAD-SPECTRUM
```

```
; TITLE OF INVENTION: ANTIMICROBIAL PEPTIDES FROM BONY FISH
; FILE REFERENCE: 6899-6/PAR
; CURRENT APPLICATION NUMBER: US/10/525,126
; CURRENT FILING DATE: 2005-02-18
; PRIOR APPLICATION NUMBER: PCT/CA03/01323
; PRIOR FILING DATE: 2003-08-22
; PRIOR APPLICATION NUMBER: 60/404,922
; PRIOR FILING DATE: 2002-08-22
; NUMBER OF SEQ ID NOS: 329
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 300
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Salmo salar
US-10-525-126-300

Query Match 10.5%; Score 54.5; DB 6; Length 88;
Best Local Similarity 22.2%; Pred. No. 11;
Matches 10; Conservative 9; Mismatches 11; Indels 15; Gaps 1;

QY 32 SEEDRIDGPAQAEPD-----RAHNYIVFCKC 61
DB 32 TEVESIDSPVGEHQPGGTSMNLPMHFRKROSHSLCRWCNC 76

RESULT 35
US-10-953-349-20549
; Sequence 20549, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 20549
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-20549

Query Match 10.5%; Score 54.5; DB 6; Length 255;
Best Local Similarity 27.7%; Pred. No. 34;
Matches 13; Conservative 7; Mismatches 26; Indels 1; Gaps 1;

QY 2 HGDPTLHEVMDLOPETTDLYXXQLNDSSEEDRIDGPAQAEPD 48
DB 94 HNPENAKAVKFDI-PEEDDDYTDLDLDPDDDDDDDFDDDDMD 139

RESULT 36
US-10-953-349-20548
; Sequence 20548, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 20548
; LENGTH: 269
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-20548

Query Match 10.5%; Score 54.5; DB 6; Length 269;
```

Best Local Similarity 27.7%; Pred. No. 36;  
Matches 13; Conservative 7; Mismatches 26; Indels 1; Gaps 1;

QY 2 HCGPTLHEHYMDLPETDLYXXQXQNDSEEDIDGPAGQAEPP 48  
DB 108 HNPENKAVKVPDI-PEEDDYTDDELDDDDDDDFDDDD 153

## RESULT 37

US-11-293-697-2988  
; Sequence 2988, Application US/11293697  
; Publication No. US20060105376A1  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: Novel full length cDNA  
; FILE REFERENCE: H1-A0106  
; CURRENT APPLICATION NUMBER: US/11/293,697  
; CURRENT FILING DATE: 2005-12-05  
; PRIOR APPLICATION NUMBER: US/10/108,260  
; PRIOR FILING DATE: 2002-03-28  
; NUMBER OF SEQ ID NOS: 5458  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2988  
; LENGTH: 489  
; TYPE: PRT  
; ORGANISM: Homo sapiens

US-11-293-697-2988

Query Match 10.5%; Score 54.5; DB 7; Length 489;  
Best Local Similarity 24.7%; Pred. No. 69;  
Matches 20; Conservative 10; Mismatches 26; Indels 25; Gaps 3;

QY 8 LHEHYMDLPETDLYXXQXQNDSEEDIDGPAGQAEPPRAHNYIVTFCKCDSTLR 67  
DB 187 LQELREKLRPPAVD-----KGIILKTRPPAQKDLGVCC---DPLVL 226

QY 68 CVQSTHVDIRTL-----EDLL 83  
DB 227 AQLTHIELDRVSSIVPEDLM 247

## RESULT 38

US-10-953-349-1526  
; Sequence 1526, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nickolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1526  
; LENGTH: 278  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana

US-10-953-349-1526

Query Match 10.4%; Score 54; DB 6; Length 278;  
Best Local Similarity 27.4%; Pred. No. 42;  
Matches 20; Conservative 10; Mismatches 29; Indels 14; Gaps 2;

QY 7 TLHEHYMDLPETDLYXXQXQNDSEEDIDGPAGQAEPPRAHNYIVTFCKCDSTLR 66  
DB 62 TLNEPTIGDLKESIDLNGEKVN--SESNRDSAPGDDKPPYASVNV----- 107

QY 67 LCVQSTHVDIRTL 79  
DB 108 LKQALHADRSLL 120

## RESULT 39

US-10-518-414-1  
; Sequence 1, Application US/10518414  
; Publication No. US20060099588A1  
; GENERAL INFORMATION:  
; APPLICANT: Chr. Hansen A/S  
; APPLICANT: Maarten van den Brink, Johannes  
; APPLICANT: Harboe, Marianne K  
; APPLICANT: Petersen, Steen Guldager  
; APPLICANT: Rahbek-Nielsen, Henrik  
; TITLE OF INVENTION: IMPROVED METHOD OF PRODUCING AN ASPARTIC PROTEASE POLYPEPTIDE IN  
; FILE REFERENCE: P1031US00  
; CURRENT APPLICATION NUMBER: US/10/518,414  
; CURRENT FILING DATE: 2004-12-17  
; PRIOR APPLICATION NUMBER: PA 2002 0092  
; PRIOR FILING DATE: 2002-06-17  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1  
; LENGTH: 323  
; TYPE: PRT  
; ORGANISM: Bos taurus

US-10-518-414-1

Query Match 10.4%; Score 54; DB 6; Length 323;  
Best Local Similarity 28.4%; Pred. No. 50;  
Matches 29; Conservative 13; Mismatches 30; Indels 30; Gaps 8;

QY 4 DPTLHEHYMDLP-----PETDLYXXQXQNDSEEDIDGPAGQAEPPRA-HNYIV 55  
DB 89 DTVTVSN-IDYDIOQTGVLSTQEPGDVFTYA-----EFGGILGMAYPSLASEYSIP 137

QY 56 TFCKCDSTL--RLCVQ---STHVDIRTLIEDLMTGLGVXP 92  
DB 138 VF---DNMMNRHLVAQDLFVYMDRNGQESML--TLGAIDP 173

## RESULT 40

US-10-953-349-35808  
; Sequence 35808, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nickolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 35808  
; LENGTH: 630  
; TYPE: PRT  
; ORGANISM: Zea mays subsp. mays

US-10-953-349-35808

Query Match 10.4%; Score 54; DB 6; Length 630;  
Best Local Similarity 28.6%; Pred. No. 1e+02;  
Matches 18; Conservative 10; Mismatches 27; Indels 8; Gaps 3;

QY 13 LDLPET--TDLYXXQXQNDSEEDIDGPAGQAEPPRAHNYIVTFCKCDSTLR 70  
DB 32 VELRAETDSDEVYAQMLQGTQSEPTSPDPRPEREC--NIHSFC-----KTLGLASDT 85

QY 71 STH 73  
DB 86 STH 88

## RESULT 41

US-10-953-349-35807  
; Sequence 35807, Application US/10953349

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; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 35807
; LENGTH: 676
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-35807

Query Match
Best Local Similarity 10.4%; Score 54; DB 6; Length 676;
Matches 18; Conservative 10; Mismatches 27; Indels 8; Gaps 3;

QY 13 LDIQPT-TDLYXXYQLNDSSEDEIDGPAGQAEPRAHYNIWTFCKCDSTLRICVQ 70
Db 78 VELRAETDSDVYAQIWLQPTQSEPTSPDPPEPERC--NIHSFC---KTLFASPT 131
QY 71 STH 73
Db 132 STH 134

RESULT 42
US-10-953-349-31198
; Sequence 31198, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31198
; LENGTH: 533
; TYPE: PRT
; ORGANISM: Trifolium aestivum
US-10-953-349-31198

Query Match
Best Local Similarity 10.3%; Score 53.5; DB 6; Length 533;
Matches 17; Conservative 6; Mismatches 21; Indels 3; Gaps 1;

QY 49 RAHNYITFCKCDSTLRICVQSTHVDIRITLEDLLMGTGIVXPIC 95
Db 4 RSPANVTKOSKCRPRTRVDPGSGCHRPILDRQLTGLV--ICS 47

RESULT 43
US-10-953-349-23351
; Sequence 23351, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23351
; LENGTH: 639
; TYPE: PRT
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; ORGANISM: Glycine max
US-10-953-349-23351

Query Match
Best Local Similarity 10.3%; Score 53.5; DB 6; Length 639;
Matches 16; Conservative 7; Mismatches 31; Indels 5; Gaps 2;

QY 30 DSSEEDER-DGPAGQAEPRAHYNIWTFCKCDSTLRICVQSTHVDIRITLEDLL 83
Db 19 EEESEEEVWDWEGEDGERSEFVCLFCDNRYSGSLFDHCASLHRRDFTIRTTL 77

RESULT 44
US-10-953-349-23350
; Sequence 23350, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23350
; LENGTH: 656
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-23350

Query Match
Best Local Similarity 10.3%; Score 53.5; DB 6; Length 656;
Matches 16; Conservative 7; Mismatches 31; Indels 5; Gaps 2;

QY 30 DSSEEDER-DGPAGQAEPRAHYNIWTFCKCDSTLRICVQSTHVDIRITLEDLL 83
Db 36 EEESEEEVWDWEGEDGERSEFVCLFCDNRYSGSLFDHCASLHRRDFTIRTTL 94

RESULT 45
US-10-953-349-23349
; Sequence 23349, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23349
; LENGTH: 664
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-23349

Query Match
Best Local Similarity 10.3%; Score 53.5; DB 6; Length 664;
Matches 16; Conservative 7; Mismatches 31; Indels 5; Gaps 2;

QY 30 DSSEEDER-DGPAGQAEPRAHYNIWTFCKCDSTLRICVQSTHVDIRITLEDLL 83
Db 44 EEESEEEVWDWEGEDGERSEFVCLFCDNRYSGSLFDHCASLHRRDFTIRTTL 102

RESULT 46
US-10-953-349-34172
; Sequence 34172, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
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; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 34172
; LENGTH: 263
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-34172
Query Match          10.3%; Score 53; DB 6; Length 263;
Best Local Similarity 25.0%; Pred. No. 51;
Matches 25; Conservative 9; Mismatches 34; Indels 32; Gaps 4;

QY 27 QUNDSSEEDRIDGPAGQAE-----DRAHY-----NIVTFCKCDST 64
Db 32 QVSDALRLHDEIMQPGSLPEPKAIALIEHIRTGEGELDRHQLDGLDNSWFDGGRV 91
QY 65 LRLCVGSTHVDIRLTEDLL-----MGTLGIVXPICSQ 96
Db 92 LLYCVQHNYPDAAI--DLLKQIREKDEMTYVVDQVFCQ 129

RESULT 47
US-10-953-349-34171
; Sequence 34171, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 34171
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-34171
Query Match          10.3%; Score 53; DB 6; Length 283;
Best Local Similarity 25.0%; Pred. No. 55;
Matches 25; Conservative 9; Mismatches 34; Indels 32; Gaps 4;

QY 27 QUNDSSEEDRIDGPAGQAE-----DRAHY-----NIVTFCKCDST 64
Db 52 QVSDALRLHDEIMQPGSLPEPKAIALIEHIRTGEGELDRHQLDGLDNSWFDGGRV 111
QY 65 LRLCVGSTHVDIRLTEDLL-----MGTLGIVXPICSQ 96
Db 112 LLYCVQHNYPDAAI--DLLKQIREKDEMTYVVDQVFCQ 149

RESULT 48
US-10-953-349-34170
; Sequence 34170, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 34170
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; LENGTH: 286
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-34170
Query Match          10.3%; Score 53; DB 6; Length 286;
Best Local Similarity 25.0%; Pred. No. 56;
Matches 25; Conservative 9; Mismatches 34; Indels 32; Gaps 4;

QY 27 QUNDSSEEDRIDGPAGQAE-----DRAHY-----NIVTFCKCDST 64
Db 55 QVSDALRLHDEIMQPGSLPEPKAIALIEHIRTGEGELDRHQLDGLDNSWFDGGRV 114
QY 65 LRLCVGSTHVDIRLTEDLL-----MGTLGIVXPICSQ 96
Db 115 LLYCVQHNYPDAAI--DLLKQIREKDEMTYVVDQVFCQ 152

RESULT 49
US-10-953-349-12021
; Sequence 12021, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12021
; LENGTH: 377
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (224)..(224)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (228)..(228)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (252)..(252)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (314)..(314)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (325)..(325)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-953-349-12021
Query Match          10.3%; Score 53; DB 6; Length 377;
Best Local Similarity 21.4%; Pred. No. 76;
Matches 27; Conservative 19; Mismatches 40; Indels 40; Gaps 7;

QY 5 TPT-LHEWMLDLPETTDLYXXYL-----NDSSEEDRIDGPAGQ-----AEFDRA 50
Db 34 TPNSHPKLHFPBRSVSESTQKAEPAVLGESEEDDDDDPSAELSYVDPTVDESI 93
QY 51 HNYIVTFCKC-----CDSTRLCVGSTH-----VDIRLTEDLLMGR--- 86
Db 94 TEMELDFCSRPIILDARGKVMELVCDKTSL--QYTKFPNNVINSTITKDAIVASDQ 151
QY 87 LGIVXP 92
Db 152 LGVPLP 157
```

RESULT 50  
US-11-293-697-3292  
; Sequence 3292, Application US/11293697  
; Publication No. US20060105376A1  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: Novel full length cDNA  
; FILE REFERENCE: HI-A0106  
; CURRENT APPLICATION NUMBER: US/11/293,697  
; CURRENT FILING DATE: 2005-12-05  
; PRIOR APPLICATION NUMBER: US/10/108,260  
; PRIOR FILING DATE: 2002-03-28  
; NUMBER OF SEQ ID NOS: 5458  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3292  
; LENGTH: 423  
; TYPE: PR  
; ORGANISM: Homo sapiens  
US-11-293-697-3292

Query Match 10.3%; Score 53; DB 7; Length 423;  
Best Local Similarity 23.5%; Pred. No. 86;  
Matches 23; Conservative 10; Mismatches 29; Indels 36; Gaps 3;

Qy 22 LYYXQUNDS-----SEEDDEIDGPAGQAE-----DRAHYIVT 56  
Db 291 LVYVNOQNDYRKLKIFSESVPLFGPPLPTPVFTDQBFDFLLVYLINGEKATLETPT 350

Qy 57 FCCKDSTLRKCVOSTVVDI-----RTLEDLL 83  
Db 351 FAQKRRITLMLIRSLHODLMPDLHKMLMRSSDVL 388

RESULT 51  
US-10-505-928-443  
; Sequence 443, Application US/10505928  
; Publication No. US20060088532A1  
; GENERAL INFORMATION:  
; APPLICANT: Ludwig Institute for Cancer Research et al.  
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES  
; FILE REFERENCE: 28967/39178  
; CURRENT APPLICATION NUMBER: US/10/505,928  
; CURRENT FILING DATE: 2004-08-27  
; PRIOR APPLICATION NUMBER: US 60/363,019  
; PRIOR FILING DATE: 2002-03-07  
; NUMBER OF SEQ ID NOS: 866  
; SOFTWARE: PatentIn 3.2  
; SEQ ID NO 443  
; LENGTH: 749  
; TYPE: PR  
; ORGANISM: Homo sapiens  
US-10-505-928-443

Query Match 10.3%; Score 53; DB 6; Length 749;  
Best Local Similarity 34.0%; Pred. No. 1.6e+02;  
Matches 17; Conservative 8; Mismatches 17; Indels 8; Gaps 3;

Qy 3 GDTPTLHEVMDLQPETTDLYXXYQUNDS-----SEEDDEIDGPAGQAE 48  
Db 484 GRAGKVNFMFLGMLNMTS--YPLSPLSDFATQDSFDDDEL--AAVADPD 529

RESULT 52  
US-10-953-349-15959  
; Sequence 15959, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nickolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349

CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 15959  
; LENGTH: 109  
; TYPE: PR  
; ORGANISM: Glycine max  
US-10-953-349-15959

Query Match 10.2%; Score 52.5; DB 6; Length 109;  
Best Local Similarity 24.2%; Pred. No. 22;  
Matches 16; Conservative 10; Mismatches 33; Indels 7; Gaps 2;

Qy 3 GDT---PTLHEVMDLQPETTDLYXXYQ-----LNDSEEDDEIDGPAGQAEPPRAHYIV 55  
Db 9 GETDMLQTMQDAMDLSKALDFDVTETAIKIRFTIKCFDRMHGFMQCI VTGDFGSFV 68

Qy 56 TPCCCK 61  
Db 69 THCCGC 74

RESULT 53  
US-11-293-697-3886  
; Sequence 3886, Application US/11293697  
; Publication No. US20060105376A1  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: Novel full length cDNA  
; FILE REFERENCE: HI-A0106  
; CURRENT APPLICATION NUMBER: US/11/293,697  
; CURRENT FILING DATE: 2005-12-05  
; PRIOR APPLICATION NUMBER: US/10/108,260  
; PRIOR FILING DATE: 2002-03-28  
; NUMBER OF SEQ ID NOS: 5458  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3886  
; LENGTH: 275  
; TYPE: PR  
; ORGANISM: Homo sapiens  
US-11-293-697-3886

Query Match 10.2%; Score 52.5; DB 7; Length 275;  
Best Local Similarity 30.0%; Pred. No. 61;  
Matches 18; Conservative 8; Mismatches 19; Indels 15; Gaps 4;

Qy 44 QAEPPRAHYIVTFCCKDSTLRKCVOST---HVDIR-TLEDLLM-----GTIGIVAPIC 94  
Db 180 QAKPSRLH-----GSHCDFTYTLPPQNGTIKLYKELRCPLDDELVLVMSGSGKSYPLC 233

RESULT 54  
US-10-953-349-11222  
; Sequence 11222, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nickolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 11222  
; LENGTH: 288  
; TYPE: PR  
; ORGANISM: Arabidopsis thaliana  
US-10-953-349-11222

Query Match 10.2%; Score 52.5; DB 6; Length 288;  
Best Local Similarity 27.8%; Pred. No. 64;  
Matches 15; Conservative 9; Mismatches 19; Indels 11; Gaps 2;

Qy 15 LQPTDLYXXYXQLNDSSEDEIDG-----PAGQAEPPRAHNYITVFC 58  
Db 232 IEPETEEYEESEDEDEDEVMGLENVNSRCVQGDRE-NRGLNWSFC 264

RESULT 55  
US-10-511-937-2561  
; Sequence 2561, Application US/10511937  
; Publication No. US20060088836A1  
; GENERAL INFORMATION:  
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.  
; APPLICANT: Mohlgemuth, Jay  
; APPLICANT: Fry, Kirk  
; APPLICANT: Woodward, Robert  
; APPLICANT: Ly, Ngoc  
; APPLICANT: Prentice, James  
; APPLICANT: Morris, Macdonald  
; APPLICANT: Rosenberg, Steven  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING  
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION  
; FILE REFERENCE: 506612000104  
; CURRENT APPLICATION NUMBER: US/10/511,937  
; CURRENT FILING DATE: 2004-10-19  
; PRIOR APPLICATION NUMBER: PCT/US2003/012946  
; PRIOR FILING DATE: 2003-04-24  
; PRIOR APPLICATION NUMBER: US 10/131,831  
; PRIOR FILING DATE: 2002-04-24  
; PRIOR APPLICATION NUMBER: US 10/325,899  
; PRIOR FILING DATE: 2002-12-20  
; NUMBER OF SEQ ID NOS: 3117  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2561  
; LENGTH: 1912  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-511-937-2561

Query Match 10.2%; Score 52.5; DB 6; Length 1912;  
Best Local Similarity 29.6%; Pred. No. 5.1e+02;  
Matches 16; Conservative 9; Mismatches 14; Indels 15; Gaps 4;  
Qy 30 DSSEDEIDGPAQAEPPRAHNYITVFC-----CDSTLRICVOSTHV 74  
Db 426 DNSEGEETLEBVGDDLEEDDH--MEFCRVCKXGGEILCCDT----CPSSTYH 473  
RESULT 56  
US-10-525-126-296  
; Sequence 296, Application US/10525126  
; Publication No. US20060093596A1  
; GENERAL INFORMATION:  
; APPLICANT: NATIONAL RESEARCH COUNCIL OF CANADA  
; TITLE OF INVENTION: A GENOMIC APPROACH TO IDENTIFICATION OF NOVEL BROAD-SPECTRUM  
; TITLE OF INVENTION: ANTIMICROBIAL PEPTIDES FROM BONY FISH  
; FILE REFERENCE: 6899-6/PAR  
; CURRENT APPLICATION NUMBER: US/10/525,126  
; CURRENT FILING DATE: 2005-02-18  
; PRIOR APPLICATION NUMBER: PCT/CA03/01323  
; PRIOR FILING DATE: 2003-08-22  
; PRIOR APPLICATION NUMBER: 60/404,922  
; PRIOR FILING DATE: 2002-08-22  
; NUMBER OF SEQ ID NOS: 329  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 296  
; LENGTH: 90  
; TYPE: PRT  
; ORGANISM: Oryzias latipes  
US-10-525-126-296

Query Match 10.1%; Score 52; DB 6; Length 90;  
Best Local Similarity 20.0%; Pred. No. 20;  
Matches 13; Conservative 8; Mismatches 24; Indels 20; Gaps 1;

Qy 4 DPTLEHYMLDLPETTDLYXXYXQLNDSSEDEIDGPAQAEPPRAHNYITVFCCKDS 63  
Db 40 DTVAAARHEHSMQPMWL-----PNHRRKQSHISMCTMCKCK 79

Qy 64 TLRIC 68  
Db 80 NYKGC 84  
RESULT 57  
US-10-953-349-15960  
; Sequence 15960, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nikolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 15960  
; LENGTH: 97  
; TYPE: PRT  
; ORGANISM: Glycine max  
US-10-953-349-15960

Query Match 10.1%; Score 52; DB 6; Length 97;  
Best Local Similarity 23.7%; Pred. No. 22;  
Matches 14; Conservative 9; Mismatches 32; Indels 4; Gaps 1;  
Qy 7 TLHEHYMLDLPETTDLYXXYQ-----LNDSEDEIDGPAQAEPPRAHNYITVFCCKC 61  
Db 4 TWQDAMDALASKALDFPDVTETAIKIAFTKPEBRMHGPEWQCI VGTDFGFSVTHCCG 62

RESULT 58  
US-10-953-349-21799  
; Sequence 21799, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nikolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 21799  
; LENGTH: 324  
; TYPE: PRT  
; ORGANISM: Glycine max  
US-10-953-349-21799

Query Match 10.1%; Score 52; DB 6; Length 324;  
Best Local Similarity 21.5%; Pred. No. 83;  
Matches 17; Conservative 13; Mismatches 29; Indels 20; Gaps 3;  
Qy 10 EYMLDLPETTDLYXXYXQLNDSSEDEIDGPAQAEPPRAHNYITVFCCKDSTLRICV 69  
Db 113 EHKLDMPFTASERKSF-----KKHBDLNDP-----IOFGCQVSKPLP 152  
Qy 70 QSTHVDIRTLEDLMTLG 88  
Db 153 EERKTEVDLQSSQSGSLG 171

RESULT 59  
US-10-953-349-21798  
; Sequence 21798, Application US/10953349

```
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 21798
; LENGTH: 348
; TYPE: PRT
; ORGANISM: Glycine max
; US-10-953-349-21798

Query Match          10.1%; Score 52; DB 6; Length 348;
Best Local Similarity 21.5%; Pred. No. 90;
Matches 17; Conservative 13; Mismatches 29; Indels 20; Gaps 3;

QY 10 EYMLDLPETTDLYXXYQLNDSSEEDIDGPAQAEPDRAHNYIVTFCKCDSTLRVCV 69
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 137 EHKLDMDPTASFKSF-----KHEHDLNDP-----IQFCGCVSKLPL-P 176
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 70 QSTHVDIRLTEDLLMGTLG 88
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 177 EERKTEVDLQSSSGSGSLG 195
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 60
US-10-953-349-21797
; Sequence 21797, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 21797
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Glycine max
; US-10-953-349-21797

Query Match          10.1%; Score 52; DB 6; Length 352;
Best Local Similarity 21.5%; Pred. No. 91;
Matches 17; Conservative 13; Mismatches 29; Indels 20; Gaps 3;

QY 10 EYMLDLPETTDLYXXYQLNDSSEEDIDGPAQAEPDRAHNYIVTFCKCDSTLRVCV 69
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 141 EHKLDMDPTASFKSF-----KHEHDLNDP-----IQFCGCVSKLPL-P 180
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 70 QSTHVDIRLTEDLLMGTLG 88
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 181 EERKTEVDLQSSSGSGSLG 199
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 61
US-10-953-349-31968
; Sequence 31968, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
```

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; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31968
; LENGTH: 357
; TYPE: PRT
; ORGANISM: Triticum aestivum
; US-10-953-349-31968

Query Match          10.1%; Score 52; DB 6; Length 357;
Best Local Similarity 24.7%; Pred. No. 92;
Matches 19; Conservative 9; Mismatches 33; Indels 16; Gaps 2;

QY 1 MHGDTPLHEHYMDLPETTDLYXXYQLNDSSEEDIDGPAQAEPDRAHNYI--VTFC 58
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 249 VHQFAPTYMEYVL-----YHNBEESAPTKPSSGSAVSDVDELGITVM 294
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 59 CKCDSTLRCLCVOSTHVD 75
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 295 PPSNSPVTSSVSSNHVD 311
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 62
US-10-953-349-31967
; Sequence 31967, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31967
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Triticum aestivum
; US-10-953-349-31967

Query Match          10.1%; Score 52; DB 6; Length 405;
Best Local Similarity 24.7%; Pred. No. 11e+02;
Matches 19; Conservative 9; Mismatches 33; Indels 16; Gaps 2;

QY 1 MHGDTPLHEHYMDLPETTDLYXXYQLNDSSEEDIDGPAQAEPDRAHNYI--VTFC 58
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 297 VHQFAPTYMEYVL-----YHNBEESAPTKPSSGSAVSDVDELGITVM 342
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 59 CKCDSTLRCLCVOSTHVD 75
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 343 PPSNSPVTSSVSSNHVD 359
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 63
US-10-953-349-31966
; Sequence 31966, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31966
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Triticum aestivum
; US-10-953-349-31966

Query Match          10.1%; Score 52; DB 6; Length 475;
Best Local Similarity 24.7%; Pred. No. 1.3e+02;
```

Matches 19; Conservative 9; Mismatches 33; Indels 16; Gaps 2;  
QY 1 MHGDTPLHMYMDLOPETTDLYXXOLNDSSEDELDGAGQAPDRAHNY--VTFPC 58  
Db 367 VHQAPFYNEYVL-----YNHGESAPTKFPGSVAVSDVDELAGITVM 412  
QY 59 CKCDSTLRLCQSTHVD 75  
Db 413 PPSNSPVTSSVSSNHVD 429

RESULT 64  
US-10-514-462-4  
; Sequence 4, Application US/10514462  
; Publication No. US20060088909A1  
; GENERAL INFORMATION:  
; APPLICANT: Emory University  
; TITLE OF INVENTION: Virus-Like Particles, Methods of Preparation, And Immunogenic  
; FILE REFERENCE: 050508-2210  
; CURRENT APPLICATION NUMBER: US/10/514,462  
; CURRENT FILING DATE: 2004-11-12  
; PRIOR APPLICATION NUMBER: 60/381,557  
; PRIOR FILING DATE: 2002-05-17  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 4  
; LENGTH: 507  
; TYPE: PRT  
; ORGANISM: RVFV GC  
US-10-514-462-4

Query Match 10.1%; Score 52; DB 6; Length 507;  
Best Local Similarity 30.0%; Pred. No. 1.4e+02;  
Matches 18; Conservative 9; Mismatches 25; Indels 8; Gaps 3;  
QY 37 EIDGPAQAPDRAHNYIVTFCKCDSTLRLCQSTHVDIRTL---EDLLMGTLGIYXP 92  
Db 329 EVDVFGAANVSCDAFLNL-TGCTSCNAGARVCLSTGTGSLSAHNKD---GSLHIVLP 384

RESULT 65  
US-11-293-3174  
; Sequence 3174, Application US/11293697  
; Publication No. US20060105376A1  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: Novel full length cDNA  
; FILE REFERENCE: H1-A0106  
; CURRENT APPLICATION NUMBER: US/11/293,697  
; CURRENT FILING DATE: 2005-12-05  
; PRIOR APPLICATION NUMBER: US/10/108,260  
; PRIOR FILING DATE: 2002-03-28  
; NUMBER OF SEQ ID NOS: 5458  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3174  
; LENGTH: 634  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-293-697-3174

Query Match 10.1%; Score 52; DB 7; Length 634;  
Best Local Similarity 34.4%; Pred. No. 1.7e+02;  
Matches 21; Conservative 9; Mismatches 21; Indels 10; Gaps 4;  
QY 29 NDSSEDEIDGP---AGQAPDRAHNYIVTFCKCD---STL--RLCQSTHVDIRTL 79  
Db 183 HEMMEEBEELPKPSVVAAPGAPKKEHNVV-FIGHVDAGKSTIGQIMVLTGMVDKRTL 241

QY 80 E 80  
Db 242 E 242

RESULT 66  
US-10-514-462-2  
; Sequence 2, Application US/10514462  
; Publication No. US20060088909A1  
; GENERAL INFORMATION:  
; APPLICANT: Emory University  
; TITLE OF INVENTION: Virus-Like Particles, Methods of Preparation, And Immunogenic  
; FILE REFERENCE: 050508-2210  
; CURRENT APPLICATION NUMBER: US/10/514,462  
; CURRENT FILING DATE: 2004-11-12  
; PRIOR APPLICATION NUMBER: 60/381,557  
; PRIOR FILING DATE: 2002-05-17  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2  
; LENGTH: 1067  
; TYPE: PRT  
; ORGANISM: RVFV Glycoprotein a.a.  
US-10-514-462-2

Query Match 10.1%; Score 52; DB 6; Length 1067;  
Best Local Similarity 30.0%; Pred. No. 3e+02;  
Matches 18; Conservative 9; Mismatches 25; Indels 8; Gaps 3;  
QY 37 EIDGPAQAPDRAHNYIVTFCKCDSTLRLCQSTHVDIRTL---EDLLMGTLGIYXP 92  
Db 889 EVDVFGAANVSCDAFLNL-TGCTSCNAGARVCLSTGTGSLSAHNKD---GSLHIVLP 944

RESULT 67  
US-10-525-126-302  
; Sequence 302, Application US/10525126  
; Publication No. US20060093596A1  
; GENERAL INFORMATION:  
; APPLICANT: NATIONAL RESEARCH COUNCIL OF CANADA  
; TITLE OF INVENTION: A GENOMIC APPROACH TO IDENTIFICATION OF NOVEL BROAD-SPECTRUM  
; FILE REFERENCE: 6899-6/PAR  
; CURRENT APPLICATION NUMBER: US/10/525,126  
; CURRENT FILING DATE: 2005-02-18  
; PRIOR APPLICATION NUMBER: PCT/CA03/013323  
; PRIOR FILING DATE: 2003-08-22  
; PRIOR APPLICATION NUMBER: 60/404,922  
; PRIOR FILING DATE: 2002-08-22  
; NUMBER OF SEQ ID NOS: 329  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 302  
; LENGTH: 61  
; TYPE: PRT  
; ORGANISM: Oncorhynchus mykiss  
; FEATURE:  
; NAME/KEY: MOD RES  
; LOCATION: (37)  
; OTHER INFORMATION: Variable amino acid  
; FEATURE:  
; NAME/KEY: MOD RES  
; LOCATION: (55)  
; OTHER INFORMATION: Variable amino acid  
US-10-525-126-302

Query Match 10.0%; Score 51.5; DB 6; Length 61;  
Best Local Similarity 24.4%; Pred. No. 15;  
Matches 11; Conservative 8; Mismatches 11; Indels 15; Gaps 2;  
QY 32 SEEDSIDGPQAE-----PDR-----AHNYIVTFCKC 61  
Db 5 TEEVGSIDSPVGHQPGGSMRLPEHFRPKRXSHLSLCWCNC 49

RESULT 68  
US-10-953-349-6871

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: Sequence 6871, Application US/10953349
: Publication No. US20060107345A1
:
: GENERAL INFORMATION:
: APPLICANT: ALEXANDROV, Nikolai et al.
: TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
: TITLE OF INVENTION: ENCODED THERBY
: FILE REFERENCE: 2750-1579PU52
: CURRENT APPLICATION NUMBER: US/10/953,349
: CURRENT FILING DATE: 2004-09-30
: NUMBER OF SEQ ID NOS: 40252
: SOFTWARE: PatentIn version 3.3
: SEQ ID NO 6871
:
: LENGTH: 145
:
: TYPE: PRT
:
: ORGANISM: Arabidopsis thaliana
US-10-953-349-6871

```

Query Match	10.0%	Score 51.5	DB 6	Length 145
Best Local Similarity	30.4%	Pred. No. 39		
Matches 14	Conservative	7	Mismatches 24	Indels 1
				Gaps 1

```

QY      13 LDLPQETTDLYXXKQLNDSSEED-EIDGPAGQAEPRRAHNYITP 57
      : | : : | : : : | : : | : : |
Db      20 IKLPPIITNLEAFLLQPKPRPATIDANAPKPTGEKEPLKSTYEITVP 65

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RESULT 69  
US-10-953-349-6870

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: APPLICANT: ALEXANDROV, Nikolai et al.
: TITLE OR INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
: TITLE OF INVENTION: ENCODED THERBY
: FILE REFERENCE: 2750-1579PUS2
: CURRENT APPLICATION NUMBER: US/10/953,349
: CURRENT FILING DATE: 2004-09-30
: NUMBER OF SEQ ID NOS: 40252
: SOFTWARE: PatentIn version 3.3
: SEQ ID NO 6870
: LENGTH: 158
: TYPE: PRT
: ORGANISM: Arabidopsis thaliana
: US-10-953-349-6870

```

Query Match	10.0%	Score 51.5	DB 6	Length 158
Best Local Similarity	30.4%	Pred. No. 43		
Matches 14	Conservative	7	Mismatches	24
			Indels	1
			Gaps	1

```

Qy      13 LDLPETTDLYXXQQLNDSSEED-EIDGPAQAEPRRAHNYTF 57
          :|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      33 IKLPFITNLEAFLOKPPRATIDANAPKPTGEKEPLKSTYEITYF 78

```

RESULT 70  
US-11-297-160-7  
Sequence 7, Application US/11297160  
Publication No. US20060088886A1  
GENERAL INFORMATION:  
APPLICANT: Wang, Xin wei  
APPLICANT: Harris, Curtis C.  
APPLICANT: Fornace Jr., Albert J.  
APPLICANT: Coorsen, Jill D.  
APPLICANT: Zhan, Qimian  
APPLICANT: The Government of the United States of America  
as represented by the Secretary of the  
APPLICANT: Department of Health and Human Services  
TITLE OF INVENTION: Methods for Identifying Inhibitors of GADD45  
FILE REFERENCE: 015280-367100US  
CURRENT APPLICATION NUMBER: US/11/297,160  
CURRENT FILING DATE: 2005-12-07  
PRIORITY APPLICATION NUMBER: US/10/600,158

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:
:
: PRIOR FILING DATE: 2003-06-20
: PRIOR APPLICATION NUMBER: US/09/534, 811
: PRIOR FILING DATE: 2000-03-24
: PRIOR APPLICATION NUMBER: US 60/126, 069
: PRIOR FILING DATE: 1999-03-25
: NUMBER OF SEQ ID NOS: 32
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 7
: LENGTH: 159
: TYPE: prt
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: human growth arrest and DNA-damage-inducible
: OTHER INFORMATION: protein (hGADD45gamma)
US-11-297-160-7

```

Query Match	10.0%	Score 51.5;	DB 7;	length 159;
Best Local Similarity	24.7%;	Pred. No. 43;		
Matches 19;	Conservative 13;	Mismatches 24;	Indels 21;	Gaps 4;

```

OY      1 MHGDTPTLHYMLDLP-----TTLDYXXYQLND-----SSEESBEIDPGQAE 46
        | | | | | : | : : : : | | | |
DB      19 MQGAGKALHELLLSAQRQCGCTAGVYBSAKLVNDPNTVFCVLAAGEBEGDLAL---- 74

```

QY 47 PDRAHYNIV-TECCCKD 62  
::: |||:  
Db 75 --QIHFTLIQAFCCEND 89

```

RESULT 71
US-10-953-349-24841
: Sequence 24841, Application US/10953349
: Publication No. US20060107345A1
: GENERAL INFORMATION:
: APPLICANT: ALEXANDROV, Nikolai et al.
: TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
: FILE REFERENCE: ENCODED THERBY
: FILE REFERENCE: 2750-1579PUS2
: CURRENT APPLICATION NUMBER: US/10/953,349
: CURRENT FILING DATE: 2004-09-30
: NUMBER OF SEQ ID NOS: 40252
: SOFTWARE: PatentIn version 3.3
: SEQ ID NO 24841
: LENGTH: 315
: TYPE: PRT
: ORGANISM: Glycine max
US-10-953-349-24841

```

Query Match	10.0%	Score 51.5;	DB 6;	length 315;
Best Local Similarity	23.5%	Pred. No.91;		
Matches 20; Conservative	7;	Mismatches 15;	Indels 43;	Gaps 4;

CY 5 TPTLHEWMLD-----IQPE---TDTLYXXYQLN-----DSSEEDIED 39  
Db : : : : :  
58 TKIVYNISLPKRRVWALQIPSPSSNVVPAPFDNLVEYTPSPNNHGFEEDHSEDEGV 116

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QY      40 GPAGQAEPPDRAHYNIVTFCCCKDST 64
          ||| |||
Db      117 -----LCCVCQST 124

```

```

RESULT 72
US-10-953-349-24840
; Sequence. 24840, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERAPY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252

```

SOFTWARE: Patentin version 3.3  
; SEQ ID NO 24840  
; LENGTH: 323  
; TYPE: PRT  
; ORGANISM: Glycine max  
US-10-953-349-24840

Query Match 10.0%; Score 51.5; DB 6; Length 323;  
Best Local Similarity 23.5%; Pred. No. 94;  
Matches 20; Conservative 7; Mismatches 15; Indels 43; Gaps 4;

QY 5 TPTLHYMD-----LOPE---TTDLYXXQLN-----DSSEDEID 39  
DB 66 TKTVYVNSLPKAKKRWALQPSPPSNDVVPAPFDLNVETPSPNNHGFDEHSDSDGV- 124  
QY 40 GPAGQAEPPDRAHNYIVTFCKCDST 64  
DB 125 -----LCCVCQST 132

RESULT 73  
US-11-121-154-195  
; Sequence 195, Application US/11121154  
; Publication No. US20060105914A1  
; GENERAL INFORMATION:  
; APPLICANT: TAYLOR, LARRY EDMUND  
; APPLICANT: WEINER, RONALD M.  
; APPLICANT: HUTCHESON, STEVEN WAYNE  
; APPLICANT: EKBORG, NATHAN A.  
; APPLICANT: HOWARD, MICHAEL  
; TITLE OF INVENTION: PLANT WALL DEGRADATIVE COMPOUNDS AND SYSTEMS  
; FILE REFERENCE: 108172-00121  
; CURRENT APPLICATION NUMBER: US/11/121,154  
; CURRENT FILING DATE: 2005-05-04  
; PRIOR APPLICATION NUMBER: 60/567,971  
; PRIOR FILING DATE: 2004-05-04  
; NUMBER OF SEQ ID NOS: 214  
; SOFTWARE: Patentin version 3.3  
; SEQ ID NO 195  
; LENGTH: 500  
; TYPE: PRT  
; ORGANISM: Microbulbifer degradans  
US-11-121-154-195

Query Match 10.0%; Score 51.5; DB 7; Length 500;  
Best Local Similarity 42.4%; Pred. No. 1.5e+02;  
Matches 14; Conservative 6; Mismatches 8; Indels 5; Gaps 1;

QY 62 DSTLRLCVQSTHVDIRLTDLMTGTL---LGI 89  
DB 219 EHTLRIVQAGNFNINMLLELLAGTQOPDMLGV 251

RESULT 74  
US-10-953-349-22956  
; Sequence 22956, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, NIKOLAI et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: Patentin version 3.3  
; SEQ ID NO 22956  
; LENGTH: 155  
; TYPE: PRT  
; ORGANISM: Glycine max  
US-10-953-349-22956

Query Match 9.9%; Score 51; DB 6; Length 155;

Best Local Similarity 30.3%; Pred. No. 48;  
Matches 20; Conservative 10; Mismatches 26; Indels 10; Gaps 4;

QY 31 SSEBEDIDGPAGQAEPPDRAHNYIVTFCKCDSTLRICVQ--STHVDIRLTDLMTGTL- 87  
DB 75 AQEGEGGLRDKPKR--RDHYH---TCYCLSGLSICQYWSKHGPPPLPVLVLPYS 127  
QY 88 GIVXPI 93  
DB 128 NLEPI 133

RESULT 75  
US-10-953-349-22955  
; Sequence 22955, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, NIKOLAI et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: Patentin version 3.3  
; SEQ ID NO 22955  
; LENGTH: 171  
; TYPE: PRT  
; ORGANISM: Glycine max  
US-10-953-349-22955

Query Match 9.9%; Score 51; DB 6; Length 171;  
Best Local Similarity 30.3%; Pred. No. 53;  
Matches 20; Conservative 10; Mismatches 26; Indels 10; Gaps 4;

QY 31 SSEBEDIDGPAGQAEPPDRAHNYIVTFCKCDSTLRICVQ--STHVDIRLTDLMTGTL- 87  
DB 91 AQEGEGGLRDKPKR--RDHYH---TCYCLSGLSICQYWSKHGPPPLPVLVLPYS 143  
QY 88 GIVXPI 93  
DB 144 NLEPI 149

RESULT 76  
US-10-953-349-16871  
; Sequence 16871, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, NIKOLAI et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: Patentin version 3.3  
; SEQ ID NO 16871  
; LENGTH: 549  
; TYPE: PRT  
; ORGANISM: Glycine max  
US-10-953-349-16871

Query Match 9.9%; Score 51; DB 6; Length 549;  
Best Local Similarity 31.4%; Pred. No. 1.9e+02;  
Matches 16; Conservative 7; Mismatches 18; Indels 10; Gaps 1;

QY 22 LYXXYQLNDSSEBEDIDGPAGQAEPPDRAHNYIVTFCKCDSTLRICVQST 72  
DB 478 LHLSSKLSDDSNVCLDVD-----NNNIVTNACKLSRDRCDPSS 518

RESULT 77

US-10-953-349-16870  
; Sequence 16870, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nikolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 16870  
; LENGTH: 557  
; TYPE: PRT  
; ORGANISM: Glycine max  
US-10-953-349-16870

Query Match  
Best Local Similarity 9.9%; Score 51; DB 6; Length 557;  
Matches 16; Conservative 7; Mismatches 18; Indels 10; Gaps 1;

Qy 22 LYYXQXNDSEEDIDGPAGAEPPRAHYNIVTFCCCKDSTLRCLCVQST 72  
Db 486 LHSLSKLSDDSNVCLDVD-----NNNIVTNACKCLSRDRTCDPSS 526

RESULT 78  
US-10-953-349-16869  
; Sequence 16869, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nikolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 16869  
; LENGTH: 585  
; TYPE: PRT  
; ORGANISM: Glycine max  
US-10-953-349-16869

Query Match  
Best Local Similarity 9.9%; Score 51; DB 6; Length 585;  
Matches 16; Conservative 7; Mismatches 18; Indels 10; Gaps 1;

Qy 22 LYYXQXNDSEEDIDGPAGAEPPRAHYNIVTFCCCKDSTLRCLCVQST 72  
Db 514 LHSLSKLSDDSNVCLDVD-----NNNIVTNACKCLSRDRTCDPSS 554

RESULT 79  
US-11-293-697-4398  
; Sequence 4398, Application US/11293697  
; Publication No. US20060105376A1  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: Novel full length cDNA  
; FILE REFERENCE: H1-A0106  
; CURRENT APPLICATION NUMBER: US/11/293,697  
; CURRENT FILING DATE: 2005-12-05  
; PRIOR APPLICATION NUMBER: US/10/108,260  
; PRIOR FILING DATE: 2002-03-28  
; NUMBER OF SEQ ID NOS: 5458  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4398  
; LENGTH: 764  
; TYPE: PRT  
; ORGANISM: Homo sapiens

US-11-293-697-4398

Query Match  
Best Local Similarity 9.9%; Score 51; DB 7; Length 764;  
Matches 18; Conservative 4; Mismatches 20; Indels 8; Gaps 3;

Qy 31 SSEEEDIDGPAGQ-----AEPRAHYNIVTFCCCKDSTLRCLCVQSTHV 74  
Db 510 SCHEHMADDPKSKYTLRFVABQVSHHPISCFYCEBER-RLCV-NTHV 557

RESULT 80  
US-10-953-349-13813  
; Sequence 13813, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nikolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 13813  
; LENGTH: 176  
; TYPE: PRT  
; ORGANISM: Glycine max  
US-10-953-349-13813

Query Match  
Best Local Similarity 9.8%; Score 50.5; DB 6; Length 176;  
Matches 18; Conservative 12; Mismatches 31; Indels 11; Gaps 4;

Qy 1 MHGDTPLHEWYLDL--QETDLYXXQXNDSEEDIDGPAGAEPPRAHYNIVTF 57  
Db 8 LHNENPGIHLILSLYAKQDSDSLRFLQSKFGKGP---NGPEFFYDPKYA----LRL 60

Qy 58 CCKCDSTLRCLCV 69  
Db 61 CLK-EKRMRACV 71

RESULT 81  
US-10-953-349-23159  
; Sequence 23159, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nikolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 23159  
; LENGTH: 218  
; TYPE: PRT  
; ORGANISM: Glycine max  
US-10-953-349-23159

Query Match  
Best Local Similarity 9.8%; Score 50.5; DB 6; Length 218;  
Matches 26; Conservative 13; Mismatches 37; Indels 59; Gaps 5;

Qy 1 MHGDTPL-----LHEWYLD-----LOPETT-----PLYYXQXND----- 29  
Db 1 MYGDEITSMLTITRYRMHELIMDSKSKELVSKIKAPSVTAHMLYDLGVRKRNSTPTL 60

Qy 30 -----DSSEEDIDGPAGAEPPRAHYNIVTFCCCKDSTLRCLCVQSTHVDIRTLED 81  
Db 61 LLDITAGCDMEKKEDSDSFPNGEAL-----VVTYHAKRLVQSG 100

```
QY      82 LLMGTLGIVXPICSQ 96
      91  ::||:|::|
Db      101 VLPSDIGITPYAAQ 115
```

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1 RESULT 82
2 US-10-953-349-36029
3 ; Sequence 36029, Application US/10953349
4 ; Publication No. US20060107345A1
5 ;
6 ; GENERAL INFORMATION:
7 ;
8 ; APPLICANT: ALEXANDROV, NICKOLAI et al.
9 ;
10 ; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
11 ;
12 ; TITLE OF INVENTION: ENCODED THERBY
13 ;
14 ; FILE REFERENCE: 2750-1579PUS2
15 ;
16 ; CURRENT APPLICATION NUMBER: US/10/953,349
17 ;
18 ; CURRENT FILING DATE: 2004-09-30
19 ;
20 ; NUMBER OF SEQ ID NOS: 40252
21 ;
22 ; SOFTWARE: PatentIn version 3.3
23 ;
24 ; SEQ ID NO 36029
25 ;
26 ; LENGTH: 235
27 ;
28 ; TYPE: PRT
29 ;
30 ; ORGANISM: Zea mays subsp. mays
31 ;
32 ; US-10-953-349-36029

```

```

RESULT 83
US-10-953-349-23158
: Sequence 23158, Application US/10953349
: Publication No. US20060107345A1
: GENERAL INFORMATION:
: APPLICANT: ALEXANDROV, Nickolai et al.
: TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
: FILE REFERENCE: 2750-1579PUS2
: CURRENT APPLICATION NUMBER: US/10/953,349
: CURRENT FILING DATE: 2004-09-30
: NUMBER OF SEQ ID NOS: 40252
: SOFTWARE: PatentIn version 3.3
: SEQ ID NO 23158
: LENGTH: 343
: TYPE: PRT
: ORGANISM: Glycine max
: US-10-953-349-23158

```

```

Query Match      9.8% Score 50.5; DB 6; Length 343;
Best Local Similarity 19.3%; Pred. No. 1.3e+02;
Matches 26; Conservative 13; Mismatches 37; Indels 59; Gaps 5

QY    1 MHGDTPT-----LHEYMLD-----LOPETT-----DLVXXYXOLN-----29
       |||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db    126 MYGDBITSMLTIQYNMHELIMDSKELYSKIYKHPSVTAMLVLDLBEVKRKTNSTEPTL 185
               |||::||::||::||::||::||::||::||::||::||::||::||::||
QY    30 -----DSSSEDEIDGPACQAEPDRAHYNI VTFCCCKDSTLRLCVQSTHVDITRLD 81
               |||::|||::||::||::||::||::||::||::||::||::||::||
Db    186 LLIDPAGCDMEKKDEDSTFNEGEAE-----VVTHAKRLVVGSG 225
               |||::|||::||::||::||::||::||::||::||::||::||::||
QY    82 LLMGTGLGVXPICSQ 96
       |||::|||::||::||::||::||::||::||::||::||::||::||
Db    226 VLPSDIGIITPYAAQ 240
       |||::|||::||::||::||::||::||::||::||::||::||::||

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RESULT 84  
US-10-953-349-36028  
; Sequence 36028, Application US/10953349

```

? Publication No. US20060107345A1
? GENERAL INFORMATION:
? APPLICANT: ALEXANDROV, Nikolai et al.
? TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
? TITLE OF INVENTION: ENCODED THERBY
? FILE REFERENCE: 2750-1579PUS2
? CURRENT APPLICATION NUMBER: US/10/953,349
? CURRENT FILING DATE: 2004-09-30
? NUMBER OF SEQ ID NOS: 40252
? SOFTWARE: PatentIn version 3.3
? SEQ ID NO 36028
? LENGTH: 369
? TYPE: prt
? ORGANISM: Zea mays subsp. mays
US-10-953-349-36028

```

```

RESULT 85
US-10-953-349-23157
; Sequence 23157, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953.349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23157
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-23157

```

[illegible]

```

RESULT 86
US-10-953-349-0399
; Sequence 9399, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERAPY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252

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; SOFTWARE: Patentin version 3.3
; SEQ ID NO 9399
; LENGTH: 57
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-9399

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```

Query Match          9.7%; Score 50; DB 6; Length 57;
Best Local Similarity 24.6%; Pred. No. 21;
Matches 15; Conservative 6; Mismatches 18; Indels 22; Gaps 2;

```

```

QY 3 GDTPTLHEVYLDLOPETTDLYXXQLNDSSEEDIDGPAGQAPDRAHNYITFCCKCD 62
DB 9 GDTTETETVVLGVAPAMKQY-----EASGESNNMEND-----ACKCG 46

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QY 63 S 63
DB 47 S 47

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RESULT 87
US-10-953-349-9398
; Sequence 9398, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 9398
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-9398

```

```

Query Match          9.7%; Score 50; DB 6; Length 81;
Best Local Similarity 24.6%; Pred. No. 30;
Matches 15; Conservative 6; Mismatches 18; Indels 22; Gaps 2;

```

```

QY 3 GDTPTLHEVYLDLOPETTDLYXXQLNDSSEEDIDGPAGQAPDRAHNYITFCCKCD 62
DB 33 GDTTETETVVLGVAPAMKQY-----EASGESNNMEND-----ACKCG 70
QY 63 S 63
DB 71 S 71

```

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RESULT 88
US-10-953-349-27383
; Sequence 27383, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 27383
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Trillium aestivum
US-10-953-349-27383

```

```

Query Match          9.7%; Score 50; DB 6; Length 205;
Best Local Similarity 21.3%; Pred. No. 84;

```

```

Matches 20; Conservative 16; Mismatches 40; Indels 18; Gaps 3;

```

```

QY 4 DTPTLHEVY-----LDLOPETTDLY-XXQLNDSSEEDIDGPAGQAE 46
DB 7 DAPKLNQRMVSSLSKRTAAASHWHDLEIGPEAPLIRNAVVEITKGSKVYEIDKKTGMIK 66
QY 47 PDRAHNYITFCCKCDSTLR-LCVQSTHVDIRTL 79
DB 67 VDRILYSSVYVPHNYGVPRTLCEDGDPIDVVL 100

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RESULT 89
US-10-953-349-38511
; Sequence 38511, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 38511
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-38511

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```

Query Match          9.7%; Score 50; DB 6; Length 211;
Best Local Similarity 27.9%; Pred. No. 86;
Matches 17; Conservative 7; Mismatches 27; Indels 10; Gaps 1;

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```

QY 43 GQAEPP-----RAHNYITFCCKCDSTLR-LCVQSTHVDIRTLMDLMTGLGIYXP 92
DB 73 GQAEPRERFVEAIGVRHKNLVRLLGYCAEGQRILIVEYVQNGNLHGQVGAIVSP 132
QY 93 I 93
DB 133 I 133

```

```

RESULT 90
US-10-953-349-27382
; Sequence 27382, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 27382
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Trillium aestivum
US-10-953-349-27382

```

```

Query Match          9.7%; Score 50; DB 6; Length 231;
Best Local Similarity 21.3%; Pred. No. 95;
Matches 20; Conservative 16; Mismatches 40; Indels 18; Gaps 3;

```

```

QY 4 DTPTLHEVY-----LDLOPETTDLY-XXQLNDSSEEDIDGPAGQAE 46
DB 33 DAPKLNQRMVSSLSKRTAAASHWHDLEIGPEAPLIRNAVVEITKGSKVYEIDKKTGMIK 92
QY 47 PDRAHNYITFCCKCDSTLR-LCVQSTHVDIRTL 79
DB 93 VDRILYSSVYVPHNYGVPRTLCEDGDPIDVVL 126

```

```
RESULT 91
US-10-511-937-2618
; Sequence 2618, Application US/10511937
; Publication No. US2006008836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, Macdonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2618
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937-2618

Query Match
Best Local Similarity 25.4%; Score 50; DB 6; Length 272;
Matches 16; Conservative 9; Mismatches 22; Indels 16; Gaps 3;

QY
9 HEYMLDLPQETTDLYXXQLNDSEDEIDGPAGQAEPRAHYNIYVFCCKC---DST 64
Db
222 HDVALPVGKQKQDLDL-----EEDDSAGVGLHVDKDKVS---VFCSGCAKXKSSS 269
QY
65 LRL 67
Db
270 LKM 272

RESULT 92
US-10-953-349-12546
; Sequence 12546, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12546
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-12546

Query Match
Best Local Similarity 28.1%; Score 50; DB 6; Length 293;
Matches 18; Conservative 6; Mismatches 18; Indels 22; Gaps 3;

QY
17 PETTDLYXXQLNDSEED-----EIDGPAGQAEPRDAHNIYVFCCKCSTLRLCVQST 72
Db
18 PENISL-----DRNKKAGNVEFVSPNGE-----VFICKSPLIEGLCHQDK 59
```

```
QY
73 HVDI 76
Db
60 LEVEL 63

RESULT 93
US-10-953-349-38510
; Sequence 38510, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 38510
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-38510

Query Match
Best Local Similarity 27.9%; Score 50; DB 6; Length 343;
Matches 17; Conservative 7; Mismatches 27; Indels 10; Gaps 1;

QY
43 GOAEPD-----RAHYNIYVFCCKCDSTRLCVQSTHVDIRLTDLMLGTLGIYXP 92
Db
205 GOAEREFREVEAIGRVHKNLIVRLGYCAEGAQRILVEYVDNGLQWLHGDVGAVSP 264
QY
93 I 93
Db
265 L 265

RESULT 94
US-10-953-349-8835
; Sequence 8835, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8835
; LENGTH: 438
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-8835

Query Match
Best Local Similarity 21.6%; Score 50; DB 6; Length 438;
Matches 19; Conservative 17; Mismatches 38; Indels 14; Gaps 2;

QY
15 LQPETTDLYXXQLNDSE-----SEDEIDGPAGQAEPRDAHNIYVFCCKC 61
Db
118 LSVEMPEIEFARALDDAEFAIFVRHFKPEVWMQGLIGVALKLRRAHAFDRVCSKC 177
QY
62 DSTRLCVQSTHVDIRLTDLMLGTLGI 89
Db
178 IASKRDEI-SQGISSSSKDLMSINV 204

RESULT 95
US-10-953-349-8834
; Sequence 8834, Application US/10953349
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Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 8834
LENGTH: 476
TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-10-953-349-8834

Query Match
Best Local Similarity 9.7%; Score 50; DB 6; Length 476;
Matches 19; Conservative 17; Mismatches 38; Indels 14; Gaps 2;

QY 15 LQPTTDLYXXYXQNDSS-----EEDIDGPAQAEPDRAHYNIVTFCKC 61
DB 156 LSVEMPEIEFARALDDAEBAIFRHFKEVVMKQRLIGVAGALKKRAHAIFDRVCSKC 215

QY 62 DSTLRFCVOSTHVDIRLTEDLMTGLGI 89
DB 216 IASKRDEI-SQGISSSSKDLMSINV 242

RESULT 96
US-10-953-349-8833
Sequence 8833, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 8833
LENGTH: 516
TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-10-953-349-8833

Query Match
Best Local Similarity 9.7%; Score 50; DB 6; Length 516;
Matches 19; Conservative 17; Mismatches 38; Indels 14; Gaps 2;

QY 15 LQPTTDLYXXYXQNDSS-----EEDIDGPAQAEPDRAHYNIVTFCKC 61
DB 196 LSVEMPEIEFARALDDAEBAIFRHFKEVVMKQRLIGVAGALKKRAHAIFDRVCSKC 255

QY 62 DSTLRFCVOSTHVDIRLTEDLMTGLGI 89
DB 256 IASKRDEI-SQGISSSSKDLMSINV 282

RESULT 97
US-10-953-349-13398
Sequence 13398, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 13398
LENGTH: 527
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
NAME/KEY: misc feature
LOCATION: (9)..(9)
OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-953-349-13398

Query Match
Best Local Similarity 9.7%; Score 50; DB 6; Length 527;
Matches 18; Conservative 15; Mismatches 38; Indels 8; Gaps 2;

QY 27 QLNDSSEDEID-CPAQAEPDRAHYNIVTFCKCDSTLRFCVOSTHVDIRT----- 78
DB 340 EVVKDRTSADSDSLASGKKDPFVRQRELLIKSGLDSTLDICIESVGELIRSNLGEVYL 399

QY 79 LEDLMTGLGIYXPTCSOK 97
DB 400 YEVA TGSDGIMHPVLDK 418

RESULT 98
US-10-953-349-13397
Sequence 13397, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 13397
LENGTH: 548
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
NAME/KEY: misc feature
LOCATION: (30)..(30)
OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-953-349-13397

Query Match
Best Local Similarity 9.7%; Score 50; DB 6; Length 548;
Matches 18; Conservative 15; Mismatches 38; Indels 8; Gaps 2;

QY 27 QLNDSSEDEID-CPAQAEPDRAHYNIVTFCKCDSTLRFCVOSTHVDIRT----- 78
DB 361 EVVKDRTSADSDSLASGKKDPFVRQRELLIKSGLDSTLDICIESVGELIRSNLGEVYL 420

QY 79 LEDLMTGLGIYXPTCSOK 97
DB 421 YEVA TGSDGIMHPVLDK 439

RESULT 99
US-10-953-349-13396
Sequence 13396, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
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; SEQ ID NO 13396
; LENGTH: 634
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (116)..(116)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-953-349-13396

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Query Match          9.7%; Score 50; DB 6; Length 634;
Best Local Similarity 22.8%; Pred. No. 2.9e+02;
Matches 18; Conservative 15; Mismatches 38; Indels 8; Gaps 2;

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QY      27 QLNDSSEEDID-GPAGQAEPPDRAHNYIVFCCCKDSTLRLCVQSTHVDIRT----- 78
Db      447 EVNKKDTSADSDLAESGKDPFVRRQELIKSLGLADSLDICTESVGEIIRSNLGKVL 506
QY      79 LEDLMGTLGIVXPICSQK 97
Db      507 YEVA TGSDGIMHPVLDXK 525

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RESULT 100
US-11-293-697-3814
; Sequence 3814, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3814
; LENGTH: 878
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-3814

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Query Match          9.7%; Score 50; DB 7; Length 878;
Best Local Similarity 24.3%; Pred. No. 4.1e+02;
Matches 25; Conservative 15; Mismatches 39; Indels 24; Gaps 4;

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QY      5 TPTL--HEVMDLQPERTTLYXYQLN-----DSSEEDRIDGPAGQAE--- 47
Db      591 TPRLSADLPDDIANEIAIDIPHDELNQEDFSVDLPRLPDDLQDPDFEFGKNGDLPTTE 650
QY      48 -----DRAHNYIVFCCCKDSTLRLCVQSTHVDIRTLEDLMG 85
Db      651 EAETLERALQAVTSL--ECLSTIGVLAQSDGVPVQELSDRGIG 691

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Search completed: May 27, 2006, 05:38:15  
 Job time : 8.69076 secs